

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
6 September 2002 (06.09.2002)

PCT

(10) International Publication Number  
**WO 02/068623 A2**

(51) International Patent Classification <sup>7</sup> : C12N 9/62, 15/57, 15/63, C07K 16/40, C12Q 1/37, G01N 33/573			01000320.0	30 July 2001 (30.07.2001)	EP
			01000321.8	30 July 2001 (30.07.2001)	EP
			01000322.6	30 July 2001 (30.07.2001)	EP
(21) International Application Number: PCT/EP02/01984			01000323.4	30 July 2001 (30.07.2001)	EP
			01000327.5	30 July 2001 (30.07.2001)	EP
(22) International Filing Date: 22 February 2002 (22.02.2002)			01000341.6	2 August 2001 (02.08.2001)	EP
			01000342.4	2 August 2001 (02.08.2001)	EP
(25) Filing Language: English			01000343.2	2 August 2001 (02.08.2001)	EP
			01000344.0	2 August 2001 (02.08.2001)	EP
(26) Publication Language: English			01000357.2	9 August 2001 (09.08.2001)	EP
			01000374.7	16 August 2001 (16.08.2001)	EP
(30) Priority Data:			01000377.0	16 August 2001 (16.08.2001)	EP
01200660.7	23 February 2001 (23.02.2001)	EP	01000478.6	20 September 2001 (20.09.2001)	EP
01200658.1	23 February 2001 (23.02.2001)	EP	01000483.6	20 September 2001 (20.09.2001)	EP
01200657.3	23 February 2001 (23.02.2001)	EP	01000552.8	22 October 2001 (22.10.2001)	EP
01200707.6	26 February 2001 (26.02.2001)	EP	01000553.6	22 October 2001 (22.10.2001)	EP
01200708.4	26 February 2001 (26.02.2001)	EP	01000554.4	22 October 2001 (22.10.2001)	EP
01200719.1	26 February 2001 (26.02.2001)	EP	01000556.9	22 October 2001 (22.10.2001)	EP
01200706.8	26 February 2001 (26.02.2001)	EP	01000557.7	22 October 2001 (22.10.2001)	EP
01000075.0	28 March 2001 (28.03.2001)	EP	01000558.5	22 October 2001 (22.10.2001)	EP
01000078.4	28 March 2001 (28.03.2001)	EP	01204464.0	15 November 2001 (15.11.2001)	EP
01000080.0	28 March 2001 (28.03.2001)	EP	01205117.3	21 December 2001 (21.12.2001)	EP
01000084.2	28 March 2001 (28.03.2001)	EP			
01000085.9	28 March 2001 (28.03.2001)	EP	(71) Applicant (for all designated States except US): DSM N.V.		
01000087.5	28 March 2001 (28.03.2001)	EP	[NL/NL]; Het Overloon 1, NL-6411 TE Heerlen (NL).		
01000088.3	28 March 2001 (28.03.2001)	EP			
01000156.8	21 May 2001 (21.05.2001)	EP	(72) Inventors; and		
01000159.2	21 May 2001 (21.05.2001)	EP	(75) Inventors/Applicants (for US only): EDENS, Luppö		
01000160.0	21 May 2001 (21.05.2001)	EP	[NL/NL]; Hoflaan 118, NL-3062 JL Rotterdam (NL).		
01000162.6	21 May 2001 (21.05.2001)	EP	DIJK VAN, Albertus, Alard [NL/NL]; Cederdreef 32,		
01000165.9	21 May 2001 (21.05.2001)	EP	NL-3137 PB Vlaardingen (NL). KRUBASIK, Philipp		
01000166.7	21 May 2001 (21.05.2001)	EP	[DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE).		
01000168.3	21 May 2001 (21.05.2001)	EP	ALBERMANN, Kaj [DE/DE]; Lochhamer Str. 11, 82152		
01000225.1	20 June 2001 (20.06.2001)	EP	Martinsried (DE). STOCK, Alex [DE/DE]; Lochhamer		
01000229.3	20 June 2001 (20.06.2001)	EP	Str. 11, 82152 Martinsried (DE). KIMPEL, Erik		
01000234.3	21 June 2001 (21.06.2001)	EP	[DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE).		
01000237.6	21 June 2001 (21.06.2001)	EP	KLUGBAUER, Sabine [DE/DE]; Lochhamer Str. 11,		
01000238.4	21 June 2001 (21.06.2001)	EP	82152 Martinsried (DE). WAGNER, Christian [DE/DE];		
01000240.0	21 June 2001 (21.06.2001)	EP	Lochhamer Str. 11, 82152 Martinsried (DE). FRITZ,		
01000242.6	21 June 2001 (21.06.2001)	EP	Andreas [DE/DE]; Lochhamer Str. 11, 82152 Martinsried		
01000244.2	21 June 2001 (21.06.2001)	EP	(DE). GUSTEDT VON, Wilk [DE/DE]; Lochhamer		
01000246.7	21 June 2001 (21.06.2001)	EP	Str. 11, 82152 Martinsried (DE). HEINRICH, Oliver		
01000280.6	12 July 2001 (12.07.2001)	EP	[DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE).		
01000285.5	12 July 2001 (12.07.2001)	EP	MAIER, Dieter [DE/DE]; Lochhamer Str. 11, 82152 Mar- tinsried (DE). SPREAFICO, Fabio [IT/DE]; Lochhamer		
01000286.3	12 July 2001 (12.07.2001)	EP	Str. 11, 82152 Martinsried (DE). FOLKERS, Ulrike		
01000287.1	12 July 2001 (12.07.2001)	EP			

[Continued on next page]

(54) Title: NOVEL GENES ENCODING NOVEL PROTEOLYTIC ENZYMES

(57) Abstract: The invention relates to newly identified gene sequences that encode novel proteases obtainable from *Aspergillus niger*. The invention features the full length gene sequence of the novel genes, their cDNA sequences as well as the full-length functional protein and fragments thereof. The invention also relates to methods of using these enzymes in industrial processes and methods of diagnosing fungal infections. Also included in the invention are cells transformed with DNA according to the invention and cells wherein a protease according to the invention is genetically modified to enhance or reduce its activity and/or level of expression.

WO 02/068623 A2



[DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE). **HOPPER, Sylvia** [DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE). **KEMMNER, Wolfram** [DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE). **TAN, Pamela** [DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE). **STIEBLER, Josephine** [DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE). **ALBANG, Richard** [DE/DE]; Lochhamer Str. 11, 82152 Martinsried (DE).

(74) Agent: **HABETS, Winand, Johannes, Antonius**; DSM Patents & Trademarks, P.O. Box 9, NL-6160 MA Geleen (NL).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,

SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## NOVEL GENES ENCODING NOVEL PROTEOLYTIC ENZYMES

5

### Field of the invention

The invention relates to newly identified polynucleotide sequences comprising genes that encode novel proteases isolated from *Aspergillus niger*. The invention features the full length nucleotide sequence of the novel genes, the cDNA sequences comprising the full length coding sequences of the novel proteases as well as the amino acid sequences of the full-length functional proteins and fragments and variants thereof. The invention also relates to methods of using these enzymes in industrial processes and methods of diagnosing fungal infections. Also included in the invention are cells transformed with a polynucleotide according to the invention and cells wherein a protease according to the invention is genetically modified to enhance or reduce its activity and/or level of expression.

### Background of the invention

20

#### Proteolytic Enzymes

Proteins can be regarded hetero-polymers that consist of amino acid building blocks connected by a peptide bond. The repetitive unit in proteins is the central alpha carbon atom with an amino group and a carboxyl group. Except for glycine, a so-called amino acid side chain substitutes one of the two remaining alpha carbon hydrogen atoms. The amino acid side chain renders the central alpha carbon asymmetric. In general, in proteins the L-enantiomer of the amino acid is found. The following terms describe the various types of polymerized amino acids. *Peptides* are short chains of amino acid residues with defined sequence. Although there is not really a maximum to the number of residues, the term usually indicates a chain which properties are mainly determined by its amino acid composition and which does not have a fixed three-dimensional conformation. The term *polypeptide* is usually used for the longer chains, usually of defined sequence and length and in principle of the appropriate length to fold into a three-dimensional structure. *Protein* is reserved for polypeptides that occur naturally and exhibit a defined three-dimensional structure. In case the proteins main function is to catalyze a chemical reaction it usually is called an *enzyme*. Proteases are the

enzymes that catalyze the hydrolysis of the peptide bond in (poly)peptides and proteins.

Under physiological conditions proteases catalyse the hydrolysis of the peptide bond.

- 5 The International Union of Biochemistry and Molecular Biology (1984) has recommended to use the term *peptidase* for the subset of peptide bond hydrolases (Subclass E.C 3.4.). The terms *protease* and *peptide hydrolase* are synonymous with *peptidase* and may also be used here. *Proteases* comprise two classes of enzymes: the endo-peptidases and the exo-peptidases, which cleave peptide bonds at points
- 10 within the protein and remove amino acids sequentially from either N or C-terminus respectively. *Proteinase* is used as a synonym for *endo-peptidase*. The peptide bond may occur in the context of di-, tri-, tetra-peptides, peptides, polypeptides or proteins. In general the amino acid composition of natural peptides and polypeptides comprises 20 different amino acids, which exhibit the L-configuration (except for glycine which does
- 15 not have a chiral centre). However the proteolytic activity of proteases is not limited to peptides that contain only the 20 natural amino acids. Peptide bonds between so-called non-natural amino acids can be cleaved too, as well as peptide bonds between modified amino acids or amino acid analogues. Some proteases do accept D enantiomers of amino acids at certain positions. In general the remarkable stereo-
- 20 selectivity of proteases makes them very useful in the process of chemical resolution. Many proteases exhibit interesting side activities such as esterase activity, thiol esterase activity and (de)amidase activity. These side activities are usually not limited to amino acids only and might turn out to be very useful in bioconversions in the area of fine chemicals.

25

- There are a number of reasons why proteases of filamentous fungi, eukaryotic microorganisms, are of particular interest. The basic process of hydrolytic cleavage of peptide bonds in proteins appears costly and potentially detrimental to an organism if not properly controlled. The desired limits to proteolytic action are achieved through the
- 30 specificity of proteinases, by compartmentalization of proteases and substrates within the cell, through modification of the substrates allowing recognition by the respective proteases, by regulation via zymogen activation, and the presence or absence of specific inhibitors, as well through the regulation of protease gene expression. In fungi, proteases are also involved in other fundamental cellular processes, including intracellular protein
- 35 turnover, processing, translocation, sporulation, germination and differentiation. In fact, *Aspergillus nidulans* and *Neurospora crassa* have been used as model organisms for



analyzing the molecular basis of a range of physiological and developmental processes. Their genetics enable direct access to biochemical and genetical studies, under defined nutrient and cultivation conditions. Furthermore, a large group of fungi pathogenic to humans, live-stock and crop, has been isolated and proteolysis has been suggested to play a role in their pathogenicity (host penetration, countering host defense mechanisms and/or nutrition during infection). Proteases are also frequently used in laboratory, clinical and industrial processes; both microbial and non-microbial proteases are widely used in the food industry (baking, brewing, cheese manufacturing, meat tenderizing), in tanning industry and in the manufacture of biological detergents (Aunstrup, 1980). The commercial interest in exploiting certain filamentous fungi, especially the *Aspergilli*, as hosts for the production of both homologous and heterologous proteins, has also recently renewed interests in fungal proteases (van Brunt, 1986ab). Proteases often cause problems in heterologous expression and homologous overexpression of proteins in fungi. In particular, heterologous expression is hampered by the proteolytic degradation of the expressed products by homologous proteases. These commercial interests have resulted in detailed studies of proteolytic spectra and construction of protease deficient strains and have improved the knowledge about protease expression and regulation in these organisms. Consequently there is a great need to identify and eliminate novel proteases in filamentous fungi.

Micro-organisms such as for example fungi are particularly useful in the large scale production of proteins. In particular when such proteins are secreted into the medium. Proteolytic enzymes play a role in these production processes. On the one hand particular proteolytic enzymes are in general required for proper processing of the target protein and the metabolic well-being of the production host. On the other hand proteolytic degradation may significantly decrease the yield of secreted proteins. Poor folding in the secretion pathway may lead to degradation by intracellular proteases. This might be a particular problem with producing heterologous proteins. The details of the proteolytic processes, which are responsible for the degradation of the proteins that are diverted from the secretory process in fungi are not exactly known. In eukaryotes the degradation of cellular proteins is achieved by a proteasome and usually involves ubiquitin labelling of proteins to be degraded. In fungi, proteasomal and vacuolar proteases are also likely candidates for the proteolytic degradation of poorly folded secretory proteins. The proteolytic degradation is likely cytoplasmic, but endoplasmic reticulum resident proteases cannot be excluded. From the aspect of production host strain improvement the proteolytic system may be an interesting target for genetic

engineering and production strain improvement. Additional copies of protease genes, over-expression of certain proteases, modification of transcriptional control, as well as knock out procedures for deletion of protease genes may provide a more detailed insight in the function a given protease. Deletion of protease encoding genes can be a valuable strategy for host strain improvement in order to improve production yield for homologous as well as heterologous proteins.

Eukaryotic microbial proteases have been reviewed by North (1982). More recently, Suarez Rendueles and Wolf (1988) have reviewed the *S. cerevisiae* proteases and their function.

Apart from the hydrolytic cleavage of bonds, proteases may also be applied in the formation of bonds. Bonds in this aspect comprise not only peptide and amide bonds but also ester bonds. Whether a protease catalyses the cleavage or the formation of a particular bond does in the first place depend on the thermodynamics of the reaction. An enzyme such as a protease does not affect the equilibrium of the reaction. The equilibrium is dependent on the particular conditions under which the reaction occurs. Under physiological conditions the thermodynamics of the reactions is in favour of the hydrolysis of the peptide due to the thermodynamically very stable structure of the zwitterionic product. By application of physical-chemical principles to influence the equilibrium, or by manipulating the concentrations or the nature of the reactants and products, or by exploiting the kinetic parameters of the enzyme reaction it is possible to apply proteases for the purpose of synthesis of peptide bonds. The addition of water miscible organic solvents decreases the extent of ionisation of the carboxyl component, thereby increasing the concentration of substrate available for the reaction. Biphasic systems, water mimetics, reverse micelles, anhydrous media, or modified amino and carboxyl groups to invoke precipitation of products are often employed to improve yields. When the proteases with the right properties are available the application of proteases for synthesis offers substantial advantages. As proteases are stereo-selective as well as regio-selective, sensitive groups on the reactants do usually not need protection and reactants do not need to be optically pure. As conditions of enzymatic synthesis are mild, racemization and decomposition of labile reactants or products can be prevented. Apart from bonds between amino acids, also other compounds exhibiting a primary amino group, a thiol group or a carboxyl group may be linked by properly selected proteases. In addition esters, thiol esters and amides may be synthesized by certain proteases. Protease have been shown to exhibit

regioselectively in the acylation of mono, di- and tri- saccharides, nucleosides, and riboflavin. Problems with stability under the sometimes harsh reaction conditions may be prevented by proper formulation. Encapsulation and immobilisation do not only stabilise enzymes but also allow easy recovery and separation from the reaction medium. Extensive crosslinking, treatment with aldehydes or covering the surface with certain polymers such as dextrans, polyethyleneglycol, polyimines may substantially extend the lifetime of the biocatalyst.

#### The Natural Roles of Proteases

Traditionally, proteases have been regarded as degrading enzymes, capable of cleaving proteins into small peptides and/or amino acids, and whose role it is to digest nutrient protein or to participate in the turnover of cellular proteins. In addition, it has been shown that proteases also play key roles in a wide range of cellular processes, via mechanisms of selective modification by limited proteolysis, and thus can have essential regulatory functions (Holzer and Tschensche 1979; Holzer and Heinrich, 1980). The specificity of a proteinase is assumed to be closely related to its physiological function and its mode of expression. With respect to the function of a particular protease, its localisation is often very important; for example, a lot of the vacuolar and periplasmic proteases are involved in protein degradation, while many of the membrane-bound proteases are important in protein processing (Suarez Rendueles and Wolf, 1988). The different roles of proteases in many cellular processes can be divided into four main functions of proteases: 1) protein degradation, 2) posttranslational processing and (in)activation of specific proteins, 3) morphogenesis, and 4) pathogenesis.

An obvious role for proteases in organisms which utilise protein as a nutrient source is in the hydrolysis of nutrients. In fungi, this would involve the degradation outside the cells by extracellular broad specificity proteases. Protein degradation is also important for rapid turnover of cellular proteins and allows the cell to remove abnormal proteins and to adapt their complement of protein to changing physiological conditions. Generally, proteases of rather broad specificity should be extremely well-controlled in order to protect the cell from random degradation of other than correct target proteins.

Contrary to the hydrolysis the synthesis of polypeptides occurs *in vivo* by an ATP driven process on the ribosome. Ultimately the sequence in which the amino acids are linked is dictated by the information derived from the genome. This process is known as the transcription. Primary translation products are often longer than the final functional

products, and after the transcription usually further processing of such precursor proteins by proteases is required. Proteases play a key role in the maturation of such precursor proteins to obtain the final functional protein. In contrast to the very controlled trimming and reshaping of proteins, proteases can also be very destructive and may completely degrade polypeptides into peptides and amino acids. In order to avoid that proteolytic activity is unleashed before it is required, proteases are subject to extensive regulation. Many proteases are synthesized as larger precursors known as zymogens, which become activated when required. Remarkably this activation always occurs by proteolysis. Apart from direct involvement in the processing, selective activation and inactivation of individual proteins are well-known phenomena catalyzed by specific proteases.

The selectivity of limited proteolysis appears to reside more directly in the proteinase-substrate interaction. Specificity may be derived from the proteolytic enzyme which recognizes only specific amino acid target sequences. On the other hand, it may also be the result of selective exposure of the 'processing site' under certain conditions such as pH, ionic strength or secondary modifications, thus allowing an otherwise non-specific protease to catalyze a highly specific event. The activation of vacuolar zymogens by limited proteolysis gives an example of the latter kind.

Morphogenesis or differentiation can be defined as a regulated series of events leading to changes from one state to another in an organism. Although direct relationships between proteases and morphological effects could not be established in many cases, the present evidence suggests a significant involvement of proteases in fungal morphogenesis; apart from the observed extensive protein turnover during differentiation, sporulation and spore germination, proteases are thought to be directly involved in normal processes as hyphal tip branching and septum formation, (Deshpande, 1992).

Species of *Aspergillus*, in particular *A. fumigatus* and *A. flavus*, have been implicated as the causative agents of a number of diseases in humans and animals called aspergillosis (Bodey and Vartivarian, 1989). It has been repeatedly suggested that proteases are involved in virulence of *A. fumigatus* and *A. flavus* like there are many studies linking secreted proteases and virulence of bacteria. In fact, most human infections due to *Aspergillus* species are characterised by an extensive degradation of the parenchyma of the lung which is mainly composed of collagen and elastin (Campbell et al., 1994). Research has been focussed on the putative role of the secreted proteases in virulence

of *A. fumigatus* and *A. flavus* which are the main human pathogens and are known to possess elastinolytic and collagenic activities (Kolattukudy et al., 1993). These elastinolytic activities were shown to correlate *in vitro* with infectivity in mice (Kothary et al., 1984). Two secreted proteases are known to be produced by *A. fumigatus* and *A. flavus*, an alkaline serine protease (ALP) and a neutral metallo protease (MEP). In *A. fumigatus* both the genes encoding these proteases were isolated, characterised and disrupted (Reicherdt et al., 1990; Tang et al., 1992, 1993; Jatón-Ogay et al., 1994). However, *alp mep* double mutants showed no differences in pathogenicity when compared with wild type strains. Therefore, it must be concluded that the secreted *A. fumigatus* proteases identified *in vitro* are not essential factors for the invasion of tissue (Jatón Ogay et al., 1994). Although *A. fumigatus* accounts for only a small proportion of the airborne mould spores, it is the most frequently isolated fungus from lung and sputum (Schmitt et al., 1991). Other explanations for the virulence of the fungus could be that the conditions in the bronchia (temperature and nutrients) are favourable for the parasitic growth of *A. fumigatus*. As a consequence, invasive aspergillosis could be a circumstantial event, when the host pathogenic defences have been weakened by immunosuppressive treatments or diseases like AIDS.

Four major classes of proteases are known and are designated by the principal functional groups in their active site: the 'serine', the 'thiol' or 'cysteine', the 'aspartic' or 'carboxyl' and the 'metallo' proteases. A detailed state of the art review on these major classes of proteases, minor classes and unclassified proteases can be found in Methods in Enzymology part 244 and 248 (A.J.Barrett ed, 1994 and 1995).

## 25 Specificity of Proteases

Apart from the catalytic machinery of proteases another important aspect of proteolytic enzymes is the specificity of proteases. The specificity of a protease indicates which substrates the protease is likely to hydrolyze. The twenty natural amino acids offer a large number of possibilities to make up peptides. Eg with twenty amino acids one can make up already 400 dipeptides and 800 different tripeptide, and so on. With longer peptides the number of possibilities will become almost unlimited. Certain proteases hydrolyze only particular sequences at a very specific position. The interaction of the protease with the peptide substrate may encompass one up to ten amino acid residues of the peptide substrate. With large proteinacious substrates there may be even more residues of the substrate that interact with the proteases. However this likely involves less specific interactions with protease residues outside the active site binding cleft. In

general the specific recognition is restricted to the linear peptide, which is bound in the active site of the protease.

The nomenclature to describe the interaction of a substrate with a protease has been introduced in 1967 by Schechter and Berger (Biochem. Biophys. Res. Com., 1967, 27, 157-162) and is now widely used in the literature. In this system, it is considered that the amino acid residues of the polypeptide substrate bind to so-called *sub-sites* in the active site. By convention, these sub-sites on the protease are called S (for sub-sites) and the corresponding amino acid residues are called P (for peptide). The amino acid residues of the N-terminal side of the scissile bond are numbered P3, P2, P1 and those residues of the C-terminal side are numbered P1', P2', P3'. The P1 or P1' residues are the amino acid residues located near the scissile bond. The substrate residues around the cleavage site can then be numbered up to P8. The corresponding sub-sites on the protease that complement the substrate binding residues are numbered S3, S2, S1, S1', S2', S3', etc, etc. The preferences of the sub-sites in the peptide binding site determine the preference of the protease for cleaving certain specific amino acid sequences at a particular spot. The amino acid sequence of the substrate should conform with the preferences exhibited by the sub-sites. The specificity towards a certain substrate is clearly dependant both on the binding affinity for the substrate and on the velocity at which subsequently the scissile bond is hydrolysed. Therefore the specificity of a protease for a certain substrate is usually indicated by its  $k_{cat}/K_m$  ratio, better known as the specificity constant. In this specificity constant  $k_{cat}$  represents the turn-over rate and  $K_m$  is the dissociation constant.

Apart from amino acid residues involved in catalysis and binding, proteases contain many other essential amino acid residues. Some residues are critical in folding, some residues maintain the overall three dimensional architecture of the protease, some residues may be involved in regulation of the proteolytic activity and some residue may target the protease for a particular location. Many proteases contain outside the active site one or more binding sites for metal ions. These metal ions often play a role in stabilizing the structure. In addition secreted eukaryotic microbial proteases may be extensively glycosylated. Both N- and O-linked glycosylation occurs. Glycosylation may aid protein folding, may increase solubility, prevent aggregation and as such stabilize the mature protein. In addition the extent of glycosylation may influence secretion as well as water binding by the protein.

### Regulation of Proteolytic Activity

A substantial number of proteases are subject to extensive regulation of the proteolytic activity in order to avoid undesired proteolytic damage. To a certain extent this regulation takes place at transcription level. For example in fungi the transcription of secreted protease genes appears to be sensitive to external carbon and nitrogen sources, whereas genes encoding intracellular proteases are insensitive. The extracellular pH is sensed by fungi and some genes are regulated by pH. In this process transcriptional regulator proteins play a crucial role. Proteolytic processing of such regulator proteins is often the switch that turns the regulator proteins either on or off.

Proteases are subject to intra- as well as intermolecular regulation. This implies certain amino acids in the proteolytic enzyme molecule that are essential for such regulation. Proteases are typically synthesized as larger precursors known as zymogens, which are catalytically inactive. Usually the peptide chain extension rendering the precursor protease inactive is located at the amino terminus of the protease. The precursor is better known as pro-protein. As many of the proteases processed in this way are secreted from the cells they contain in addition a signal sequence (pre sequence) so that the complete precursor is synthesized as a pre-pro-protein. Apart from rendering the protease inactive the pro-peptide often is essential for mediating productive folding. Examples of proteases include serine proteases (alpha lytic protease, subtilisin, aqualysin, prohormone convertase), thiol proteases (cathepsin L and cruzian), aspartic proteases (proteinase A and cathepsin D) and metalloproteases. In addition the pro-peptide might play a role in cellular transport either alone or in conjunction with signal peptides. It may facilitate interaction with cellular chaperones or it may facilitate transport over the membrane. The size of the extension in the precursor pre-pro-protein may vary substantially, ranging from a short peptide fragment to a polypeptide, which can exist as an autonomous folding unit. In particular these larger extensions are often observed to be strong inhibitors of the protease even after cleavage from the protease. It was observed that even after cleavage such pro-peptides could assist in proper folding of the proteases. As such pro-peptides can be considered to function as molecular chaperones and separate or additional co-expression of such pro-peptides could be advantageous for protease production.

There is substantial difference in the level of regulation between proteases that are secreted into the medium and proteases that remain intracellular. Proteases secreted

into the medium are usually after activation no longer subject to control and therefore are usually relatively simple in their molecular architecture consisting of one globular module. Intracellular proteases are necessarily subject to continuous control in order to avoid damage to the cells. In contrast with zymogens of secreted proteases in more

5 complex regulatory proteases very large polypeptide segments may be inserted between the signal and the zymogen activation domain of the proteolytic module. Structure-function studies indicate that such non-protease parts may be involved in interactions with macroscopic structures, membranes, cofactors, substrates, effectors, inhibitors, ions, that regulate activity and activation of the proteolytic module(s) or its

10 (their) zymogens. The non-proteolytic modules exhibit remarkable variation in size and structure. Many of the modules can exist as such independently from the proteolytic module. Therefore such modules can be considered to correspond to independent structural and functional units that are autonomous with respect to folding. The value of such a modular organization is that acquisition of new modules can endow the recipient

15 protease with new novel binding specificities and can lead to dramatic changes in its activity, regulation and targeting. The principle of modular organized proteolytic enzymes may also be exploited by applying molecular biology tools in order to create novel interactions, regulation, specificity, and/or targeting by shuffling of modules. Although in general such additional modules are observed as N or C terminal

20 extension, also large insertions within the exterior loops of the catalytic domain have been observed. It is believed that also in this case the principal fold of the protease represents still the essential topology to form a functional proteolytic entity and that the insertion can be regarded as substructure folded onto the surface of the proteolytic module.

25

#### Molecular Structure

In principle the modular organization of larger proteins is a general theme in nature. In particular within the larger multimodular frameworks typical proteolytic modules show sizes of 100 to 400 amino acids on the average. This corresponds with the average

30 size of most of the globular proteolytic enzymes that are secreted into the medium. As discussed above polypeptide modules are polypeptide fragments, which can fold and function as independent entities. Another term for such modules is domains. However domain is used in a broader context than module. The term domain as used herein refers usually to a part of the polypeptide chain that depicts in the three-dimensional

35 structure a typical folding topology. In a protein domains interact to varying extents, but less extensively than do the structural elements within domains. Other terms such as



subdomain and folding unit are also used in literature. As such it is observed that many proteins that share a particular functionality may share the same domains. Such domains can be recognized from the primary structure that may show certain sequence patterns, which are typical for a particular domain. Typical examples are the mononucleotide binding fold, cellulose binding domains, helix-turn-helix DNA binding motif, zinc fingers, EF hands, membrane anchors. Modules refer to those domains which are expected to be able to fold and function autonomously. A person skilled in the art knows how to identify particular domains in a primary structure by applying commonly available computersoftware to said structure and homologous sequences from other organisms or species.

Although multimodular or multidomain proteins may appear as a string of beads, assemblies of substantial more complex architecture have been observed. In case the various beads reside on the same polypeptide chain the beads are generally called modules or domains. When the beads do not reside on one and same polypeptide chain but form assemblies via non-covalent interactions then the term *subunit* is used to designate the bead. Subunits may be transcribed by one and the same gene or by different genes. The multi-modular protein may become proteolytically processed after transcription leading to multiple subunits. Individual subunits may consist of multiple domains. Typically the smaller globular proteins of 100-300 amino acids usually consist only of one domain.

#### Molecular Classification of Proteolytic Enzymes

In general proteases are classified according to their molecular properties or according to their functional properties. The molecular classification is based on the primary structure of the protease. The primary structure of a protein represents its amino acid sequence, which can be derived from the nucleotide sequence of the corresponding gene. Tracing extensively the similarities in the primary structures may allow for the notice of similarities in catalytic mechanism and other properties, which even may extend to functional properties. The term *family* is used to describe a group of proteases that show evolutionary relationship based on similarity between their primary structures. The members of such a family are believed to have arisen by divergent evolution from the same ancestor. Within a family further sub-grouping of the primary structures based on more detailed refinement of sequence comparisons results in

subfamilies. Classification according to three-dimensional fold of the proteases may comprise secondary structure, tertiary structure and quaternary structure. In general the classification on secondary structure is limited to content and gross orientation of secondary structure elements. Similarities in tertiary structure have led to the

5 recognition of superfamilies or clans. A superfamily or a clan is a group of families that are thought to have common ancestry as they show a common 3-dimensional fold. In general tertiary structure is more conserved than the primary structure. As a consequence similarity of the primary structure does not always reflect similar functional properties. In fact functional properties may have diverged substantially

10 resulting in interesting new properties. At present quaternary structure has not been applied to classify various proteases. This might be due to a certain bias of the structural databases towards simple globular proteases. Many proteolytic systems that are subject to activation, regulation, or complex reaction cascades are likely to consist of multiple domains or subunits. General themes in the structural organization of such

15 protease systems may lead to new types of classification.

Classification according to specificity.

In absence of sequence information proteases have been subject to various type of

20 functional classification. The classification and naming of enzymes by reference to the reactions which are catalyzed is a general principle in enzyme nomenclature. This approach is also the underlying principle of the EC numbering of enzymes (*Enzyme Nomenclature* 1992 Academic Press, Orlando). Two types of proteases (EC 3.4) can be recognized within *Enzyme Nomenclature* 1992, those of the exo-peptidases (EC

25 3.4.11-19) and those of the endo-peptidases (EC 3.4.21-24, 3.4.99). Endo-peptidases cleave peptide bonds in the inner regions of the peptide chain, away from the termini. Exo-peptidases cleave only residues from the ends of the peptide chain. The exo-peptidases acting at the free N-terminus may liberate a single amino acid residue, a dipeptide or a tripeptide and are called respectively amino peptidases (EC 3.4.11),

30 dipeptidyl peptidases (EC 3.4.14) and tripeptidyl peptidase (EC 3.3.14). Proteases starting peptide processing from the carboxyl terminus liberating a single amino acid are called carboxy peptidase (EC 3.4.16-18). Peptidyl-dipeptidases (EC 3.4.15) remove a dipeptide from the carboxyl terminus. Exo- and endo-peptidase in one are the dipeptidases (EC 3.4.13), which cleave specifically only dipeptides in their two amino

35 acid halves. Omega peptidases (EC 3.4.19) remove terminal residues that are either substituted, cyclic, or linked by isopeptide bonds

Apart from the position where the protease cleaves a peptide chain, for each type of protease a further division is possible based on the nature of the preferred amino acid residues in the substrate. In general one can distinguish proteases with broad, medium and narrow specificity. Some proteases are simply named after the specific proteins or polypeptides that they hydrolyze, e.g. keratinase, collagenase, elastase. A narrow specificity may pin down to one particular amino acid or one particular sequence which is removed or which is cleaved respectively. When the protease shows a particular preference for one amino acid in the P1 or P1' position the name of this amino acid may be a qualifier. For example prolyl amino peptidase removes proline from the amino terminus of a peptide (proline is the P1 residue). X-Pro or proline is used when the bond on the imino side of the proline is cleaved (proline is P1' residue), eg proline carboxypeptidase removes proline from the carboxyl terminus. Prolyl endopeptidase (or Pro-X) cleaves behind proline while proline endopeptidase (X-Pro) cleaves in front of a proline. Amino acid residue *in front of* the scissile peptide bond refers to the amino acid residue that contributes the carboxyl group to the peptide bond. The amino acids residue *behind* the scissile peptide bond refers to the amino acid residue that contributes the amino group to the peptide bond. According to the general convention an amino acid chain runs from amino terminus (the start) to the carboxyl terminus (the end) and is numbered accordingly. Endo proteases may also show clear preference for a particular amino acid in the P1 or P1' position, eg glycyl endopeptidase, peptidyl-lysine endopeptidase, glutamyl endopeptidase. In addition proteases may show a preference for a certain group of amino acids that share a certain resemblance. Such a group of preferred amino acids may comprise the hydrophobic amino acids, only the bulky hydrophobic amino acids, small hydrophobic, or just small amino acids, large positively charged amino acids, etc, etc. Apart from preferences for P1 and P1' residues also particular preferences or exclusions may exist for residues preferred by other subsites on the protease. Such multiple preferences can result in proteases that are very specific for only those sequences that satisfy multiple binding requirements at the same time. In general it should be realized that protease are rather promiscuous enzymes. Even very specific protease may cleave peptides that do not comply with the generally observed preference of the protease. In addition it should be realized that environmental conditions such as pH, temperature, ionic strength, water activity, presence of solvents, presence of competing substrates or inhibitors may influence the preferences of the proteases. Environmental condition may not only influence the protease but also influence the way the proteinaceous substrate is presented to the protease.

### Classification by catalytic mechanism.

- Proteases can be subdivided on the basis of their catalytic mechanism. It should be understood that for each catalytic mechanism the above classification based on specificity leads to further subdivision for each type of mechanism. Four major classes of proteases are known and are designated by the principal functional group in the active site: the serine proteases (EC 3.4.21 endo peptidase, EC 3.4.16 carboxy peptidase), the thiol or cysteine proteases (EC 3.4.22 endo peptidase, EC 3.4.18 carboxy peptidase), the carboxyl or aspartic proteases (EC 3.4.23 endo peptidase) and metallo proteases (EC 3.4.24 endo peptidase, EC 3.4.18 carboxy peptidase). There are characteristic inhibitors of the members of each catalytic type of protease. These small inhibitors irreversibly modify an amino acid residue of the protease active site. For example, the serine protease are inactivated by Phenyl Methane Sulfonyl Fluoride (PMSF) and Diisopropyl Fluoro Phosphate (DFP), which react with the active Serine whereas the chloromethylketone derivatives react with the Histidine of the catalytic triad. Phosphoramidon and 1,10 Phenanthroline typically inhibit metallo proteases. Inhibition by Pepstatin generally indicates an aspartic protease. E64 inhibits thiol protease specifically. Amastatin and Bestatin inhibit various aminopeptidases.
- Substantial variations in susceptibility of the proteases to the inhibitors are observed, even within one catalytic class. To a certain extent this might be related to the specificity of the protease. In case binding site architecture prevents a mechanism based inhibitor to approach the catalytic site, then such a protease escapes from inhibition and identification of the type of mechanism based on inhibition is prohibited.
- Chymostatin for example is a potent inhibitor for serine protease with chymotrypsin like specificity, Elastatinal inhibits elastase like serine proteases and does not react with trypsin or chymotrypsin, 4 amido PMSF (APMSF) inhibits only serine proteases with trypsin like specificity. Extensive accounts of the use of inhibitors in the classification of proteases include Barret and Salvesen, *Proteinase Inhibitors*, Elsevier Amstardam, 1986; Bond and Beynon (eds), *Proteolytic Enzymes, A Practical Approach*, IRL Press, Oxford, 1989; Methods in Enzymology, eds E.J.Barret, volume 244, 1994 and volume 248, 1995; E.Shaw, *Cysteinylnl proteinases and their selective inactivation*, Adv Enzymol. 63:271-347 (1990)
- Classification according to optimal performance conditions.

The catalytic mechanism of a proteases and the requirement for its conformational integrity determine mainly the conditions under which the protease can be utilized. Finding the protease that performs optimal under application conditions is a major challenge. Often conditions at which proteases have to perform are not optimal and do  
5 represent a compromise between the ideal conditions for a particular application and the conditions which would suit the protease best. Apart from the particular properties of the protease it should be realized that also the presentation of a proteinaceous substrates is dependant on the conditions, and as such determines also which conditions are most effective for proteolysis. Specifications for the enzyme that are  
10 relevant for application comprise for example the pH dependence, the temperature dependence, sensitivity for or the dependence of metal ions, ionic strength, salt concentration, solvent compatibility. Another factor of major importance is the specific activity of a protease. The higher the enzyme's specific activity, the less enzyme is needed for a specific conversion. Lower enzyme requirements imply lower costs and  
15 lower protein contamination levels.

The pH is a major parameter that determines protease performance in an application. Therefor pH dependence is an important parameter to group proteases. The major groups that are recognized are the acid proteases, the neutral proteases, the alkaline proteases and the high alkaline proteases. The optimum pH matches only to some  
20 extent the proteolytic mechanism, eg aspartic protease show often an optimum at acidic pH, metalloproteases and thiol proteases often perform optimal around neutral pH to slightly alkaline, serine peptidases are mainly active in the alkaline and high alkaline region. For each class exceptions are known. In addition the overall water activity of the system plays a role. The pH optimum of a protease is defined as the pH  
25 range where the protease exhibits an optimal hydrolysis rate for the majority of its substrates in a particular environment under particular conditions. This range can be narrow, e.g. one pH unit, as well as quite broad, 3-4 pH units. In general the pH optimum is also dependant on the nature of the proteinaceous substrate. Both the turnover rate as well as the specificity may vary as a function of pH. For a certain  
30 efficacy it can be desirable to use the protease far from its pH optimum because production of less desired peptides is avoided. Less desired peptides might be for example very short peptides or peptides causing a bitter taste. In addition a more narrow specificity can be a reason to choose conditions that deviate from optimal conditions with respect to turnover rate. Dependant on the pH the specificity may be  
35 narrow, e.g. only cleaving the peptide chain in one particular position or before or after one particular amino acid, or broader, e.g. cleaving a chain at multiple positions or

cleaving before or after more different types of amino acids. In fact the pH dependence might be an important tool to regulate the proteolytic activity in an application. In case the pH shifts during the process the proteolysis might cease spontaneously without the need for further treatment to inactivate the protease. In some cases the proteolysis  
5 itself may be the driver of the pH shift.

Very crucial for application of proteases is their handling and operating stability. As protease stability is strongly affected by the working temperature, stability is often also referred to as thermostability. In general the stability of a protease indicates how long a  
10 protease retains its proteolytic activity under particular conditions. Particular conditions may comprise fermentation conditions, conditions during isolation and down stream processing of the enzyme, storage conditions, formulation and operating or application conditions. In case particular conditions encompass elevated temperatures stability in general refers to thermostability. Apart from the general causes for enzyme inactivation  
15 such as chemical modification, unfolding, aggregation etc, main problem with proteases is that they are easy subject to autodegradation. Especially for the utilization of proteases the temperature optimum is a relevant criterion to group proteases. Although there are different definitions, economically the most useful definition is the temperature or the temperature range in which the protease is most productive in a  
20 certain application. Protease productivity is a function of both the stability and the turnover rate. Where elevated temperature in general will increase the turnover rate, rapid inactivation will counteract the increase in turnover rate and ultimately lead to low productivity. The conformational stability of the protease under a given process condition will determine its maximum operating temperature. The temperature at which  
25 the protease loses its active conformation, often indicated as unfolding or melting point, can be determined according various methods, for example NMR, Circular Dichroism Spectroscopy, Differential Scanning Calorimetry etc etc. For protease unfolding is usually accompanied by a tremendous increase in autodegradation rate.

30 In applications where low temperatures are required protease may be selected with emphasis on a high intrinsic activity at low to moderate temperature. As under such conditions inactivation is relatively slow, under these conditions activity might largely determine productivity. In processes where only during a short period protease activity is required, the stability of the protease might be used as a switch to turn the protease  
35 off. In such case more labile instead of very thermostable protease might be preferred.

Other environmental parameters which may play a role in selecting the appropriate protease may be its sensitivity to salts. The compatibility with metal ions which are found frequently at low concentrations in various natural materials can be crucial for certain applications. In particular with metallo proteases certain ions may replace the catalytic metal ion and reduce or even abolish activity completely. In some applications metal ions have to be added on purpose in order to prevent the washout of the metal ions coordinated to the protease. It is well known that for the sake of enzyme stability and life-time, calcium ions have to be supplied in order to prevent dissociation of protein bound calcium.

10

Most microorganisms show a certain tolerance with respect to adapting to changes in the environmental condition. As a consequence at least the proteolytic spectrum that the organism is able to produce are likely to show at least similar tolerances. Such a proteolytic spectrum might be covered by many proteases covering together the whole proteolytic spectrum or by only a few proteases of a broad spectrum. Taking into account the whole proteolytic spectrum of a microorganism it can be very important to take the location into account.

15

#### Cellular localisation and characterization of proteolytic processing and degradation

20

From an industrial point of view the proteases which are excreted from the cell have specific advantages with respect to producibility at a large scale and stress tolerance as they have to survive without protection of the cell. The large group of cellular protease can be further subdivided in soluble and membrane bound. Membrane bound protease may comprise protease at the inside as well the outside of the membrane. Intracellular soluble protease may be subdivided further according to specific compartments of the cell where they do occur. As the cell shields the proteases to some extent from the environment and because the cell controls the conditions in the cell, intracellular protease might be more sensitive to large environmental changes and their optima might correlate better with the specific intracellular conditions. Knowing the conditions of the cellular department where the protease resides might indicate their preferences. Where extracellular protease in general do not require any regulation any more once excreted from the cell, intracellular proteases are often subject to more complicated control and regulation.

35

With respect to the function of a particular protease, its localisation is often very

important; for example, a lot of the vacuolar and periplasmic proteases are involved in protein degradation, while many of the membrane-bound proteases are important in protein processing (Suarez Rendueles and Wolf, 1988).

- 5 A comprehensive review on the biological properties and evolution of proteases has been published in van den Hombergh: Thesis Landbouwwuniversiteit Wageningen: An analysis of the proteolytic system in *Aspergillus* in order to improve protein production ISBN 90-5485-545-2, which is hereby incorporated by reference herein.

10 The protease problem

An important reason for the interest in microbial proteases are protease related expression problems observed in several expression hosts used in bioprocess industry. The increasing use of heterologous hosts for the production of proteins, by recombinant  
15 DNA technology, has recently brought this problem into focus, since it seems that heterologous proteins are more prone to proteolysis (Archer et al., 1992; van den Hombergh et al., 1996b).

In *S. cerevisiae*, already in the early eighties the protease problem and the involvement  
20 of several proteases, thus complicating targetted gene disruption approaches to overcome this problem, was recognised. During secretion a protein is exposed to several proteolytic activities residing in the secretory pathway. Additionally, in a prototrophic microorganism as *Aspergillus* secreted proteins can be exposed to several extracellular proteolytic activities

25 The problem of degradation of heterologously expressed proteins is well documented in *Aspergillus* (van den Hombergh Thesis Landbouwwuniversiteit Wageningen: An analysis of the proteolytic system in *Aspergillus* in order to improve protein production ISBN 90-5485-545-2) and has been reported in the expression of cow prochymosin,  
30 human interferon  $\alpha$ -2 tPA, GMCSF, IL6, lactoferrin, chicken egg-white lysosyme, porcine pIA2, *A. niger* pectin lyase B, *E. coli* enterotoxin B and  $\beta$ -glucoronidase, and *Erwinia carotovora* pectate lyase 3.

The problem of proteolysis may be addressed at several stages in protein production.  
35 Bioprocess engineers may address the problem of proteolysis by downstream



processing at low temperatures , by early separation of product and protease(s) or by use of protease inhibitors. These may all lead to successful reduction of the problem. However it is certainly not eliminated, because much of the degradation occurs *in vivo* during the production of the protein.

5

In understanding how proteolysis is controlled in the cell, a major question concerns the recognition mechanism by which proteolysis is triggered. Into what extent are proteolytically susceptible (heterologous) proteins recognised as aberrant because of misfolding or, if correctly folded, as 'foreign', because they do not possess features essential for stability which are specific to the host. Various types of stress can cause the overall proteolysis in a cell to increase significantly. Factors known to increase rate of proteolysis include nutrient starvation and various other types of stress (i.e. elevation of temperature, osmotic stress, toxic substances and expression of certain heterologous proteins). To deal with proteolysis-related expression problems *in vivo*, several approaches have been proven successful as will be discussed below. However, we have to keep in mind that true 'non-proteolytic cells' cannot exist, since proteolysis by intracellular proteases is involved in many essential metabolic and 'housekeeping' reactions. Reducing proteolysis will therefore always be a process in which the changed genetical background which results in decreased proteolytic has to be analysed for potential secondary effects which could lead to reduced protein production (e.g. reduced growth rate or sporulation).

*Disruption of proteases in filamentous fungal expression hosts*

Berka and coworkers (1990) describe the cloning and disruption of the *A. awamori pepA* gene. More recently, three disrupted aspartyl proteases in *A. niger* have been described. Disruptants for both the major extracellular aspartyl proteases and the major vacuolar aspartyl protease were described. Double and triple disruptants were generated via recombination and tested for protease spectra and expression and secretion of the *A. niger* pectin lyase PELB protein, which is very susceptible to proteolytic degradation (van den Hombergh et al., 1995). Disruption of *pepA* and *pepB* resulted both in reduction of extracellular protease activities, 80% and 6 %, respectively. In the  $\Delta pepE$  disruptant also other (vacuolar) protease activities were severely affected caused by inactivating of the proteolytic cascade for other vacuolar proteases. Reduced extracellular activities correlated with reduced *in vitro* degradation of PELB and improved *in vivo* expression of *peB* (van den Hombergh et al., 1996f).

*Protease deficient (prt) mutants filamentous fungi*

Several *Aspergillus* protease deficient mutants have been studied whether protein production is improved. Archer and coworkers describe the reduced proteolysis of Hen egg white lysozyme in supernatants of an *A. niger* double *prt* mutant generated by Mattern and coworkers (1992) and conclude that although the degradation is not absent, it is significantly reduced. Van den Hombergh et al. (1995) show that the *in vitro* degradation of *A. niger* PELB is reduced in all seven *prt* complementation groups they have isolated. Virtually no degradation is observed in the *prtB*, *prtF* and *prtG* mutants. Recently, the expression of the *pebB* gene was shown to be improved in six complementation groups tested (*prtA-F*) and highest expression levels were observed in the *prtB*, *prtF* and *prtG* mutants. In addition to the single mutants, which contained residual extracellular proteolytic activities varying from 2-80 % compared to wild type activity, double mutants were generated both by recombination and by additional rounds of mutagenesis. Via this approach several double *prt* mutants were selected and further characterised, which showed a further reduction of PELB degradation compared to their parental strains.

Instead of elimination of protease activities via disruption or mutagenesis, reduced proteolysis can also be achieved via down-regulation of the interfering proteolytic activities. This may be achieved by genetically altering the promoter or other regulatory sequences of the gene. As shown by Fraissinet-Tachet and coworkers (1996) the extracellular proteases in *A. niger* are all regulated by carbon catabolite repression and nitrogen metabolite repression. Nutrient starvation also causes the overall proteolysis rate in a cell to increase strongly, which makes sense for a cell that lacks nutrients but possesses proteins, that under starvation conditions are not needed or needed only in smaller amounts. In expression strategies which allow high expression on media containing high glucose and ammonium concentrations reduced proteolysis has been reported. Several constitutive glycolytic promoters (*gpd* and *pkiA*) are highly expressed under these conditions and can also be used to drive (heterologous) gene expression in continuous fermentations. The type of nutrient starvation imposed can influence different proteases to varying extent, which means that the importance of nutrient conditions in a given process depend on the type of proteolysis that is involved. Specific proteolysis may therefore be induced by conditions of substrate limitation which are frequently used in many large-scale fermentation processes.

The protease problem can nowadays be addressed in part by one or more of the above

strategies. However, the residual proteolytic activity of yet unidentified proteolytic enzymes still constitutes a major problem in the art. In order to further reduce the level of unwanted proteolysis, there is a great need in the art to identify novel proteases responsible for degradation of homologously and heterologously expressed proteins.

5 This invention provides such novel protease gene sequences encoding novel proteases. Once the primary sequence of a novel protease gene is known, one or more of the above recombinant DNA strategies may be employed to produce (knock-out) mutants with reduced proteolytic activity.

10 Despite the widespread applications of proteases in a great number of industrial processes, current enzymes also have significant shortcomings with respect to at least one of the following properties.

When added to animal feed, current proteases are not sufficiently resistant to digestive  
15 enzymes present in the gastrointestinal (GI) tract of e.g. pigs and poultry.

With respect to another aspect, the currently available enzymes are not sufficiently resistant to specific (high) temperatures and (high) pressure conditions that are applied during extrusion or pelleting operations.

20

Also, the current enzymes are not sufficiently active in a pH range of 3-7, conditions prevailing in many food, beverage products as well as in the GI tract of most animals.

25 According to yet another aspect the specificity of the currently available proteases is very limited which results in the inability of the existing enzymes to degrade or to dissolve certain "protease resistant" proteins thus resulting in low peptide or amino acid yields. Moreover proteases with new specificities allow the synthesis of new peptides.

30 Yet another drawback of the currently available enzymes is their low specific activity.

It is therefore clear that for a large number of applications a strong desire exists for proteases that are more resistant to digestive enzymes, high temperature and/or pressure and which exhibit novel specificities regarding their sites of hydrolysis. The  
35 present invention provides such enzymes.

### **Object of the invention**

It is an object of the invention to provide novel polynucleotides encoding novel proteases. A further object is to provide naturally and recombinantly produced  
5 proteases as well as recombinant strains producing these. Such strains may also be used to produce classical fermentation products faster or with higher yields. Yet another object of the invention is to provide a filamentous fungus strain defective in producing a protease according to the invention. Such strains may be used for a more efficient production of heterologous or homologous proteins. Also antibodies and fusion  
10 polypeptides are part of the invention as well as methods of making and using the polynucleotides and polypeptides according to the invention.

### **Summary of the invention**

15 The invention provides for novel polynucleotides encoding novel proteases.

More in particular, the invention provides for polynucleotides having a nucleotide sequence that hybridises (preferably under highly stringent conditions) to a sequence according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ  
20 ID NO: 57 or to a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114. Consequently, the invention provides nucleic acids that are about 60%, preferably 65%, more preferably 70%, even more preferably 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% homologous to the sequences according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a  
25 sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114.

In a more preferred embodiment the invention provides for such an isolated polynucleotide obtainable from a filamentous fungus, preferably *Aspergilli*, in particular *A. niger* is preferred.

30 In one embodiment, the invention provides for an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.

35 In a further preferred embodiment, the invention provides an isolated polynucleotide

encoding at least one functional domain of a polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.

- 5 In a preferred embodiment the invention provides a protease gene according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57. In another aspect the invention provides a polynucleotide, preferably a cDNA encoding an *A. niger* protease selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or variants or fragments of that polypeptide. In a preferred embodiment the
- 10 cDNA has a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or functional equivalents thereof.

- A genomic clone encoding a polypeptide according to the invention may also be obtained by selecting suitable probes to specifically amplify a genomic region
- 15 corresponding to any of the sequences according to SEQ ID NO: 1 to SEQ ID NO: 57 or fragments thereof, hybridising that probe under suitable conditions to genomic DNA obtained from a suitable organism, such as *Aspergillus*, e.g. *A. niger*, amplifying the desired fragment e.g. by PCR (polymerase chain reaction) followed by purifying and cloning of the amplified fragment.

20

In an even further preferred embodiment, the invention provides for a polynucleotide comprising the coding sequence of the genomic polynucleotides according to the invention, preferred is a polynucleotide sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114.

25

In another preferred embodiment, the invention provides a cDNA obtainable by cloning and expressing a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 into a suitable host organism, such as *A. niger*.

- 30 A polypeptide according to the invention may also be obtained by cloning and expressing a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 into a suitable host organism, such as *A. niger*.

- The invention also relates to vectors comprising a polynucleotide sequence according
- 35 to the invention and primers, probes and fragments that may be used to amplify or detect the DNA according to the invention.

In a further preferred embodiment, a vector is provided wherein the polynucleotide sequence according to the invention is functionally linked with regulatory sequences suitable for expression of the encoded amino acid sequence in a suitable host cell, such as *A. niger* or *A. oryzae*. The invention also provides methods for preparing polynucleotides and vectors according to the invention.

The invention also relates to recombinantly produced host cells that contain heterologous or homologous polynucleotides according to the invention.

In one embodiment, the invention provides recombinant host cells wherein the expression of a protease according to the invention is significantly reduced or wherein the activity of the protease is reduced or wherein the protease is even inactivated. Such recombinants are especially useful for the expression of homologous or heterologous proteins.

In another embodiment, the invention provides recombinant host cells wherein the expression of a protease according to the invention is significantly increased or wherein the activity of the protease is increased. Such recombinants are especially useful for the expression of homologous or heterologous proteins where maturation is seriously hampered in case the required proteolytic cleavage becomes the rate limiting step.

In another embodiment the invention provides for a recombinantly produced host cell that contains heterologous or homologous DNA according to the invention, preferably DNA encoding proteins bearing signal sequences and wherein the cell is capable of producing a functional protease according to the invention, preferably a cell capable of over-expressing the protease according to the invention, for example an *Aspergillus* strain comprising an increased copy number of a gene or cDNA according to the invention.

In another embodiment the invention provides for a recombinantly produced host cell that contains heterologous or homologous DNA according to the invention and wherein the cell is capable of secreting a functional protease according to the invention, preferably a cell capable of over-expressing and secreting the protease according to the invention, for example an *Aspergillus* strain comprising an increased copy number of a gene or cDNA according to the invention.

In yet another aspect of the invention, a purified polypeptide is provided. The polypeptides according to the invention include the polypeptides encoded by the polynucleotides according to the invention. Especially preferred is a polypeptide  
5 according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.

The invention also provides for antibodies reactive with a polypeptide according to the invention. These antibodies may be polyclonal, yet especially preferred are monoclonal  
10 antibodies. Such antibodies are particularly useful for purifying the polypeptides according to the invention.

Fusion proteins comprising a polypeptide according to the invention are also within the scope of the invention. The invention also provides methods of making the  
15 polypeptides according to the invention.

The invention further relates to a method for diagnosing aspergillosis either by detecting the presence of a polypeptide according to the invention or functional equivalents thereof, or by detecting the presence of a DNA according to the invention  
20 or fragments or functional equivalents thereof.

The invention also relates to the use of the protease according to the invention in an industrial process as described herein

25

### **Detailed description of the invention**

#### **Polynucleotides**

30 The present invention provides polynucleotides encoding proteases having an amino acid sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof. The sequence of these genes was determined by sequencing a genomic clone obtained from *Aspergillus niger*. The invention provides polynucleotide sequences comprising the gene encoding these proteases as well as  
35 their complete cDNA sequence and its coding sequence. Accordingly, the invention

relates to an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or functional equivalents thereof.

5

More in particular, the invention relates to an isolated polynucleotide hybridisable under stringent conditions to a polynucleotide selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 preferably under highly stringent conditions.

10

Advantageously, such polynucleotides may be obtained from filamentous fungi, in particular from *Aspergillus niger*. More specifically, the invention relates to an isolated polynucleotide having a nucleotide sequence according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114.

15

The invention also relates to an isolated polynucleotide encoding at least one functional domain of a polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.

20

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules which may be isolated from chromosomal DNA, which include an open reading frame encoding a protein, e.g. an *A. niger* protease. A gene may include coding sequences, non-coding sequences, introns and regulatory sequences. Moreover, a gene refers to an isolated nucleic acid molecule as defined herein.

25

A nucleic acid molecule of the present invention, such as a nucleic acid molecule having the nucleotide sequence of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or a functional equivalent thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, using all or portion of the nucleic acid sequence of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or the nucleotide sequence of a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 as a hybridization probe, nucleic acid molecules according to the invention can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A*

35



Laboratory Manual.2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Moreover, a nucleic acid molecule encompassing all or a portion of a sequence  
5 selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence  
selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 can be  
isolated by the polymerase chain reaction (PCR) using synthetic oligonucleotide  
primers designed based upon the sequence information contained in a sequence  
selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence  
10 selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114.

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively,  
genomic DNA, as a template and appropriate oligonucleotide primers according to  
standard PCR amplification techniques. The nucleic acid so amplified can be cloned  
15 into an appropriate vector and characterized by DNA sequence analysis.

Furthermore, oligonucleotides corresponding to or hybridisable to nucleotide  
sequences according to the invention can be prepared by standard synthetic  
techniques, e. g., using an automated DNA synthesizer.  
20

In a preferred embodiment, an isolated nucleic acid molecule of the invention  
comprises the nucleotide sequence shown in a sequence selected from the group  
consisting of SEQ ID NO: 58 to SEQ ID NO: 114. The sequence of a sequence  
selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 corresponds  
25 to the coding region of the *A. niger* protease cDNA. This cDNA comprises sequences  
encoding the *A. niger* protease polypeptide according to a sequence selected from the  
group consisting of SEQ ID NO: 115 to SEQ ID NO: 171.

In another preferred embodiment, an isolated nucleic acid molecule of the invention  
30 comprises a nucleic acid molecule which is a complement of the nucleotide sequence  
shown in a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID  
NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID  
NO: 114 or a functional equivalent of these nucleotide sequences.

35 A nucleic acid molecule which is complementary to another nucleotide sequence is one  
which is sufficiently complementary to the other nucleotide sequence such that it can

hybridize to the other nucleotide sequence thereby forming a stable duplex.

One aspect of the invention pertains to isolated nucleic acid molecules that encode a polypeptide of the invention or a functional equivalent thereof such as a biologically  
5 active fragment or domain, as well as nucleic acid molecules sufficient for use as hybridisation probes to identify nucleic acid molecules encoding a polypeptide of the invention and fragments of such nucleic acid molecules suitable for use as PCR primers for the amplification or mutation of nucleic acid molecules.

10 An "isolated polynucleotide" or "isolated nucleic acid" is a DNA or RNA that is not immediately contiguous with both of the coding sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally occurring genome of the organism from which it is derived. Thus, in one embodiment, an isolated nucleic acid includes some or all of the 5' non-coding (e.g., promotor) sequences that are  
15 immediately contiguous to the coding sequence. The term therefore includes, for example, a recombinant DNA that is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other  
20 sequences. It also includes a recombinant DNA that is part of a hybrid gene encoding an additional polypeptide that is substantially free of cellular material, viral material, or culture medium (when produced by recombinant DNA techniques), or chemical precursors or other chemicals (when chemically synthesized). Moreover, an "isolated nucleic acid fragment" is a nucleic acid fragment that is not naturally occurring as a  
25 fragment and would not be found in the natural state.

As used herein, the terms "polynucleotide" or "nucleic acid molecule" are intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The  
30 nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. The nucleic acid may be synthesized using oligonucleotide analogs or derivatives (e.g., inosine or phosphorothioate nucleotides). Such oligonucleotides can be used, for example, to prepare nucleic acids that have altered base-pairing abilities or increased resistance to nucleases.

35

Another embodiment of the invention provides an isolated nucleic acid molecule which

is antisense to a protease nucleic acid molecule, e.g., the coding strand of a protease nucleic acid molecule. Also included within the scope of the invention are the complement strands of the nucleic acid molecules described herein.

## 5 Sequencing errors

The sequence information as provided herein should not be so narrowly construed as to require inclusion of erroneously identified bases. The specific sequences disclosed herein can be readily used to isolate the complete gene from filamentous fungi, in particular *A. niger* which in turn can easily be subjected to further sequence analyses thereby identifying sequencing errors.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

The person skilled in the art is capable of identifying such erroneously identified bases and knows how to correct for such errors.

## Nucleic acid fragments, probes and primers

A nucleic acid molecule according to the invention may comprise only a portion or a fragment of the nucleic acid sequence shown in a sequence selected from the group

consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114, for example a fragment which can be used as a probe or primer or a fragment encoding a portion of a protease protein. The nucleotide sequence determined from the cloning of the protease gene and cDNA

5 allows for the generation of probes and primers designed for use in identifying and/or cloning other protease family members, as well as protease homologues from other species. The probe/primer typically comprises substantially purified oligonucleotide which typically comprises a region of nucleotide sequence that hybridizes preferably under highly stringent conditions to at least about 12 or 15, preferably about 18 or 20,

10 preferably about 22 or 25, more preferably about 30, 35, 40, 45, 50, 55, 60, 65, or 75 or more consecutive nucleotides of a nucleotide sequence shown in a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or of a functional equivalent thereof.

15

Probes based on the protease nucleotide sequences can be used to detect transcripts or genomic protease sequences encoding the same or homologous proteins for instance in other organisms. In preferred embodiments, the probe further comprises a label group attached thereto, e.g., the label group can be a radioisotope, a fluorescent

20 compound, an enzyme, or an enzyme cofactor. Such probes can also be used as part of a diagnostic test kit for identifying cells which express a protease protein.

#### Identity & homology

25 The terms "homology" or "percent identity" are used interchangeably herein. For the purpose of this invention, it is defined here that in order to determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a

30 second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the

35 number of identical positions shared by the sequences (i.e., % identity = number of identical positions/total number of positions (i.e. overlapping positions) x 100).

Preferably, the two sequences are the same length.

- The skilled person will be aware of the fact that several different computer programs are available to determine the homology between two sequences. For instance, a
- 5 comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (J. Mol. Biol. (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available
- 10 at <http://www.gcg.com>), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. The skilled person will appreciate that all these different parameters will yield slightly different results but that the overall percentage identity of two sequences is not significantly altered when using different algorithms.
- 15 In yet another embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity two amino acid or nucleotide sequence is determined using the algorithm of E.
- 20 Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0) (available at <http://vega.igh.cnrs.fr/bin/align-guess.cgi>), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.
- 25 The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403—10. BLAST nucleotide searches can be performed with the NBLAST
- 30 program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to protease nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to protease protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as
- 35 described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the

respective programs (e.g., XBLAST and NBLAST) can be used. See  
<http://www.ncbi.nlm.nih.gov>.

#### Hybridisation

5

As used herein, the term "hybridizing" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least about 50%, at least about 60%, at least about 70%, more preferably at least about 80%, even more preferably at least about 85% to 90%, more preferably at least 95% homologous to  
10 each other typically remain hybridized to each other.

A preferred, non-limiting example of such hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45 °C, followed by one or more washes in 1 X SSC, 0.1 % SDS at 50 °C, preferably at 55 °C, preferably at 60 °C and  
15 even more preferably at 65 °C.

Highly stringent conditions include, for example, hybridizing at 68 °C in 5x SSC/5x Denhardt's solution/1.0% SDS and washing in 0.2x SSC/0.1% SDS at room temperature. Alternatively washing may be performed at 42 °C.

20

The skilled artisan will know which conditions to apply for stringent and highly stringent hybridisation conditions. Additional guidance regarding such conditions is readily available in the art, for example, in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, N.Y.; and Ausubel et al. (eds.), 1995,  
25 Current Protocols in Molecular Biology, (John Wiley & Sons, N.Y.).

Of course, a polynucleotide which hybridizes only to a poly A sequence (such as the 3' terminal poly(A) tract of mRNAs), or to a complementary stretch of T (or U) residues, would not be included in a polynucleotide of the invention used to specifically hybridize  
30 to a portion of a nucleic acid of the invention, since such a polynucleotide would hybridize to any nucleic acid molecule contain a poly (A) stretch or the complement thereof (e.g., practically any double-standed cDNA clone).

#### Obtaining full length DNA from other organisms

35

In a typical approach, cDNA libraries constructed from other organisms, e.g.

filamentous fungi, in particular from the species *Aspergillus* can be screened.

For example, *Aspergillus* strains can be screened for homologous protease polynucleotides by Northern blot analysis. Upon detection of transcripts homologous to  
5 polynucleotides according to the invention, cDNA libraries can be constructed from RNA isolated from the appropriate strain, utilizing standard techniques well known to those of skill in the art. Alternatively, a total genomic DNA library can be screened using a probe hybridisable to a protease polynucleotide according to the invention.

10 Homologous gene sequences can be isolated, for example, by performing PCR using two oligonucleotide primers or two degenerate oligonucleotide primer pools designed on the basis of nucleotide sequences as taught herein.

The template for the reaction can be cDNA obtained by reverse transcription of mRNA  
15 prepared from strains known or suspected to express a polynucleotide according to the invention. The PCR product can be subcloned and sequenced to ensure that the amplified sequences represent the sequences of a new protease nucleic acid sequence, or a functional equivalent thereof.

20 The PCR fragment can then be used to isolate a full length cDNA clone by a variety of known methods. For example, the amplified fragment can be labeled and used to screen a bacteriophage or cosmid cDNA library. Alternatively, the labeled fragment can be used to screen a genomic library.

25 PCR technology also can be used to isolate full length cDNA sequences from other organisms. For example, RNA can be isolated, following standard procedures, from an appropriate cellular or tissue source. A reverse transcription reaction can be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis.

30 The resulting RNA/DNA hybrid can then be "tailed" (e.g., with guanines) using a standard terminal transferase reaction, the hybrid can be digested with RNase H, and second strand synthesis can then be primed (e.g., with a poly-C primer). Thus, cDNA sequences upstream of the amplified fragment can easily be isolated. For a review of  
35 useful cloning strategies, see e.g., Sambrook et al., supra; and Ausubel et al., supra.

## Vectors

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a protease protein or a functional equivalent thereof.

- 5 As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are
- 10 capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the
- 15 expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. The terms "plasmid" and "vector" can be used interchangeably herein as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression
- 20 vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which
- 25 means that the recombinant expression vector includes one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows
- 30 for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signal). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in*
- 35 *Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many



- types of host cells and those which direct expression of the nucleotide sequence only in a certain host cell (e.g. tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, encoded by nucleic acids as described herein (e.g. protease proteins, mutant forms of protease proteins, fragments, variants or functional equivalents thereof, fusion proteins, etc.).
- 10 The recombinant expression vectors of the invention can be designed for expression of protease proteins in prokaryotic or eukaryotic cells. For example, protease proteins can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185,
- 15 Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors e.g., vectors derived from bacterial plasmids, bacteriophage, yeast episome, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic elements, such as cosmids and phagemids.

- 25 The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli* lac, trp and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled person. In a specific embodiment, promoters are preferred that are capable of directing a high expression level of proteases in filamentous fungi. Such promoters are known in the art. The expression constructs may contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will include a translation initiating AUG at the beginning
- 30 and a termination codon appropriately positioned at the end of the polypeptide to be translated.
- 35

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, transduction, infection, lipofection, cationic lipid-mediated transfection or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al. (*Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup>, ed. Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), Davis et al., *Basic Methods in Molecular Biology* (1986) and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding a protease protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g. cells that have incorporated the selectable marker gene will survive, while the other cells die).

Expression of proteins in prokaryotes is often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, e.g. to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa,

thrombin and enterokinase.

As indicated, the expression vectors will preferably contain selectable markers. Such markers include dihydrofolate reductase or neomycin resistance for eukarotic cell culture and tetracycline or ampicilling resistance for culturing in *E. coli* and other bacteria. Representative examples of appropriate host include bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9; animal cells such as CHO, COS and Bowes melanoma; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria are pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16A, pNH18A, pNH46A, available from Stratagene; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are PWLNEO, pSV2CAT, pOG44, pZT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters for use in the present invention include *E. coli* lacI and lacZ promoters, the T3 and T7 promoters, the gpt promoter, the lambda PR, PL promoters and the trp promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus ("RSV"), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion

signal may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

5 The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate  
10 purification.

#### Polypeptides according to the invention

The invention provides an isolated polypeptide having an amino acid sequence  
15 selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171, an amino acid sequence obtainable by expressing a polynucleotide according to the invention or in a preferred embodiment of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 in an appropriate host, as well as an amino acid sequence obtainable by expressing a polynucleotide sequences selected from the group  
20 consisting of SEQ ID NO: 58 to SEQ ID NO: 114 in an appropriate host. Also, a peptide or polypeptide comprising a functional equivalent of the above polypeptides is comprised within the present invention. The above polypeptides are collectively comprised in the term "polypeptides according to the invention".

25 The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least two amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than seven amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written  
30 from left to right and in the direction from amino terminus to carboxy terminus. The one-letter code of amino acids used herein is commonly known in the art and can be found in Sambrook, et al. (*Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup>, ed. Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989)

35

By "isolated" polypeptide or protein is intended a polypeptide or protein removed from

its native environment. For example, recombinantly produced polypeptides and proteins expressed in host cells are considered isolated for purpose of the invention as are native or recombinant polypeptides which have been substantially purified by any suitable technique such as, for example, the single-step purification method disclosed  
5 in Smith and Johnson, Gene 67:31-40 (1988).

The protease according to the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,  
10 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. For analytical purposes most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

15 Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be  
20 glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes.

Moreover, a protein according to the invention may be a precursor protein such as a  
25 zymogen, a hybrid protein, a protein obtained as a pro sequence or pre-pro sequence, or any other type of immature form.

#### Protein fragments

30 The invention also features biologically active fragments of the polypeptides according to the invention.

Biologically active fragments of a polypeptide of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino  
35 acid sequence of the protease protein (e.g., the amino acid sequence of a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171), which

include fewer amino acids than the full length protein, and exhibit at least one biological activity of the corresponding full-length protein. Typically, biologically active fragments comprise a domain or motif with at least one activity of the protease protein. A biologically active fragment of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the biological activities of the native form of a polypeptide of the invention.

- 10 The invention also features nucleic acid fragments which encode the above biologically active fragments of the protease protein.

#### Fusion proteins

- 15 The proteins of the present invention or functional equivalents thereof, e.g., biologically active portions thereof, can be operatively linked to a non-protease polypeptide (e.g., heterologous amino acid sequences) to form fusion proteins. As used herein, a protease "chimeric protein" or "fusion protein" comprises a protease polypeptide operatively linked to a non-protease polypeptide. A "protease polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a polypeptide sequence according to the invention, whereas a "non-protease polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to a protein according to the invention, e.g., a protein which is different from the protease protein and which is derived from the same or a different organism. Within a protease fusion protein the protease polypeptide can correspond to all or a portion of a protein according to the invention. In a preferred embodiment, a protease fusion protein comprises at least one biologically active fragment of a protein according to the invention. In another preferred embodiment, a protease fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the protease polypeptide and the non-protease polypeptide are fused in-frame to each other. The non-protease polypeptide can be fused to the N-terminus or C-terminus of the protease polypeptide.
- 35 For example, in one embodiment, the fusion protein is a GST-protease fusion protein in which the protease sequences are fused to the C-terminus of the GST sequences.

- Such fusion proteins can facilitate the purification of recombinant protease. In another embodiment, the fusion protein is a protease protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian and Yeast host cells), expression and/or secretion of protease can be increased through use of a
- 5 heterologous signal sequence.
- In another example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (*Current Protocols in Molecular Biology*, Ausubel et al., eds., John Wiley & Sons, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human
- 10 placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook et al., *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).
- 15 A signal sequence can be used to facilitate secretion and isolation of a protein or polypeptide of the invention. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass
- 20 through the secretory pathway. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which
- 25 facilitates purification, such as with a GST domain. Thus, for instance, the sequence encoding the polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide, which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among
- 30 others, many of which are commercially available. As described in *Gentz et al, Proc. Natl. Acad. Sci. USA 86:821-824 (1989)*, for instance, hexa-histidine provides for convenient purification of the fusion protein. The HA tag is another peptide useful for purification which corresponds to an epitope derived of influenza hemagglutinin protein, which has been described by Wilson *et al.*, *Cell 37:767 (1984)*, for instance.
- 35 Preferably, a protease chimeric or fusion protein of the invention is produced by

standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, 5 filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene 10 fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g, a GST polypeptide). A protease-encoding nucleic acid can be cloned into such an expression vector such that 15 the fusion moiety is linked in-frame to the protease protein.

#### Functional equivalents

The terms "functional equivalents" and "functional variants" are used interchangeably 20 herein. Functional equivalents of a DNA according to the invention are isolated DNA fragments that encode a polypeptide that exhibits a particular function of an *A. niger* protease as defined herein. A functional equivalent of a polypeptide according to the invention is a polypeptide that exhibits at least one function of an *A. niger* protease as defined herein.

25

Functional protein or polypeptide equivalents may contain only conservative substitutions of one or more amino acids of a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or substitutions, insertions or deletions of non-essential amino acids. Accordingly, a non-essential amino acid is a 30 residue that can be altered in a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 without substantially altering the biological function. For example, amino acid residues that are conserved among the protease proteins of the present invention, are predicted to be particularly unamenable to alteration. Furthermore, amino acids conserved among the protease proteins according to the 35 present invention and other proteases are not likely to be amenable to alteration.



The term "conservative substitution" is intended to mean that a substitution in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

These families are known in the art and include amino acids with basic side chains (e.g. lysine, arginine and histidine), acidic side chains (e.g. aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine).

10

Functional nucleic acid equivalents may typically contain silent mutations or mutations that do not alter the biological function of encoded polypeptide. Accordingly, the invention provides nucleic acid molecules encoding protease proteins that contain changes in amino acid residues that are not essential for a particular biological activity.

15

Such protease proteins differ in amino acid sequence from a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 yet retain at least one biological activity. In one embodiment the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises a substantially homologous amino acid sequence of at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more homologous to the amino acid sequence shown in a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171.

20

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J.U. et al., Science 247:1306-1310 (1990) wherein the authors indicate that there are two main approaches for studying the tolerance of an amino acid sequence to change. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selects or screens to identify sequences that maintain functionality. As the authors state, these studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require non-polar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described in Bowie et al, supra, and the references cited therein.

30

35

An isolated nucleic acid molecule encoding a protease protein homologous to the protein selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 can be created by introducing one or more nucleotide substitutions, additions or deletions  
5 into the coding nucleotide sequences according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 such that one or more amino acid substitutions, deletions or insertions are introduced into the encoded protein. Such mutations may be introduced by standard techniques, such as site-directed  
10 mutagenesis and PCR-mediated mutagenesis.

The term "functional equivalents" also encompasses orthologues of the *A. niger* protease protein. Orthologues of the *A. niger* protease protein are proteins that can be isolated from other strains or species and possess a similar or identical biological  
15 activity. Such orthologues can readily be identified as comprising an amino acid sequence that is substantially homologous to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171.

As defined herein, the term "substantially homologous" refers to a first amino acid or  
20 nucleotide sequence which contains a sufficient or minimum number of identical or equivalent (e.g., with similar side chain) amino acids or nucleotides to a second amino acid or nucleotide sequence such that the first and the second amino acid or nucleotide sequences have a common domain. For example, amino acid or nucleotide sequences which contain a common domain having about 60%, preferably 65%, more preferably  
25 70%, even more preferably 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identity or more are defined herein as sufficiently identical.

Also, nucleic acids encoding other protease family members, which thus have a nucleotide sequence that differs from a sequence selected from the group consisting of  
30 SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114, are within the scope of the invention. Moreover, nucleic acids encoding protease proteins from different species which thus have a nucleotide sequence which differs from a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting  
35 of SEQ ID NO: 58 to SEQ ID NO: 114 are within the scope of the invention.

Nucleic acid molecules corresponding to variants (e.g. natural allelic variants) and homologues of the protease DNA of the invention can be isolated based on their homology to the protease nucleic acids disclosed herein using the cDNAs disclosed herein or a suitable fragment thereof, as a hybridisation probe according to standard  
5 hybridisation techniques preferably under highly stringent hybridisation conditions.

In addition to naturally occurring allelic variants of the protease sequence, the skilled person will recognise that changes can be introduced by mutation into the nucleotide sequences of a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ  
10 ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 thereby leading to changes in the amino acid sequence of the protease protein without substantially altering the function of the protease protein.

In another aspect of the invention, improved protease proteins are provided. Improved  
15 protease proteins are proteins wherein at least one biological activity is improved. Such proteins may be obtained by randomly introducing mutations along all or part of the protease coding sequence, such as by saturation mutagenesis, and the resulting mutants can be expressed recombinantly and screened for biological activity. For instance, the art provides for standard assays for measuring the enzymatic activity of  
20 proteases and thus improved proteins may easily be selected.

In a preferred embodiment the protease protein has an amino acid sequence according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171. In another embodiment, the protease polypeptide is substantially homologous to  
25 the amino acid sequence according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 and retains at least one biological activity of a polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171, yet differs in amino acid sequence due to natural variation or mutagenesis as described above.

30 In a further preferred embodiment, the protease protein has an amino acid sequence encoded by an isolated nucleic acid fragment capable of hybridising to a nucleic acid according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ  
35 ID NO: 114, preferably under highly stringent hybridisation conditions.

Accordingly, the protease protein is a protein which comprises an amino acid sequence at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more homologous to the amino acid sequence shown in a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 and retains at least one  
5 functional activity of the polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171.

Functional equivalents of a protein according to the invention can also be identified e.g. by screening combinatorial libraries of mutants, e.g. truncation mutants, of the protein  
10 of the invention for protease activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or  
15 alternatively, as a set of larger fusion proteins (e.g., for phage display). There are a variety of methods that can be used to produce libraries of potential variants of the polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) Tetrahedron 39:3; Itakura et al. (1984) Annu. Rev. Biochem. 53:323; Itakura et al. (1984) Science 198:1056; Ike et al. (1983) Nucleic Acid Res. 11:477).  
20

In addition, libraries of fragments of the coding sequence of a polypeptide of the invention can be used to generate a variegated population of polypeptides for screening a subsequent selection of variants. For example, a library of coding  
25 sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by  
30 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the protein of interest.

Several techniques are known in the art for screening gene products of combinatorial  
35 libraries made by point mutations of truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are

amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the  
5 vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan (1992) Proc. Natl. Acad. Sci. USA 89:7811-7815; Delgrave et al. (1993) Protein Engineering 6(3):327-331).

10

In addition to the protease gene sequence shown in a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57, it will be apparent for the person skilled in the art that DNA sequence polymorphisms that may lead to changes in the amino acid sequence of the protease protein may exist within a given population. Such  
15 genetic polymorphisms may exist in cells from different populations or within a population due to natural allelic variation. Allelic variants may also include functional equivalents.

Fragments of a polynucleotide according to the invention may also comprise  
20 polynucleotides not encoding functional polypeptides. Such polynucleotides may function as probes or primers for a PCR reaction. Such polynucleotides may also be useful when it is desired to abolish the functional activity of a protease in a particular organism (knock-out mutants).

25 Nucleic acids according to the invention irrespective of whether they encode functional or non-functional polypeptides, can be used as hybridization probes or polymerase chain reaction (PCR) primers. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having a protease activity include, inter alia,  
30 (1) isolating the gene encoding the protease protein, or allelic variants thereof from a cDNA library e.g. from other organisms than *A. niger*; (2) in situ hybridization (e.g. FISH) to metaphase chromosomal spreads to provide precise chromosomal location of the protease gene as described in Verma et al., Human Chromosomes: a Manual of Basic Techniques, Pergamon Press, New York (1988); (3) Northern blot analysis for detecting expression of protease mRNA in specific tissues and/or cells and 4) probes  
35 and primers that can be used as a diagnostic tool to analyse the presence of a nucleic acid hybridisable to the protease probe in a given biological (e.g. tissue) sample.

Also encompassed by the invention is a method of obtaining a functional equivalent of a protease gene or cDNA. Such a method entails obtaining a labelled probe that includes an isolated nucleic acid which encodes all or a portion of the sequence  
5 according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or a variant thereof; screening a nucleic acid fragment library with the labelled probe under conditions that allow hybridisation of the probe to nucleic acid fragments in the library, thereby forming nucleic acid duplexes, and preparing a full-length gene sequence from the nucleic acid fragments in any labelled duplex to obtain  
10 a gene related to the protease gene.

In one embodiment, a protease nucleic acid of the invention is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more homologous to a nucleic acid sequence shown in a sequence selected from the group  
15 consisting of SEQ ID NO: 1 to SEQ ID NO: 57, a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or the complement thereof.

In another preferred embodiment a protease polypeptide of the invention is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,  
20 99%, or more homologous to the amino acid sequence shown in a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171.

#### Host cells

25 In another embodiment, the invention features cells, e.g., transformed host cells or recombinant host cells that contain a nucleic acid encompassed by the invention. A "transformed cell" or "recombinant cell" is a cell into which (or into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a nucleic acid according to the invention. Both prokaryotic and eukaryotic cells are included, e.g.,  
30 bacteria, fungi, yeast, and the like, especially preferred are cells from filamentous fungi, in particular *Aspergillus niger*.

A host cell can be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in a specific, desired fashion. Such  
35 modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may facilitate optimal functioning of the protein.

Various host cells have characteristic and specific mechanisms for post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems familiar to those of skill in the art of molecular biology and/or microbiology  
5 can be chosen to ensure the desired and correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product can be used. Such host cells are well known in the art.

10 Host cells also include, but are not limited to, mammalian cell lines such as CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, and choroid plexus cell lines.

If desired, the polypeptides according to the invention can be produced by a stably-  
15 transfected cell line. A number of vectors suitable for stable transfection of mammalian cells are available to the public, methods for constructing such cell lines are also publicly known, e.g., in Ausubel et al. (supra):

#### Antibodies

20 The invention further features antibodies, such as monoclonal or polyclonal antibodies, that specifically bind protease proteins according to the invention.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to  
25 include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')<sub>2</sub> fragments) which are capable of specifically binding to protease protein. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding of an intact antibody (Wahl et al., *J. Nucl. Med.* 24:316-325 (1983)). Thus, these fragments are preferred.

30 The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing the protease protein or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of protease  
35 protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal

antisera of greater specific activity.

- In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protease protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology (Kohler *et al.*, *Nature* 256:495 (1975);
- 5 Kohler *et al.*, *Eur. J. Immunol.* 6:511 (1976); Hammerling *et al.*, In: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981)). In general, such procedures involve immunizing an animal (preferably a mouse) with a protease protein antigen or, with a protease protein expressing cell. The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma
- 10 cell line may be employed in accordance with the present invention; however, it is preferably to employ the parent myeloma cell line (SP<sub>2</sub>O), available from the American Type Culture Collection, Rockville, Maryland. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands *et al.* (*Gastro-enterology* 80:225-232 (1981)). The hybridoma cells
- 15 obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the protease protein antigen. In general, the polypeptides can be coupled to a carrier protein, such as KtH, as described in Ausubel *et al.*, supra, mixed with an adjuvant, and injected into a host mammal.
- 20 In particular, various host animals can be immunized by injection of a polypeptide of interest. Examples of suitable host animals include rabbits, mice, guinea pigs, and rats. Various adjuvants can be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), adjuvant mineral gels such as aluminum hydroxide, surface active substances such as
- 25 lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*. Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of the immunized animals.
- 30 Such antibodies can be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD, and any subclass thereof. The hybridomas producing the mAbs of this invention can be cultivated *in vitro* or *in vivo*.
- Once produced, polyclonal or monoclonal antibodies are tested for specific recognition
- 35 of an protease polypeptide or functional equivalent thereof in an immunoassay, such as a Western blot or immunoprecipitation analysis using standard techniques, e.g., as



described in Ausubel et al., supra. Antibodies that specifically bind to protease proteins or functional equivalents thereof are useful in the invention. For example, such antibodies can be used in an immunoassay to detect protease in pathogenic or non-pathogenic strains of *Aspergillus* (e.g., in *Aspergillus* extracts).

5

Preferably, antibodies of the invention are produced using fragments of the protease polypeptides that appear likely to be antigenic, by criteria such as high frequency of charged residues. For example, such fragments may be generated by standard techniques of PCR, and then cloned into the pGEX expression vector (Ausubel et al., supra). Fusion proteins may then be expressed in *E. coli* and purified using a glutathione agarose affinity matrix as described in Ausubel, et al., supra. If desired, several (e.g., two or three) fusions can be generated for each protein, and each fusion can be injected into at least two rabbits. Antisera can be raised by injections in a series, typically including at least three booster injections. Typically, the antisera are checked for their ability to immunoprecipitate a recombinant protease polypeptide or functional equivalents thereof whereas unrelated proteins may serve as a control for the specificity of the immune reaction.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778 and 4,704,692) can be adapted to produce single chain antibodies against a protease polypeptide or functional equivalents thereof. Kits for generating and screening phage display libraries are commercially available e.g. from Pharmacia.

Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223, 409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 20791; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J.* 12:725-734.

Polyclonal and monoclonal antibodies that specifically bind protease polypeptides of functional equivalents thereof can be used, for example, to detect expression of a protease gene or a functional equivalent thereof e.g. in another strain of *Aspergillus*.

For example, protease polypeptide can be readily detected in conventional immunoassays of *Aspergillus* cells or extracts. Examples of suitable assays include, without limitation, Western blotting, ELISAs, radioimmune assays, and the like.

- 5 By "specifically binds" is meant that an antibody recognizes and binds a particular antigen, e.g., a protease polypeptide, but does not substantially recognize and bind other unrelated molecules in a sample.

- Antibodies can be purified, for example, by affinity chromatography methods in which  
10 the polypeptide antigen is immobilized on a resin.

- An antibody directed against a polypeptide of the invention (e.g., monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to  
15 detect the protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polypeptide. The antibodies can also be used diagnostically to monitor protein levels in cells or tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen or in the diagnosis of Aspergillosis..

20

- Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline  
25 phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable  
30 radioactive materials include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

- Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, e.g., hydrophilic regions. Hydrophobicity plots of the proteins of the invention can be used to identify hydrophilic regions.
- 35 The antigenic peptide of a protein of the invention comprises at least 7 (preferably 10, 15, 20, or 30) contiguous amino acid residues of the amino acid sequence of a

sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein.

- Preferred epitopes encompassed by the antigenic peptide are regions of protease that
- 5 are located on the surface of the protein, e.g., hydrophilic regions, hydrophobic regions, alpha regions, beta regions, coil regions, turn regions and flexible regions.

#### Immunoassays

- 10 Qualitative or quantitative determination of a polypeptide according to the present invention in a biological sample can occur using any art-known method. Antibody-based techniques provide special advantages for assaying specific polypeptide levels in a biological sample.
- 15 In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunocomplex is obtained.

- Accordingly, the invention provides a method for diagnosing whether a certain
- 20 organism is infected with *Aspergillus* comprising the steps of:
- Isolating a biological sample from said organism suspected to be infected with *Aspergillus*,
  - reacting said biological sample with an antibody according to the invention,
  - determining whether immunocomplexes are formed.

25

Tissues can also be extracted, e.g., with urea and neutral detergent, for the liberation of protein for Western-blot or dot/slot assay. This technique can also be applied to body fluids.

- 30 Other antibody-based methods useful for detecting protease gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). For example, protease-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify the protease protein. The amount of protease protein present in the sample
- 35 can be calculated by reference to the amount present in a standard preparation using a

linear regression computer algorithm. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect protease protein in a biological fluid. In this assay, one of the antibodies is used as the immuno-absorbent and the other as the enzyme-labeled probe.

5

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting protease protein with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled  
10 antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample.

15 Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labelled antibody/substrate reaction.

20 Besides enzymes, other suitable labels include radioisotopes, such as iodine ( $^{125}\text{I}$ ,  $^{127}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulphur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{112}\text{In}$ ), and technetium ( $^{99\text{m}}\text{Tc}$ ), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Specific binding of a test compound to a protease polypeptide can be detected, for  
25 example, in vitro by reversibly or irreversibly immobilizing the protease polypeptide on a substrate, e.g., the surface of a well of a 96-well polystyrene microtitre plate. Methods for immobilizing polypeptides and other small molecules are well known in the art. For example, the microtitre plates can be coated with a protease polypeptide by adding the polypeptide in a solution (typically, at a concentration of 0.05 to 1 mg/ml in a volume of  
30 1-100  $\mu\text{l}$ ) to each well, and incubating the plates at room temperature to 37  $^{\circ}\text{C}$  for 0.1 to 36 hours. Polypeptides that are not bound to the plate can be removed by shaking the excess solution from the plate, and then washing the plate (once or repeatedly) with water or a buffer. Typically, the polypeptide is contained in water or a buffer. The plate is then washed with a buffer that lacks the bound polypeptide. To block the free  
35 protein-binding sites on the plates, the plates are blocked with a protein that is unrelated to the bound polypeptide. For example, 300  $\mu\text{l}$  of bovine serum albumin

(BSA) at a concentration of 2 mg/ml in Tris-HCl is suitable. Suitable substrates include those substrates that contain a defined cross-linking chemistry (e.g., plastic substrates, such as polystyrene, styrene, or polypropylene substrates from Corning Costar Corp. (Cambridge, MA), for example) . If desired, a beaded particle, e.g., beaded agarose or  
5 beaded sepharose, can be used as the substrate.

Binding of the test compound to the polypeptides according to the invention can be detected by any of a variety of artknown methods. For example, a specific antibody can be used in an immunoassay. If desired, the antibody can be labeled (e.g., fluorescently  
10 or with a radioisotope) and detected directly (see, e.g., West and McMahon, J. Cell Biol. 74:264, 1977). Alternatively, a second antibody can be used for detection (e.g., a labeled antibody that binds the Fc portion of an anti-AN97 antibody). In an alternative detection method, the protease polypeptide is labeled, and the label is detected (e.g.,  
15 by labeling a protease polypeptide with a radioisotope, fluorophore, chromophore, or the like). In still another method, the protease polypeptide is produced as a fusion protein with a protein that can be detected optically, e.g., green fluorescent protein (which can be detected under UV light). In an alternative method, the protease polypeptide can be covalently attached to or fused with an enzyme having a detectable enzymatic activity, such as horse radish peroxidase, alkaline phosphatase, a-  
20 galactosidase, or glucose oxidase. Genes encoding all of these enzymes have been cloned and are readily available for use by those of skill in the art. If desired, the fusion protein can include an antigen, and such an antigen can be detected and measured with a polyclonal or monoclonal antibody using conventional methods. Suitable antigens include enzymes (e.g., horse radish peroxidase, alkaline phosphatase, and a-  
25 galactosidase) and non-enzymatic polypeptides (e.g., serum proteins, such as BSA and globulins, and milk proteins, such as caseins).

#### Epitopes, antigens and immunogens.

30 In another aspect, the invention provides a peptide or polypeptide comprising an epitope-bearing portion of a polypeptide of the invention. The epitope of this polypeptide portion is an immunogenic or antigenic epitope of a polypeptide of the invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein is the immunogen. These immunogenic  
35 epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic

epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, for instance, Geysen, H. M. et al., *Proc. Natl. Acad. Sci. USA* 81:3998-4002 (1984).

- 5 As to the selection of peptides or polypeptides bearing an antigenic epitope (i.e., that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, for instance, Sutcliffe, J. G. et al., *Science* 219:660-666 (1984). Peptides
- 10 capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (i.e., immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing
- 15 antibodies that bind to the mimicked protein; longer, soluble peptides, especially those containing proline residues, usually are effective. Sutcliffe et al., *supra* ?. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12
- 20 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

- Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a
- 25 polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. Sutcliffe et al., *supra*, at 663. The antibodies raised by antigenic epitope bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used
- 30 for tracking the fate of various regions of a protein precursor which undergoes posttranslation processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (e.g., about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays.
- 35 See, for instance, Wilson, I.A. et al., *Cell* 37:767-778 at 777 (1984). The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for

instance, by adsorption chromatography using methods well known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven,  
5 more preferably at least nine and most preferably between about 15 to about 30 amino acids contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 30 to about 50 amino acids, or any length up to and including the entire amino acid sequence of a  
10 polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (i.e., the sequence includes relatively hydrophilic residues and highly hydrophobic sequences  
15 are preferably avoided); and sequences containing proline residues are particularly preferred.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant  
20 means using nucleic acid molecules of the invention. For instance, a short epitope-bearing amino acid sequence may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies.

25 Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HAI polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four  
30 weeks. Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten et al. (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps  
35 involved in solid-phase methods.

A manual procedure allows 500-1000 or more syntheses to be conducted simultaneously. Houghten et al., *supra*, at 5134.

5 Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow, M. et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle, F.J. et al., *J. Gen. Virol.* 66:2347-2354 (1985).

10 Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemocyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde.

15 Animals such as rabbits, rats and mice are immunized with either free or carriercoupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 ug peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

25 Immunogenic epitope-bearing peptides of the invention, i.e., those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen et al., 1984, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an enzyme-linked immunosorbent assay. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen et al. with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides

30

35



covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide  
5 analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392 to Geysen (1990) describes a general method  
10 of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (i.e., a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092 to Geysen (1989) describes a method of detecting or determining a sequence of monomers which is a topographical  
15 equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. et al. (1996) on Peralkylated Oligopeptide Mixtures discloses linear C1-C7-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated  
20 oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods.

#### Removal or reduction of protease activity

25 The present invention also relates to methods for producing a mutant cell of a parent cell, which comprises disrupting or deleting a nucleic acid sequence encoding the protease or a control sequence thereof, which results in the mutant cell producing less of the protease than the parent cell.

30 The construction of strains which have reduced protease activity may be conveniently accomplished by modification or inactivation of a nucleic acid sequence necessary for expression of the protease activity in the cell. The nucleic acid sequence to be modified or inactivated may be, for example, a nucleic acid sequence encoding the  
35 protease or a part thereof essential for exhibiting protease activity, or the nucleic acid sequence may have a regulatory function required for the expression of the protease

from the coding sequence of the nucleic acid sequence. An example of such a regulatory or control sequence may be a promoter sequence or a functional part thereof, i.e., a part which is sufficient for affecting expression of the protease. Other control sequences for possible modification include, but are not limited to, a leader, a polyadenylation sequence, a propeptide sequence, a signal sequence, and a termination site.

Modification or inactivation of the nucleic acid sequence may be performed by subjecting the cell to mutagenesis and selecting for cells in which the protease producing capability has been reduced or eliminated. The mutagenesis, which may be specific or random, may be performed, for example, by use of a suitable physical or chemical mutagenizing agent, by use of a suitable oligonucleotide, or by subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the mutagenesis may be performed by use of any combination of these mutagenizing agents.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues.

When such agents are used, the mutagenesis is typically performed by incubating the cell to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions, and selecting for cells exhibiting reduced or no expression of protease activity.

Modification or inactivation of production of a protease of the present invention may be accomplished by introduction, substitution, or removal of one or more nucleotides in the nucleic acid sequence encoding the protease or a regulatory element required for the transcription or translation thereof. For example, nucleotides may be inserted or removed so as to result in the introduction of a stop codon, the removal of the start codon, or a change of the open reading frame. Such modification or inactivation may be accomplished by site-directed mutagenesis or PCR generated mutagenesis in accordance with methods known in the art.

Although, in principle, the modification may be performed *in vivo*, i.e., directly on the cell expressing the nucleic acid sequence to be modified, it is preferred that the modification be performed *in vitro* as exemplified below.

An example of a convenient way to inactivate or reduce production by a host cell of

choice is based on techniques of gene replacement or gene interruption. For example, in the gene interruption method, a nucleic acid sequence corresponding to the endogenous gene or gene fragment of interest is mutagenized in vitro to produce a defective nucleic acid sequence which is then transformed into the host cell to produce  
5 a defective gene. By homologous recombination, the defective nucleic acid sequence replaces the endogenous gene or gene fragment. It may be desirable that the defective gene or gene fragment also encodes a marker which may be used for selection of transformants in which the gene encoding the protease has been modified or destroyed.

10

Alternatively, modification or inactivation of the nucleic acid sequence encoding a protease of the present invention may be performed by established anti-sense techniques using a nucleotide sequence complementary to the protease encoding sequence. More specifically, production of the protease by a cell may be reduced or  
15 eliminated by introducing a nucleotide sequence complementary to the nucleic acid sequence encoding the protease which may be transcribed in the cell and is capable of hybridizing to the protease mRNA produced in the cell. Under conditions allowing the complementary antisense nucleotide sequence to hybridize to the protease mRNA, the amount of protease translated is thus reduced or eliminated.

20

It is preferred that the cell to be modified in accordance with the methods of the present invention is of microbial origin, for example, a fungal strain which is suitable for the production of desired protein products, either homologous or heterologous to the cell.

25 The present invention further relates to a mutant cell of a parent cell which comprises a disruption or deletion of a nucleic acid sequence encoding the protease or a control sequence thereof, which results in the mutant cell producing less of the protease than the parent cell.

30 The protease-deficient mutant cells so created are particularly useful as host cells for the expression of homologous and/or heterologous polypeptides. Therefore, the present invention further relates to methods for producing a homologous or heterologous polypeptide comprising (a) culturing the mutant cell under conditions conducive for production of the polypeptide; and (b) recovering the polypeptide. In the  
35 present context, the term "heterologous polypeptides" is defined herein as polypeptides which are not native to the host cell, a native protein in which modifications have been

made to alter the native sequence, or a native protein whose expression is quantitatively altered as a result of a manipulation of the host cell by recombinant DNA techniques.

- 5    The methods of the present invention for producing an essentially protease-free product is of particular interest in the production of eukaryotic polypeptides, in particular fungal proteins such as enzymes. The protease-deficient cells may also be used to express heterologous proteins of interest for the food industry, or of pharmaceutical interest.

10

#### Use of proteases in industrial processes

- The invention also relates to the use of the protease according to the invention in a selected number of industrial and pharmaceutical processes. Despite the long term  
15    experience obtained with these processes, the protease according to the invention features a number of significant advantages over the enzymes currently used. Depending on the specific application, these advantages can include aspects like lower production costs, higher specificity towards the substrate, less antigenic, less undesirable side activities, higher yields when produced in a suitable microorganism,  
20    more suitable pH and temperature ranges, better tastes of the final product as well as food grade and kosher aspects.

- In large scale industrial applications aimed at food or feed production, proteolytic enzymes are commonly used to improve aspects like protein solubility, extraction  
25    yields, viscosity or taste, texture, nutritional value, minimalisation of antigenicity or antinutritional factors, colour or functionality as well as processing aspects like filterability of the proteinaceous raw material. In these applications the proteinaceous raw material can be of animal or vegetable origin and examples include vegetable proteins such as soy protein, wheat gluten, rape seed protein, pea protein, alfalfa protein, sunflower  
30    protein, fabaceous bean protein, cotton or sesame seed protein, maize protein, barley protein, sorghum protein, potato protein, rice protein, coffee proteins, and animal derived protein such as milk protein (e.g. casein, whey protein), egg white, fish protein, meat protein including gelatin, collagen, blood protein (e.g. haemoglobin), hair, feathers and fish meal.

35

An important aspect of the proteases according to the invention is that they cover a

whole range of pH and temperature optima which are ideally suited for a variety of applications. For example many large scale processes benefit from relatively high processing temperatures of 50 degrees C or higher to control the risks of microbial infections. Several proteases according to the invention comply with this demand but at the same time exhibit no extreme heat stabilities so that they resist attempts to inactivate the enzyme by an additional heat treatment. The latter feature allows production routes that yield final products free of residual proteolytic activity. Similarly many feed and food products have slightly acidic pH values so that for their processing proteases with acidic or near neutral pH optima are preferred. A protease according to the invention complies with this requirement as well.

The specificity of endoproteases is usually defined in terms of preferential cleavages of bonds between the carboxyl of the amino acid residue in position P1 and the amino group of the residue in position P1' respectively. The preference may be conditioned predominantly either by P1 (e.g. positively charged residues in substrates for trypsin), by P1' (e.g. hydrophobic residues in cleavages by thermolysin) or by both P1 and P2 (e.g. specific cleavages between two positively charged residues by adrenal medulla serine endoprotease). In some cases more distant residues may determine the cleavage preference, e.g. P2 for streptococcal peptidase A. Some residues are known to influence cleavages negatively; it is well known that bonds with proline in position P1' are resistant to the action of many proteases. Most endoproteases cleave preferentially either in a hydrophobic environment or in the proximity of negatively charged residues. For example, industrially available endoproteases like chymotrypsin (obtained from bovine pancreas) or subtilisin, neutral metallo endoprotease or thermolysin (all obtained from *Bacillus* species) tend to favour cleavage "behind" hydrophobic amino acids like -Phe, -Leu and -Tyr. Other industrially available endoproteases are trypsin (obtained from bovine pancreas) preferring cleavage behind -Arg and -Lys and papain (a complex mixture of various enzymes including proteases obtained from papaya fruits) preferring cleavage behind -Arg.

In contrast, peptide bonds formed by small sized residues such as Ala, Gly, Ser, Thre as well as Ile and Pro are poor substrates (Keil, B et al.; *Protein Seq Data Anal* (1993) 5; 401-407). This situation has a profound implications for the pharmaceutical, the food and beverages, the agro and even the chemical industry. A protease according to the invention exhibits uncommon cleavage preferences.

The exopeptidases act only near the ends of polypeptide chains. Those acting at a free N-terminus liberate a single amino acid residue (socalled aminopeptidases) or a dipeptide or a tripeptide (socalled dipeptidyl-peptidases and tripeptidyl-peptidases) Those acting at a free C-terminus liberate a single residu (socalled carboxypeptidases) or a dipeptide (socalled peptidyl-dipeptidases) The carboxypeptidases are allocated to three groups on the basis of catalytic mechanism i.e. serine-type carboxypeptidases, metallocarboxypeptidases and cystein-type carboxypeptidases. Other exopeptidases are specific for dipeptides (socalled dipeptidases) or are able to cleave peptide linkages other than those of alpha-carboxyl or alpha- amino groups ( socalled omega peptidases). Examples of such new omega peptidases are the pyroglutamyl-peptidase and the acylaminoacyl-peptidase as identified in the present invention (see Table1, genes 18 and 45 respectively).

Typical examples of industrial application which depend on the use of pure endoproteases and in which the protease according to the invention can be expected to deliver a superior performance include the processing of materials of vegetable or animal origin. These processing steps can be aimed at modifying a large array of characteristics of either the crude material or the (partially) purified protein fraction. For example, these processing steps can be aimed at maximising product solubilities, filterabilities, separabilities, protein extraction yields and digestibilities or minimising toxicities, off-tastes and viscosities. Furthermore the treatment can be directed at altering physico-chemical characteristics of the crude material or the purified (or partially purified ) protein. These advantages apply not only if the endoprotease according to the invention is applied as a processing aid in industrial applications but also if applied as an active enzyme component in animal feed. Specifically the endoprotease according to the invention can be applied as bread improver in the bakery industry, e.g. to retard the staling of bread or to diminishing the viscosity of doughs. Or the endoprotease can be used in the beer and wine industry to prevent or to minimise the formation of undesirable protein hazes. Alternatively it can be used in the beer industry to optimise the protein extraction yields of cereals used in the preparation of the wort. Furthermore, it can also be advantageously used in the dairy industry as a milk clotting agent with superior characteristics or to optimise the texturising, foaming or setting characteristics of various milk components. Another application in the dairy industry is the use of the new protease in the preparation of Enzyme Modified Cheeses (EMC's).

- Moreover, various proteinaceous substrates can be subjected to an endoprotease according to the invention, usually in combination with other proteolytic enzymes to obtain hydrolysates for medical or non- medical applications. Here the endoprotease according to the invention is surprisingly effective in achieving a complete hydrolysis of the proteinaceous substrate so that even protease resistant parts are fully hydrolysed, the endoprotease is also surprisingly active in minimising the allergenicity of the final hydrolysate or in suppressing the formation of bitter off-tastes.
- 10 More specifically the endoprotease according to the invention is characterised by its preference for cleaving proteins at unusual peptide bonds, especially with the small size amino acid residues of Ala, Gly, Ser and Thr, or the residues Ile and Pro in either the P1 or the P1' position (Keil, B et al.; Protein Seq Data Anal (1993) 5; 401-407). As the result those fractions of the proteinaceous starting materials that resist hydrolysis
- 15 upon using prior art endoproteases, can be dissolved and hydrolysed using the endoprotease according to the invention. Non limiting examples of such protease resistant fractions include so-called extensins in plant materials and collagen, gelatin but also specific milk components in material of animal origin.
- 20 Various feedstuffs such as e.g. soybeans contain trypsin inhibitors. These proteins inhibit trypsin activity in the GI-tract of e.g. pigs and poultry. This trypsin inhibiting activity results in sub-optimal protein digestibility in these animals resulting in increased waste production and poor economics. This problem may partly be overcome by
- 25 toasting soybeans at high temperatures. Two different types of trypsin inhibitors have been identified in soybeans, i.e. the Bowman-Birk type trypsin inhibitors and the Kunitz type trypsin inhibitors.

This invention now provides an alternative way to degrade trypsin inhibiting activity over toasting, in that it provides a cysteine proteases (EC 3.4.22, table 1) capable of

30 cleaving at Leucine176-Aspartate177 peptide bond near the carboxyl-terminus of the Kunitz type trypsin inhibitor (as reviewed by Wilson (1988) in CRC Critical Reviews in Biotechnology 8 (3): 197-216). This results in inactivation of this trypsin inhibitor in soybean. It was surprisingly found that the cysteine proteases secreted by the fungus *Aspergillus niger* fulfilled these criteria far better than similar enzymes derived from

35 other organisms.

Proteases are also widely used in the art of cheese-making. In the production of cheese it is necessary to coagulate the cheese milk to be able to separate the cheese matters e.g. casein from the whey. Several milk coagulating enzymes, also referred to as coagulants, have been described and include (bovine) chymosin, bovine pepsin, porcine pepsin as well as microbial enzymes like *Rhizomucor miehei* protease, *Rhizomucor pusillus* protease and *Cryptonectria parasitica* protease. Chymosin can be obtained from calf stomachs but can also be produced microbially by for example *Kluyveromyces lactis*. All these enzymes are characterized by having specificity for the peptide bond between residue 105 (phenylalanine) and residue 106 (methionine) or the bond adjacent to that in  $\kappa$ -casein. This means that by employing these enzymes in cheese making, the  $\kappa$ -casein is split at the junction between para- $\kappa$ -casein and the macro-peptide moiety called glycomacropeptide (GMP) carrying the negative charges. When this occurs the macropeptide diffuses into the whey, its stabilizing effect on the solubility of the casein micelles is lost, and the casein micelles can start to aggregate once sufficient kappa-casein has been hydrolyzed. For further elaboration on the enzymatic coagulation of milk ( e.g. D.G. Dalgleish in Advanced Dairy Chemistry vol.1 ed by P.F. Fox, Elsevier, London, 1992.

The currently available coagulants allow for a rather high yield of cheese, however, it should be realised that due to the enormous volumes of cheese produced, an increased yield in the order of magnitude of tenths of percent points may constitute a substantial economical advantage. Consequently there is a great need in the art for coagulants with an (even slightly) improved yield.

Coagulants are characterized by their high substrate specificity, which is, however, dependent on pH and temperature. In a typical cheese making process the pH will change from the initial pH 6.3 to lower pH values in the range of 4.5-5.5, the end-value depends on the conditions used during the cheese production process. Some coagulants are more sensitive to pH changes than others. The *Rhizomucor pusillus* protease for example is more sensitive to pH changes than chymosin. Besides pH, also other parameters like temperature and water content may affect the protease specificity. It is well known that most coagulants show a changing substrate specificity with changing pH, resulting in altered proteolytic activity in later stages of the cheese making process. It is also well known that coagulants differ in the extent of casein proteolysis; they may also show differences in the peptide patterns produced during



proteolysis. These are relevant factors during cheese ripening and may affect cheese properties like taste, flavor and texture. In some cases coagulants give rise to undesired effects like the formation of bitter tasting peptides or off-taste. In addition, changes in proteolytic specificity may lead to a reduction in yield. Pepsin, a well known component in many bovine chymosin preparations, is an example of a protease that gives rise to lower yields and taste effects as compared to pure chymosin. There is still a need for coagulants which give rise to new, improved cheese texture and taste. Such new coagulants result in the accelerated development of taste and texture profiles related to cheese aging, therewith providing a substantial economical benefit.

10

It is well known that free amino acids are very important in taste and flavour generation. Especially the amino acids leucine, phenylalanine, methionine and valine play an important role in the generation of typical cheese taste and flavor components. The free amino acids are converted via fermentation by micro organisms that are added during the cheese manufacturing process into the actual flavor and taste generating compounds like methanediol, dimethyldisulphide, methylpropanoic acid and methylpropanal. Exo-peptidases play an important role in the generation of free amino acids. They can only be effective, however, when they are combined with an endo-protease of appropriate specificity. Appropriate combinations of exo- and endo-peptidases can be used in cheese making, resulting in the manufacture of cheeses with new and improved taste profiles.

15

20

The enzymes according to the invention may be used to hydrolyze proteinaceous materials of animal origin such as whole milk, skim milk, casein, whey protein or mixtures of casein and whey protein. Such mixtures of casein and whey protein may be used, for example, in ratios similar to those found in human milk. Furthermore, the enzyme mixture according to the invention may be used to hydrolyze proteinaceous materials of plant origin such as, for example, wheat gluten malted or unmalted barley or other cereals used for making beer, soy milk, concentrates or isolates thereof, maize protein concentrates and isolates thereof, and rice proteins.

25

30

Within the area of large scale industrial processes, some applications rely on the use of endoproteases only whereas in other applications combinations of endoproteases with exoproteases are essential. Typical examples which depend on the use of pure endoproteases and in which the protease according to the invention can deliver a

35

superior performance include applications like the processing of soy or peas or cereals proteins aimed at minimising viscosities or optimising foaming or other physico-chemical characteristics, bread improvers in the bakery industry also aimed at diminishing the viscosity of doughs, processing aids in the beer and wine industry aimed at the prevention of protein hazes or optimising the extraction yields of cereals, feed additives in the bio industry aimed at enhancing intestinal absorption or modulating microbial activities in the gut, processing aids in the dairy industry aimed at optimising the clotting, foaming or setting characteristics of various milk components. Moreover, v For specific market segments proteins derived from milk or soy or collagen are exposed to proteases to produce so-called protein hydrolysates. Although the main outlets for these protein hydrolysates are infant formula and food products for hospitalised persons, products intended for persons with non-medical needs, such as athletes or people on a slimming diet form a rapidly growing segment. In all of these applications protein hydrolysates offer attractive advantages such as lowered allergenicities, facilitated gastro-intestinal uptake, less chemical deterioration of desirable amino acids like glutamine and cysteine and finally, absence of proteinaceous precipitations in acid beverages during prolonged storage periods. All these advantages can be combined if the hydrolysate is offered as a mixture of di- and tripeptides. However, currently all commercially available hydrolysates are produced by combining several endoproteases. The latter approach implies a non-uniform and incomplete degradation of the protein. To obtain the desired mixture of di- and tripeptides, a hydrolysis process involving a combination of various di- and tripeptidylpeptidases would be ideal. Unfortunately, only few of these enzymes from food grade and industrially acceptable microorganisms are known, let alone industrially available. According to the invention several of highly useful di- and tripeptidylpeptidases are economically obtainable in a relatively pure state. Preferred are those di- or tripeptidylpeptidases that exhibit a low selectivity towards the substrate to be cleaved, i.e. exhibit minimal amino acid residue cleavage preferences only. Preferred are combinations of those di- or tripeptidylpeptidases that hydrolyse high percentage of the naturally occurring peptide bonds. Despite this high activity to naturally occurring peptide bonds, a total hydrolysis to free amino acids is prevented by the nature of the di- and tripeptidylpeptidases. Also preferred are those di- or tripeptidylpeptidases that are optimally active between pH 4 to 8 and exhibit adequate temperature stability. Adequate temperature stability implies that at least 40%, preferably at least 60%, more preferably between 70 and 100% of the initial hydrolytic activity survives after heating the enzyme together with the substrate for 1 hour at 50

degrees C.

Although the process towards an efficient production of mixtures di-or tripeptides or di-and tripeptides hinges on the availability of the enzymes according to the invention, the first enzyme incubation with the proteinaceous substrate will usually be an  
5 endoprotease. Preferably an endoprotease with a broad spectrum endopeptidase suited for the situation, e.g. subtilisin (Delvolase from DSM), neutral metallo protease (Neutrase from NOVO) or thermolysin (Thermoase from Daiwa Kasei) for the near neutral conditions and pepsin or aspergillopepsin (e.g. Sumizyme AP from Shin Nihon, Japan) for the acidic conditions. Aim of this first digestion is to improve the solubility, to  
10 reduce the viscosity and to reduce the heat setting characteristics of the water/protein mixture. Furthermore this pretreatment with an endonuclease is essential to create enough starting points for the di- and tripeptidylpeptidases hereby accelerating the process of di- or tripeptide formation. Optionally a protease intended for debittering of the hydrolysate can be included in this stage of the process or later, together with the  
15 di-or tripeptidylpeptidases.

Main aim of the latter hydrolysates is to minimize the allergenicity of the product or to facilitate gastro-intestinal uptake. In the production of such hydrolysates the use of dipeptidyl- and tripeptidyl-peptidases is of special importance as these offer an  
20 efficient way for producing hydrolysates..

Other applications in these food and feed industries totally rely upon combinations of one or more endoprotease(s) with one or more exoprotease(s). Such combinations of an endoprotease with an exoprotease are typically used in industries to improve  
25 aspects like taste and colour of the final product. The reason for this is that the development of taste and colour is largely dependent upon the presence of free amino acids. Free amino acids can not only be obtained by exoproteases such as carboxypeptidases and aminopeptidases but also by peptidyl-dipeptidases. If combined with endoproteases or even dipeptidyl-or tripeptidyl-peptidases, carboxypeptidases,  
30 aminopeptidases and peptidyl-dipeptidases can create larger quantities of free amino acids in less time. However, in all of these processes an uncontrolled release of amino acids or even non-proteinaceous components should be avoided to minimise undesirable side reactions.

35 Though free amino acids as such, can elicit a number of taste impressions, these taste impressions are very basic (bitter, sweet, sour and "umami") and the amino acid

concentration required for perceiving these tastes are high. Despite these high threshold values, free amino acids are able to create major sensory effects at much lower concentration ranges through a number of flavour enhancing mechanisms. One of these mechanism involves the combination of free amino acids with sugars in so-called Maillard reactions. Compared with free amino acids, with these Maillard products overwhelmingly complex flavour and odour systems can develop with threshold values that are several orders of magnitude lower than those recorded for the free amino acids. Maillard products are formed at elevated temperatures usually during cooking, baking or roasting when preparing food or feed products. During these treatments both colour and a large array of aromas develop. In these reactions amino groups react with reducing compounds as a first step and ultimately leading to a whole family of reaction pathways. In foods or feeds the amino compounds involved are predominantly free amino acids which are released from the proteinaceous raw material by various proteases and the required reducing compounds primarily represent reducing sugars. The implication is that during the processing of the raw material undesired release of free amino acids and sugars should be avoided to minimise off tastes that could be generated during subsequent heating steps as e.g. during spray drying or sterilisation. The latter notion emphasises once more the benefits of superior purity and low in-use costs of the enzyme according to the invention.

Apart from Maillard reactions, amino acids can also undergo important chemical transitions at ambient temperatures. The latter type of transitions are enzyme dependent and are quite common in fermented foods such as beer, yogurt, cheese ripening and meat and wine maturation processes. In these fermentation processes, free amino acids are liberated from the raw materials used by the proteases added or by proteolytic enzyme activity from the raw material or the microbial starters used. During the maturation phase microbial metabolic activity then converts the free amino acids into derivatives with increased sensoric properties. For example, L-leucine, L-isoleucine and L-valine lead to the formation of valuable fusel alcohols like amylalcohols and isobutanol in beer fermentation. Similarly cheese volatiles such as methanethiol and dimethyldisulphide have been traced back to the occurrence of methionine in cheese as well as methylpropanoic acid and methylpropanal to valine. Finally the free amino acid glutamate and can create strong savoury enhancing effects because of its synergy with the breakdown products of RNA, so-called 5'-ribonucleotides. If combined with proper concentrations of 5'-ribonucleotides such as

5'-IMP and 5'-GMP, the detection threshold of the umami taste generated by glutamate is known to be lowered by almost two orders of magnitude.

In order to obtain pronounced and precise taste effects in all of these processes, the proteinaceous substrates should be hydrolysed using a combination of an endo- and an exoprotease, wherein at least one of the endo or exoprotease, preferably both the endo- and exoprotease, are pure and preferably selective towards a specific set of amino acid(s) or preferentially release the preferred amino acid(s). So preferred proteases are characterised by a high selectivity towards the amino acid sequences that can be cleaved which notion makes the enzyme category in *Aspergillus* known as "maturases" of particular importance.

Apart from the food and feed industries, proteases are also commonly applied by the chemical, pharmaceutical, diagnostic and personal care industries.

In the personal care industry proteases are used to create peptides which are added to a variety of products to improve aspects like skin feel, gloss or protection. Moreover there is a new tendency towards direct topical application of the protease. Very similar to the enzyme use in the leather industry, the prime aim in the latter application is to clean, dehair and soften the skin .

In the chemical and pharmaceutical industry proteases are being developed as valuable tools in producing costly ingredients or intermediates. In these industries proteases are not only used because of their hydrolytic capacity but also because of their capacity to synthesise peptides from natural or non-natural amino acids. The latter option is clearly demonstrated by the possibility to synthesize aspartame from its amino acid based building blocks by using an endoprotease like thermolysin.

Unlike the situation in the food and feed industry, the stereo- and regioselectivity of proteases are also considered important assets although unusual reaction conditions may be needed to accomplish the desired chemical transformation. Typical examples of the application of proteases in this industry include the use of endoproteases, aminopeptidases as well as carboxypeptidases in the production of various intermediates for drugs like insulin, antibiotics, renin and ACE-inhibitors An overview of such uses is presented in Industrial Biotransformations, A.Liese, K. Seelbach, C. Wandrey, Wiley-VCH; ISBN 3-527-30094-5.

In view of the desired specificities, stereo- and regioselectivities, the absence of side activities and resistance to unusual reaction conditions such as high solvent

concentrations, the improved performance of the protease according to the invention offers substantial advantages.

From a pharmaceutical point of view the role of proteases is illustrated by a substantial number of references in Martindale's, "The Extra Pharmacopoeia" (Pharmaceutical Press, London, UK). Moreover the important role of very specific proteases in regulating all kinds of biological processes is illustrated by the fact that many hormones become active only after the processing of an, mostly inactive, precursor molecule by such a very specific protease. Inhibitors active towards certain categories of such specific proteases have been implicated in the development of all kinds of new drugs. Therefore new and effective inhibitors for protease may now be identified using the sequences provided herein.

The entire disclosure of each document cited herein is hereby incorporated by reference

**Table 1**

SEQ ID number			Function of encoded protein	EC number
Gene	cDNA	Protein		
1	58	115	Pepsin A <sub>3</sub>	EC3.4.23.1
2	59	116	Metalloprotease	EC3.4.24.56
3	60	117	acylaminoacyl-peptidase	EC3.4.19.1
4	61	118	Tripeptidylaminopeptidase	EC3.4.14.-
5	62	119	serine carboxypeptidase	EC3.4.16.6
6	63	120	Serine endoprotease	EC3.4.21.-
7	64	121	Carboxypeptidase Y	EC3.4.16.5
8	65	122	aspergillopepsin II - hom	EC3.4.23.19
9	66	123	Tripeptidyl peptidase	EC3.4.14.9
10	67	124	Tripeptidyl peptidase	EC3.4.14.9
11	68	125	aspergillopepsin II - hom	EC3.4.23.19
12	69	126	Tripeptidyl peptidase	EC3.4.14.9
13	70	127	Metalloprotease	EC3.4.24.-
14	71	128	aspergillopepsin I	EC3.4.23.18
15	72	129	Pepsinogen E	EC3.4.23.25
16	73	130	aspergillopepsin I - hom	EC3.4.23.18
17	74	131	aspergillopepsin II	EC3.4.23.19
18	75	132	Pyro-Glu peptidase	EC3.4.19.3
19	76	133	dipeptidyl peptidase	EC3.4.14.2
20	77	134	Secr. aminopeptidase	EC3.4.11.10
21	78	135	alkaline D-peptidase	EC3.4.16.4
22	79	136	Carboxypeptidase	EC3.4.16.1
23	80	137	Carboxypeptidase	EC3.4.16.1
24	81	138	Carboxypeptidase-II	EC3.4.16.1
25	82	139	aspartic proteinase	EC3.4.23.-
26	83	140	Tripeptidyl peptidase	EC3.4.14.9
27	84	141	Carboxypeptidase	EC3.4.16.1
28	85	142	cysteine proteinase	EC3.4.22.-
29	86	143	Metallo-carboxypeptidase	EC3.4.17.-

SEQ ID number			Function of encoded protein	EC number
Gene	cDNA	Protein		
30	87	144	Subtilisin hom.	EC3.4.21.62
31	88	145	Carboxypeptidase Y	EC3.4.16.5
32	89	146	Metalloprotease	EC3.4.24.-
33	90	147	Carboxypeptidase Y	EC3.4.16.5
34	91	148	Metalloprotease	EC3.4.24.-
35	92	149	Tripeptidyl peptidase	EC3.4.14.9
36	93	150	Aspartic protease	EC3.4.23.24
37	94	151	Aspartic protease	EC3.4.23.24
38	95	152	Pepsin A <sub>3</sub>	EC3.4.23.1
39	96	153	Aspartic protease	EC3.4.23.24
40	97	154	Aspartic protease	EC3.4.23.24
41	98	155	Kex	EC3.4.21.61
42	99	156	Serine protease	EC3.4.21.-
43	100	157	Glutamyl endoprotease	EC3.4.21.82
44	101	158	aspergillopepsin II - hom	EC3.4.23.19
45	102	159	acylaminoacyl-peptidase	EC3.4.19.1
46	103	160	Tripeptidylaminopeptidase	EC3.4.14.-
47	104	161	serine carboxypeptidase	EC3.4.16.6
48	105	162	Gly-X carboxypeptidase	EC3.4.17.4
49	106	163	aspartic proteinase	EC3.4.23.-
50	107	164	Tripeptidyl peptidase	EC3.4.14.9
51	108	165	Carboxypeptidase-I	EC3.4.16.1
52	109	166	serine carboxypeptidase	EC3.4.16.6
53	110	167	serine carboxypeptidase	EC3.4.16.6
54	111	168	Secr. aminopeptidase	EC3.4.11.10
55	112	169	Prolyl endopeptidase	EC3.4.21.26
56	113	170	aspergillopepsin I - hom	EC3.4.23.18
57	114	171	Aminopeptidase	EC 3.4.11.-



## **EXAMPLES**

### **Example 1**

#### **5     Assaying Proteolytic Activity and Specificity**

Protease specificity may be explored by using various peptide substrates. Synthetic substrates are widely used to detect proteolytic enzymes in screening, in fermentation, during isolation, to assay enzyme activity, to determine enzyme concentrations, to investigate specificity and to explore interaction with inhibitors. Peptide p-nitroanilides  
10     are preferably used to assay protease activity as the activity can be followed continuously and therefore allow for kinetic measurement. The cleavage of peptide p-nitroanilides can be followed by measuring the increase in adsorption at 410nm upon release of the 4-nitroanilide. Paranitroanilide substrates are generally used for serine and cysteine proteases. In addition peptide thioesters and 7-amino-p-methylcoumarin  
15     peptide derivatives are used. Peptide thioesters are very sensitive substrates for serine and metalloproteases that exhibit relatively high turnover rate since the thioesterbond is easier to cleave than the amide bond. Cleavage of thioesters may be followed with a thiol reagent such 4,4-dithiopyridine (324nm) or 5,5-dithiobis 2-nitrobenzoic acid (405nm). The same increased turnover rate is usually observed for the cleavage of  
20     ester bonds relative to amide bond. The most well known substrates to assay the esterase activity of proteases are p-nitrophenol derivatives. The release of p-nitrophenol can be monitored at different wavelength dependent on the pH that is used, eg around neutral pH a wavelength of 340nm is used while above pH 9 monitoring is done around 405nm. In addition the hydrolysis of esters can also be followed by titration using pH-stat equipment. In case of qualitative measurement of esterase activity pH sensitive  
25     dyes can be applied.

As an alternative, peptides may be attached to a fluorescent leaving group. Proteolysis is accompanied by an increase in fluorescence when monitored at the appropriate  
30     wavelengths. Peptidyl 2-naphtylamides and peptidyl 4-methyl-7-coumarylamides are commonly used. The release of for example 7-amino-4 methylcoumarin is measured using an excitation wavelength of 350nm and an emission wavelength of 460nm. The use of 7-amino-4 trifluoromethylcoumarin has the advantage of the leaving group being both chromogenic (absorbtion 380nm) as well as flourogenic (excitation 400nm,  
35     emission 505nm). When it is essential that at both sides of the scissile bond an amino

acid is present, the introduction of a group that quenches the fluorescence might be useful. The general characteristics of such substrates is that the peptide sequence separates a fluorescent donor group from an acceptor group that acts as a quencher of of fluorescence. Cleavage of a peptide bond between the quenching group and the fluorophore will lead to substantial increase in fluorescence. Several donor-acceptor pairs have been reported, including o-aminobenzoic acid (Abz) as the donor and 2, 4 dinitrophenyl (Dnp) as the acceptor, 5-[(2'aminoethyl)-amino]naphtalenesulfonic acid (EDANS) as the donor and 4-[[4'-(dimethylamino)phenyl]azo]-benzoic acid (DABCYL) as the acceptor. The Abz/EDDnp represents a very convenient donor-acceptor pair since after total hydrolysis, the fluorescence increases by a factor 7 to 100 and the absorption spectrum of EDDnp does not change with pH. Moreover, the peptide sequence may contain up to 10 residues without loss of the quenching effect. As the size of the connecting peptides increases, the position of the scissile bond may become less specific. Therefore in addition to establishing whether proteolysis occurred, additional analysis of the products may be required. This may be done by analysing and separating the produced peptides by HPLC and determining the the amino acid sequence of the fragments. In addition the peptide composition of the digest may be directly analysed by using combined HPLC / mass-spectroscopy technique.

20

Apart from using peptides of a defined sequence also synthetic peptide libraries can be used to study protease specificity. Peptides are synthesised by solid phase synthesis in random or semi-random fashion. E.g. Meldal et al. (PNAS USA 91,3314,1994) report the preparation of a family of protease substrates by starting with H-Lys(Abz)-resin, extending the resin with peptides to a length of six aminoacids, and finally coupling Tyr(NO<sub>2</sub>) to the peptides. Each resin bead has a unique sequence and on treatment with the proteases the most susceptible becomes fluorescent as the Tyr(NO<sub>2</sub>) containing peptide is released. Sequence analysis of the peptides on the susceptible will give information on the specificity of the protease.

30

Protease activity is usually expressed in units. Generally the international standard unit (IU) is defined as the amount of enzyme, which under defined conditions transfers one micromole of substrate per minute. Specifically with proteases the IU would relate to the hydrolysis of one micromole peptide bond per minute. However in the case of protease units deviations of the international definition are more rule than exception. Where with the model peptides, which are cleaved specifically at one bond the

35

- calculation of IU's is strait-forward, for proteinacious substrates where the protease can cleave at various positions to a various degree many deviating unit definition are used. Apart from a definition of the unit used, any hydrolysis experiment requires an adequate description of the conditions under which the units are measured. Such
- 5 conditions comprise e.g. the substrate concentration, the enzyme-substrate ratio, the pH and temperature. Typical assays for determining the specific activity of a proteases comprise a proteinacious substrate such as for example denaturated hemoglobin, insulin or casein. The polypeptide substrate is digested by a protease at fixed conditions during a fixed time interval. Undigested and large polypeptides are
- 10 precipitated with TCA and TCA soluble product is determined by measuring absorbance at 220 or 280nm, or by titrating the soluble peptides with folin reagent, ninhydrin, fluoro 2,4, dinitrobenzene/ dansylchloride, TNBS method or fluorescein. Instead of labeling the product after hydrolysis, also polypeptide substrates may be used which are already labeled by specific dyes or fluorophores such as for example
- 15 fluorescein. In addition standard methods of amino acid analysis may be applied using standard laboratory analyzers. In order to hget insight in the size distribution of the peptides generated by a protease, gel chromatography experiments may be performed. In addition to this HPLC using reverse phase techniques is applied in order to get better resolution of the peptide patterns generated by the protease.
- 20 The course of the hydrolysis of proteinacious substrates is usually expressed in the degree of hydrolysis or DH. In case pH-stat is used to follow the course of hydrolysis, DH can be derived from the base consumption during hydrolysis (Enzymatic Hydrolysis of Food Protein, J. Adler-Nissen, 1986, Elsevier Apllied Science Publishers LTD). The DH is related to various useful functional properties of the hydrolysate such as
- 25 solubility, emulsifying capacity, foaming and foam stability, whipping expansion, organoleptic quality. In addition taste is an important aspect of food grade hydrolysates. Bitterness can be a major problem in protein hydrolysates. Termination of the hydrolysis reaction may be done by changing the pH, heat inactivation, denaruring agents such as SDS, acetonitril etc.
- 30
- Polypeptides shown in Tabel 1 were expressed and at least partially purified according to standard procedures known in the art. They were analysed according to al least one of the methods described above and found to have the activities listed in Table 1.
- 35 Example 2

**Direct determination of the  $k_{cat}/K_m$  ratio for protease substrates.**

Synthetic substrates can be used to monitor the enzymatic activity during purification, to determine enzyme concentration, to determine inhibition constants or to investigate the substrate specificity. Determination of the  $k_{cat}/K_m$  ratio gives a measurement of the substrate specificity. It allows to compare the specificity of different substrates for a same enzyme or the comparison of hydrolysis rates with different enzymes cleaving the same substrate. This ratio has a unit of a second order rate constant and is then expressed as  $1/(\text{concentration} \cdot \text{time})$ . Substrates having a  $k_{cat}/K_m$  ratio in the range  $10.5\text{--}10.6 \text{ M}^{-1} \cdot \text{sec}^{-1}$  are considered to be very good substrates i.e good affinity and rapid turn-over. However, some substrates may be very specific with  $k_{cat}/K_m$  values in the  $10.4 \text{ M}^{-1} \cdot \text{sec}^{-1}$  range.

The  $k_{cat}/K_m$  ratio may be calculated after determination of individual parameters. In that case,  $K_m$  and  $V_m$  may be obtained from various linear plots (e.g Hanes or Cornish-Bowden method) or by a non-linear regression method. Knowing that  $V_m = k_{cat} \cdot E_t$  (where  $E_t$  is the final active enzyme concentration then  $k_{cat} = V_m/E_t$ ). Determination of the  $k_{cat}/K_m$  ratio by the previous method may be prevented when product or substrate inhibition occur, or when substrate precipitates at high concentration. It is however possible to obtain an accurate value of the  $k_{cat}/K_m$  ratio working under first-order conditions i.e at a substrate concentration far below the estimated  $K_m$ . In these conditions, the Michaelis-Menten equation:  $v = (V_m \cdot S)/(K_m + S)$  becomes:

$$v = (V_m \cdot S)/K_m \text{ since } S \ll K_m$$

$$\text{or } v = (V_m/K_m) \cdot S = k_{obs} \cdot S = -dS/dt$$

which integrates as  $\ln S = -k_{obs} \cdot t + \ln S_0$  where  $S_0$  is the starting substrate concentration and  $S$  the substrate concentration at a given time. The velocity is proportionnal to the substrate concentration. In other words, the substrate hydrolysis obeys a first order process with  $k_{obs}$  as the first-order rate constant.  $k_{obs} = V_m/K_m = (k_{cat} \cdot E_t)/K_m$  since  $V_m = k_{cat} \cdot E_t$

A continuously recording of the substrate hydrolysis will allow the graphical determination of  $k_{obs}$  from the  $\ln S$  vs time graph. The  $k_{cat}/K_m$  ratio is simply inferred from  $k_{obs}$  providing the active enzyme concentration is known:

$$k_{cat}/K_m = k_{obs}/E_t$$

Assay method: Use a starting substrate concentration far below the estimated  $K_m$  and a low enzyme concentration to allow the substrate hydrolysis to be recorded. You will obtain a first-order curve for the product generation:

After total hydrolysis of the substrate, the absorbance (or fluorescence units) of the

product will allow the accurate determination of  $S_0$ , since  $P_t = S_0 - k_{obs}t$ .  $k_{obs}$  is determined from the slope of the  $\ln S$  vs time graph or alternatively using a fitting software (Enzfitter, SigmaPlot...).

- 5 NB: Do not forget to calculate the substrate concentration for any given time from the product concentration ( $S = S_0 - P$ ) since plotting  $P$  vs time would not provide the correct  $k_{obs}$  ( $dP/dt = k_{obs}S$  does not integrate in the same way).

Alternatively, one can measure successive  $t_{1/2}$  (half-time) from the product apparition curve since in a first order process:

$$t_{1/2} = \ln 2 / k_{obs} = 0.693 / k_{obs} \text{ then } k_{obs} = 0.693 / t_{1/2}$$

- 10 Using this method allows to check that you have a true first order decay (identical values for the successive  $t_{1/2}$ ).

### Example 3

#### Inactivating protease genes in *Aspergillus*

- 15 The most convenient way of inactivating protease genes in the genome of *Aspergillus* is the technique of gene replacement (also called "one step gene disruption"). The basics of this technique have been described by Rothstein RJ in Meth. Enzymol. 101, p202, 1983. Essentially the technique is based on homologous recombination of transformed DNA fragments with the genomic DNA of a fungal cell. Via double
- 20 crossover the gene to be inactivated is (partly) replaced by the DNA fragment with which the cell is transformed. Preferably the transformed DNA fragment contains a selectable marker gene for *Aspergillus niger*. Basically the manipulation of DNA and generation of a inactivation construct are done using general molecular biological techniques. First, genomic DNA is isolated from the *Aspergillus niger* strain that is later
- 25 on used for the inactivation of the protease gene. Genomic DNA of *A. niger* can be isolated by any of the techniques described, e.g. by the method described by de Graaff et al. (1988) Curr. Genet. 13, 315-321, and known to the person skilled in the art. This genomic DNA is used as template for amplification of the flanking regions of the protease gene by using the polymerase chain reaction (PCR; Sambrook et al. (1989)
- 30 Molecular cloning, a laboratory manual, 2nd edition, Cold Spring Harbor Laboratory Press, New York). With flanking regions is meant here the non-coding regions upstream and downstream of the protease gene that will be inactivated. Preferably the flanking regions should each be more than 1.0 kb in length.

- Two single stranded DNA oligonucleotides are used for the priming of the PCR
- 35 amplification of each flanking region. For the 5'-flanking region, one primer is homologous to a DNA sequence upstream of the start of the coding sequence of the

protease gene. Preferably the homologous region is located more than 1.0 kb upstream of the translation start site. The second primer is homologous to the complementary and inverse DNA sequence located immediately upstream of the coding sequence of the protease gene.

- 5 For the 3'-flanking region, one primer is homologous to the DNA sequence immediately downstream of the coding sequence of the protease gene. The second primer is homologous to a complementary and inverse DNA sequence located preferably more than 1.0 kb downstream of the coding sequence of the protease gene.
- The DNA sequence included in all primers and homologous to the *A. niger* genome
- 10 should be minimally 15 nucleotides in length, preferably more than 18 nucleotides in length. Most conveniently, all primers should contain a DNA sequence coding for the recognition site of suitable restriction enzymes upstream of the sequence that is homologous to the *A. niger* genome. These extra recognition sites facilitate the cloning process.
- 15 Both primers and the genomic DNA of *A. niger* are used in a PCR reaction under conditions known to those skilled in the art. The annealing temperature of the primers can be calculated from the part of the DNA sequence that is homologous to the *A. niger* genome. Both fragments containing the 5'-flanking region and the 3'-flanking region are cloned into a vector that can be propagated in *E. coli* using general
- 20 molecular biological techniques. A gene that can be used as selection marker in *Aspergillus niger* is then cloned in between the two flanking regions. Most conveniently the marker gene is under control of a promoter that comes to expression in *A. niger*, preferably an endogenous *A. niger* promoter. The orientation of the insertion of the marker gene is preferably in the same direction as the original protease gene. The final
- 25 inactivation fragment contains the 5'-flanking region, a selection marker gene preferably under control of a *A. niger* endogenous promoter, and the 3'-flanking region, all in this direction and orientation. DNA of the final construct is cloned into a vector that can be propagated in *E. coli*.
- The inactivation construct is digested with suitable restriction enzymes to remove the
- 30 *E. coli* vector sequences and the inactivation fragment is isolated using standard techniques (Sambrook et al. (1989) *Molecular cloning, a laboratory manual*, 2nd edition, Cold Spring Harbor Laboratory Press, New York). Finally *Aspergillus niger* is transformed with the inactivation fragment using a method described in literature, e.g. by the method described by Kusters-van Someren et al. (1991) *Curr. Genet.* 20, 293-
- 35 299. Transformed cells are selected by plating the transformation mixture on agar plates that are selective for growth of *Aspergillus niger* strains that do express the

- marker gene. After purification of the transformed *Aspergillus* strains by replica plating, a representative number of strains is analysed by Southern blotting using standard methods (Sambrook et al. (1989) Molecular cloning, a laboratory manual, 2nd edition, Cold Spring Harbor Laboratory Press, New York). Therefore, genomic DNA of
- 5 mycelium of transformed strains is isolated and digested with suitable restriction enzymes. Restriction fragments are separated using agarose gelelectrophoresis, blotted to nitrocellulose membranes and probed with a labeled fragment of the marker gene. Hybridization and washing is under stringent conditions. Strains that contain labeled restriction fragments of the correct length are considered correct.
- 10 Using this method *A. niger* strains can be selected with an inactivated protease gene of choice.

#### Example 4

##### **Isolating proteases by ion exchange chromatography**

- 15 Small quantities of the protease encoded by the nucleotide sequence as provided herein are obtained by constructing an expression plasmid containing the relevant DNA sequence, transforming an *A.niger* strain with this plasmid and growing the *A. niger* strain in a suitable medium. After collecting the broth free of contaminating cells, the protease sought can be purified.
- 20 To isolate the protease as encoded by the provided nucleotide sequence in an essentially pure form several strategies can be followed. All of these strategies have been adequately described in the relevant scientific literature ( see for example the Protein Purification Handbook ,18-1132-29 Edition AA as published by Amersham Pharmacia Biotech, Uppsala, Sweden). A procedure which is applicable to purify
- 25 proteases from complex mixtures is provided hereunder. Essential is that a suitable assay is available that is selective towards the enzyme characteristics sought. For proteases typically a chromogenic, synthetic peptide substrate is used as described in Example 1. Such peptide substrates can be selective towards endoproteases, carboxypeptidases, aminopeptidases or omegapeptidases. In Example 11 the
- 30 selectivity towards a specific tripeptidylpeptidase is described. By choosing the right amino acid residues in the relevant synthetic peptide, proteases with the desired specificity can be selected.

- First it should be determined whether the protease is excreted into the medium,
- 35 depending on the expression system chosen to produce the protease, it may be excreted or contained in the cell. If the protease is excreted into the fermentation

- medium, the producing cells or fragments of these cells have to be removed by centrifugation or filtration and the resulting clear or clarified medium is the starting point for further purification. In those cases in which the protease sought is not excreted, the producing cells have to be disrupted to enable purification of the protease. In such
- 5 cases the collected cell mass is best ground with an abrasive, milled with beads, ultrasonicated or subjected to a French press or a Manton-Gaulin homogeniser and then filtered or centrifuged. In case the protease is hydrophobic or membrane bound, the addition of a non-ionic detergent to solubilise the protease before the filtering or centrifugation step may be necessary.
- 10 After the clarification step, a three phase purification strategy can be applied to obtain the unknown proteases in an essentially pure state. In all or some of these three phases addition of a detergent may be necessary.
- In the first or capture phase the target protease is isolated, partly purified and concentrated. During the subsequent intermediate purification phase most of the bulk
- 15 impurities are removed and in the final polishing phase trace amounts of remaining impurities of larger amounts of closely related substances are removed and the enzyme is dissolved in the desired buffer. Depending upon the nature and physical properties of the protease at hand, a person skilled in the art is capable of optimising the three phases using slightly modified versions of the different protein binding
- 20 materials and apply these under somewhat changed conditions. However, in all cases a selective analytical assay is indispensable as it will enable the continuous monitoring of the increasingly purified proteolytic activity. Analytical assays suitable for the purpose include the use of chromogenic peptide substrates as has been mentioned before.
- 25 In the first capturing phase of the purification a strong ion exchange resin of the anionic type is preferably used to apply the clarified and desalted enzyme containing medium. To guarantee binding of the desired proteolytic activity to the resin, three or four different pH values of medium and resin are tested under low conductivity conditions. In these tests the resin is always equilibrated with a buffer of the same pH value and
- 30 conductivity as the enzyme containing medium. The medium is then applied to the column under pH conditions which has been shown to allow adequate binding of the protease to the resin i.e. none of the desired enzymatic activity can be traced back in the run-through medium. Subsequently the desired enzymatic activity is eluted from the ion exchange resin using a continuous salt gradient which starts with the resin
- 35 equilibration buffer and ends with this buffer to which 1 mol/liter of NaCl has been added. Eluted fractions containing the desired activity according to the assay are



pooled and then prepared for an additional purification step. This additional purification step depends on the purity of the desired enzyme in the pooled fraction : if almost pure, an additional gel filtration step will prove to be adequate; if not almost pure, chromatography over a hydrophobic interaction resin is applied followed by a gel  
5 filtration step.

Chromatography over a hydrophobic interaction resin is carried out by first increasing the salt content of the pooled fraction obtained from the ion exchange resin to 4mol/liter of NaCl and by removing any precipitate formed. If the resulting clear fraction doesnot  
10 contain the desired activity, this activity is obviously present in the precipitate and can be recovered in an essentially pure state. If the resulting clear fraction still exhibits the desired activity in the assay, then the liquid is applied as such to a phenyl  
sepharose resin (Pharmacia) equilibrated in this high salt buffer with an identical pH and conductivity. If the desired enzymatic activity binds to the phenyl sepharose resin,  
15 the activity is eluted with a continuous gradient of decreasing salt content followed by a salt free wash and, if necessary, with a chaotropic agent. Like before those fractions from the gradient that exhibit activity in the assay are pooled and finally subjected to a  
gelfiltration step. If the desired enzymatic activity doesnot bind to the phenyl sepharose resin, many of the contaminants will, so the desired proteolytic activity as present in the  
20 void volume of the column requires only an additional ultrafiltration step to obtain the activity in a more concentrated form before applying it to the gelfiltration column. The gelfiltration column doesnot only remove trace contaminations but also brings the  
enzyme in the buffer which is required by subsequent use.

25 Although this method is generally applicable for the isolation and purification of proteases according to the invention, a more specific isolation technique is described in Example 4. In that Example the isolation of an *Aspergillus* protease is described by using immobilised bacitracin, a peptide antibiotic known for its selective interaction with various types of proteases.

30

Example5.

#### **Isolating proteases by affinity chromatography**

An alternative method for purifying small quantities of protease is by affinity chromatography. To obtain the protease in a purified form, a 100 milliliter culture is  
35 grown in a well aerated shake flask. After centrifugation to remove any non-soluble matter, the supernatant is applied to a 40 milliliter bacitracin-Sepharose column

equilibrated with 0.05 mol/litre sodium acetate pH 5.0. Proteases bound to the column are eluted using the acetate buffer supplemented with 1 mol/litre of NaCl and 10% (v/v) isopropanol (J.Appl.Biochem.,1983 pp420-428). Active fractions are collected, dialysed against distilled water and applied on a 20 milliliter bacitracin-Sepharose column, again  
5 equilibrated with acetate buffer. As before, elution is carried out using the acetate buffer supplemented with NaCl and isopropanol. Active fractions, i.e. fractions displaying the activities sought, are collected, dialysed against a 5 millimol/litre acetate buffer pH 5.0 and then concentrated by means of ultrafiltration with a Amicon PM-10 membrane. To obtain the protease in an essentially pure state, the concentrated liquid  
10 is chromatographed over a Superdex 75 column equilibrated with the 0.05 mol/litre sodium acetate buffer pH 5.0 and supplemented with 0.5 mol/litre NaCl. Further experiments carried out with the purified enzyme on PAGE may confirm if the molecular weight is in line with what can be expected on the basis of the available sequence data. Final confirmation can be obtained by carrying out a partial, N-terminal  
15 amino acid analysis.

#### Example 6

##### **Properties of a novel cysteine protease from *A. niger*.**

In this Example *Aspergillus* gene nr 28 was cloned and overexpressed in *A. niger* as  
20 described before. The enzyme obtained was purified according to procedures described in Example 4 and used to destroy trypsin inhibiting activity from soybeans under various conditions. As reference materials papain and bromelain were used. Bromelain was obtained from Sigma, papain was obtained from DSM Food Specialties Business Unit Beverage Ingredients, PO Box 1, 2600 MA Delft, the Netherlands. .

25 Trypsin inhibition was measured according to the method of Kakade, M.L., Rackis, J.J., McGhee, J.E. and Puski, G. (1974): J. Cereal Chemistry **51**: 376-382. Degradation of the substrate N-benzoyl-L-arginine-p-nitroaniline to N-benzoyl-L-arginine and p-nitroaniline was taken as a measure of trypsin activity. Trypsin was  
30 obtained from British Drug Houses Ltd and was derived from cow's pancreas containing more than 0.54 Anson Units per gram of product. The Kunitz inhibitor for soybeans was also obtained from Sigma.

The trypsin inhibitor was pre-incubated at a concentration of 2 mg/ml with the above  
35 mentioned cysteine protease enzymes at pH 3 in 50 mM Na-acetate buffer prior to measuring trypsin inhibition. Enzymes were added at a ratio of enzyme protein to

trypsin inhibitor of 1:100 (w/w). Albumin served as a negative control for the enzymes. Remaining trypsin activity was measured after incubation during 3 hours at 37°C. Results are shown in Table 2.

- 5 Table 2 . Effects of various cysteine proteases on the enzymatic inactivation of the Kunitz trypsin inhibitor from soybeans.

1	2	3	4	5
Enzyme tested	Remaining TI activity (%)	Remaining TI activity after pepsin treatment	Remaining TI activity after heat treatment at 75°C	Remaining TI activity after heat treatment at 90°C
Papain	25	55	78	95
Bromelain	30	62	86	99
<i>A.niger</i>	26	26	28	35
Albumin (control)	100	100	100	100

TI : Trypsin Inhibitor activity

- 10 Experiments were repeated in the presence of pepsin during the pre-incubation of cysteine proteases with the trypsin inhibitor. Pepsin was added at final concentration of 1.3 mg/ml. Results are shown in column 3.

- 15 Another series of experiments were conducted to check for heat stability. The cysteine proteases were incubated at 75 and 90°C during 5 minutes prior to the addition of these enzymes to the pre-incubation with the trypsin inhibitors. Results are shown in columns 4 and 5.

- 20 These results clearly demonstrate the superior activity of these novel cysteine proteases from *Aspergillus niger* over currently available cysteine proteases for the inactivation of trypsin inhibitors in animal feed.

Example 7.

**Exo-peptidases promoting cheese ripening and cheese taste.**

The amino-peptidases encoded by genes nr 20 and 54 (see Table 1) were overexpressed in *A.niger* according to methods described earlier. Purification of these enzymes was carried out according to procedures as described in Example 4. The activity of the purified enzyme samples was determined at pH7.2 in an aqueous phosphate buffer (50 mM) containing the para-nitro anilide derivative of a number of hydrophobic amino acids (3 mM) as the substrate. The conversion of the substrate by the amino peptidase was determined by monitoring the change in optical density at 400 nm as a result of substrate conversion, using a solution not containing the enzyme as the reference. Activity (A) was calculated as the change in OD per minute and expressed as e.g. Phe-AP, Leu-AP or Val-AP units, depending on the substrate used.

Normal cheese milk was inoculated with starter culture of the Delvo-tec™ DX 31 range (DSM Food Specialities Delft, The Netherlands) to obtain a Gouda-type cheese and coagulating was executed with an average dosis of coagulant (50 IMCU per liter of cheese milk). In addition, 25 Phe-units of each exo-protease was added to two experimental cheeses whereas the control did not contain either one of the exo-proteases. Cheese making parameters were used conform the procedure applied for semi-hard cheese for both cheeses. A difference was noted in terms of flavor and aroma development between the experimental cheeses and control cheese to such an extent that the experimental cheeses has obtained most of its organoleptical properties after three (3) weeks whereas the control cheese has obtained a similar qualification after six (6) weeks. The level of free amino acids after three weeks was shown to be twice as high in the experimental cheeses; after six weeks of ripening the levels were comparable again. Amino acid analysis was carried out according to the Picotag method of Waters (Milford MA, USA).

These data suggests that the product is ready for sale three weeks earlier without decreasing the keeping quality of the cheese. The organoleptic character of the experimental cheeses differed from the control to the extent that the bland cheese flavor with a slight tendency to bitterness of the control cheese was overcome in the experimental cheese in the presence of the amino-peptidase. The texture of the cheeses was found to be somewhat smoother as well.

## Example 8

**Novel specificity of a protease encoded by gene 55**

As explained earlier, certain proteins can resist enzymatic hydrolysis as the result of specific amino acid compositions or specific tertiary structures. In such cases the quantity of peptides that can be solubilised from protease resistant proteins can be dramatically improved by using proteases exhibiting novel specificities.

Beta-casein is a protein with very limited tertiary structure but with an extraordinary high level of proline residues. Many proteases have difficulties in cleaving proline containing sequences so that the hydrolysis of beta-casein with commonly available proteases yields a hydrolysate that is relatively rich in large, protease-resistant peptides. The latter resistant peptides can attribute to a number of undesirable properties of the hydrolysate. For example, it is well known that these larger peptides have a relatively strong effect on allergenicity and bitterness. Moreover, these peptides withstand a further degradation into free amino acids so that in certain processes the occurrence of these large, protease resistant peptides are synonymous with yield losses. Therefore, the availability and use of proteases that are capable of cleaving the protease-resistant parts of the proteins, translate into serious technical and economical benefits.

Beta-casein represents one of the major casein fractions of bovine milk. The protein has been well characterised in terms of its amino acid sequence and is commercially available in an almost pure form. As such, beta-casein offers an excellent test substrate for studying the relationship between enzyme cleavage sites and the length of various peptides formed during enzyme hydrolysis.

This Example demonstrates that despite the broad spectrum cleavage character of the endoprotease subtilisin, the addition of a very specific enzyme like a prolyl endopeptidase as encoded by gene 55 (see Table 1) has a major impact on the size of the beta-casein fragments formed.

Beta-casein from bovine milk (lyophilised, essentially salt-free powder) with a minimum 90% beta-casein was obtained from Sigma. Subtilisin from *B.licheniformis* (Delvolase®, 560 000 DU per gram) was obtained from DSM Food Specialities (Seclin, France). The proline-specific endoprotease as encoded by gene 55 was overexpressed in *A. niger* and purified using procedures described in Example 4.

35

Beta-casein powder was dissolved at a concentration of 10% (w/w) together with 0.1%

(w/w) Delvolase™ powder in a 0.1 mol/liter phosphate buffer pH7.0. After an incubation of 24 hours at 45°C in a shaking waterbath, the reaction was stopped by heating the solution for 15 minutes at 90°C. To one half of the solution (1ml containing 100milligrams of beta-casein) 100 microliter of the proline-specific protease was added  
5 and the reaction was continued for another 24 hours at 45°C. After another heat shock at 90°C, samples of both the Delvolase™ and the Delvolase™ + proline-specific endoprotease treated beta-casein material were analysed by LC/MS equipment to study the precise peptide size distributions in the two samples.

#### 10 LC/MS Analysis

HPLC using an ion trap mass spectrometer (Thermoquest™, Breda, the Netherlands) coupled to a P4000 pump (Thermoquest™, Breda, the Netherlands) was used in characterising the enzymatic protein hydrolysates produced by the inventive enzyme mixture. The peptides formed were separated using a PEPMAP C18 300A (MIC-15-03-  
15 C18-PM, LC Packings, Amsterdam, The Netherlands) column in combination with a gradient of 0.1% formic acid in Milli Q water (Millipore, Bedford, MA, USA; Solution A) and 0.1% formic acid in acetonitrile (Solution B) for elution. The gradient started at 100% of Solution A and increased to 70% of solution B in 45 minutes and was kept at the latter ratio for another 5 minutes. The injection volume used was 50 microliters, the  
20 flow rate was 50 microliter per minute and the column temperature was maintained at 30°C. The protein concentration of the injected sample was approx. 50 micrograms/milliliter.

Detailed information on the individual peptides was obtained by using the "scan  
25 dependent" MS/MS algorithm which is a characteristic algorithm for an ion trap mass spectrometer. Full scan analysis was followed by zoom scan analysis for the determination of the charge state of the most intense ion in the full scan mass range. Subsequent MS/MS analysis of the latter ion resulted in partial peptide sequence information, which could be used for database searching using the SEQUEST  
30 application from Xcalibur Bioworks (Thermoquest™, Breda, The Netherlands). Databanks used were extracted from the OWL.fasta databank, available at the NCBI (National Centre for Biotechnology informatics), containing the proteins of interest for the application used.

By using this technique as a screening method only peptides with a mass ranging from  
35 approx. 400 to 2000 Daltons were considered suitable for further analysis by MS

sequencing.

Angiotensin (M=1295.6) was used to tune for optimal sensitivity in MS mode and for optimal fragmentation in MS/MS mode, performing constant infusion of 60 µg/ml, resulting in mainly doubly and triply charged species in MS mode, and an optimal  
5 collision energy of about 35 % in MS/MS mode.

In the sample digested with Delvolase alone, the LC/MS/MS analysis identified 40 peptides covering various parts of the beta-casein molecule. Together these peptides accounted for 79% of the total beta-casein sequence. Different retention times of the  
10 peptides on the C18 column could be traced back to peptide lengths ranging from 2 to 23 amino acid residues. Together < 15% of the peptides found were smaller than 6 amino acids. The sample digested with Delvolase™ and the proline-specific protease also generated a large number of identifiable peptides from beta-casein. Together these peptides covered > 50% of the total beta-casein protein sequence. In this sample  
15 the peptide size distribution was remarkably homogeneous, as the peptides ranged in length only between 2 and 6 residues. The results show that in the hydrolysate made with the proline-specific protease contain a large fraction of di-, tri-, up to 6 AA peptides, showing the distinct beneficial effect of the co-incubation with an endoprotease featuring an unusual specificity.. It is also clear from these experiments  
20 that the endoprotease according to gene 55 encodes an endoprotease that cleaves the peptide chain at the carboxyterminus of the proline residue.

#### Example 9

##### **The selective release of specific amino acids to promote flavour formation.**

25 Free amino acids like leucine and phenylalanine have not only been implicated in Maillard reactions but also as precursor for desirable aromas in various food fermentations. To promote the formation of such aromas in food fermentations or during the heating, roasting or baking phase of food, it would be advantageous to incorporate into these products a protein hydrolysate that contains relatively high levels  
30 of these specific amino acids in a free form. In this Example we describe the production of yeast extracts selectively enriched in leucine and phenylalanine. This enrichment is obtained by combining an endoprotease with a cleavage preference for a selected set of amino acid residues with an exoprotease favouring the release of a similar set of amino acid residues. The preference of the endoprotease should match with the  
35 preference of the exoprotease used. For example we have established that the

- aminopeptidases encoded by genes 20 and 54 (see Table1) feature a definite preference for releasing leucine and phenylalanine residues which matches with the cleavage preferences of thermolysin. The carboxypeptidases encoded by genes 23 and 24 have a preference for releasing arginine and lysine residues which matches the cleavage preferences of trypsin. Carboxypeptidase encoded by gene 5 features a highly unusual preference for releasing glycine which could be combined with certain endoproteases present in papaine. The carboxypeptidase encoded by gene 51 is capable of removing glutamate residues which matches the glutamate specific protease encoded by gene 43.
- 10 The endoprotease thermolysin (commercially available as Thermoase)C 180 from Daiwa Kasei KK (Osaka, Japan) is known to cleave peptide bonds at the amino terminal side of bulky, hydrophobic amino acids like Leu and Phe. To liberate the thus exposed amino acids from the newly formed peptides, we used the amino-peptidases encoded by genes nr 20 and 54 (see Table 1). These genes were overexpressed in
- 15 A.niger according to methods described earlier and purification of these enzymes was carried out according to procedures as described in Example 4.
- To release as much leucine and phenylalanine as possible without concomitant release of undesired amino acids with this combination of enzymes, it is evident that the conditions used during enzymatic hydrolysis should be carefully selected. Moreover,
- 20 the yeasts own endogeneous (and probably aspecific) proteases have to be inactivated. After a number of test incubations, a protocol was worked out that leads to a surprisingly selective and effective release of leucine and phenylalanine from the yeast proteins using these two new enzymes.
- 25 To inactivate the yeasts endogeneous proteases, the yeast suspension was kept for 5 minutes at 95 degrees C. Then the suspension was quickly cooled down to the required temperature and the pH was adjusted to 7.0 using 4N NaOH. The yeast, the thermolysin and one of the aminopeptidases were all incubated simultaneously under the following conditions. After the heat shock, the pH of the 2000 milliliters yeast
- 30 suspension was adjusted to 7.0 after which 680 milligrams of Thermoase were added and, after stirring, the purified aminopeptidase. The mixture was incubated with stirring at 50 degrees C for 3 hours and centrifuged. To stop all enzymatic activities the pH of the supernatant was adjusted to 4 and subjected to another heat treatment of 45 minutes at 95 degrees C. After another centrifugation a sample for amino acid analysis
- 35 was obtained from the supernatant. Precipitated or non-dissolved matter was removed by centrifugation for 15 minutes at 3500 rpm in an Hereaus Megafuge 2.0 R



centrifuge. Supernatant was removed and kept frozen at  $-20^{\circ}\text{C}$ .

Samples of the supernatant, were analysed for amino acid content according to the Picotag method of Waters (Milford MA, USA) immediately after thawing.

- 5 In the amino acid analysis Trp and Cys values were omitted And Asp and Asn values were summed as one value. According to the data obtained, in the resulting hydrolysate the ratio between alanine and leucine (21.3 : 11.7) was 1: 0.5. Commercially available yeast hydrolysates typically exhibit alanine versus leucine ratio's of 1: 0.3 .

10

- In a second experiment a yeast extract was prepared that was enriched in free glutamate. To achieve this, use was made of an endoprotease exhibiting a preference for cleaving at the C-terminal end of glutamate residues (encoded by gene nr 43 in Table 1) and a carboxypeptidase ( encoded by gene nr 51 in Table 1) capable of removing these glutamate residues thus exposed. The endoprotease encoded by gene 15 nr 43 and the carboxypeptidase encoded by gene 51 (see Table 1) were overexpressed in *A.niger* according to methods described earlier. Purification of these enzymes was carried out according to procedures as described in Example 4.

- 20 The essential role of free glutamate in a number of aroma forming processes is well documented and MSG, the sodium salt of glutamic acid, is recognized as the single most important taste enhancing component.

- In this Example the pH of the 200 ml heat shocked yeast suspension is adjusted to 8.0, then the purified enzyme product encoded by gene 43 is added and the mixture was 25 incubated for 4 hours at 50 degrees C. Then the pH was lowered to 5.0 and the suspension was centrifuged. To 100milliliters of supernatant the purified gene product of gene 51 is added. Incubation with this carboxypeptidase took place for 30 minutes at 50 degrees C with continuous pH adjustments. After stopping the enzyme incubation by a heat treatment of 5 minutes by 95 degrees C, the material was again centrifuged 30 (see above) and a sample was obtained for amino acid analysis.

According to the amino acid data obtained (see above), in the resulting hydrolysate the ratio between alanine and glutamate (30.0 : 48.7) was 1: 1.6. Commercially available yeast hydrolysates typically exhibit alanine versus glutamate ratio's of 1: 1.

35

**Example 10****Flavour evaluation of yeast hydrolysates enriched in specific amino acids.**

To prove that a protein hydrolysate enriched in specific amino acids according to the invention can generate specific aroma's, a number of experiments were carried out

5 with the yeast hydrolysates described in an earlier Example. To that end larger portions of these hydrolysates were prepared and lyophilised. The performance of the resulting powders were compared with the performance of a commercially available yeast extract (Gistex LS, obtainable from DSM Food Specialties, Delft, The Netherlands) in a standardised mixture under several reaction conditions. The standardised mixture

10 consisted of one of the hydrolysates, base mixture and water.

The base mixture contained 22 grams of Maxarome Plus Powder (a specialised yeast extract with a high content of natural nucleotides, also obtainable from DSM Food Specialties), 29.2 grams of glucose, 9 grams of REFEL-F fat (hydrogenated soy oil, obtainable from Barentz, Hoofddorp, The Netherlands) and 0.2 grams of calcium

15 stearyl lactylate ( emulsifier, obtainable from Abitec, Northampton, UK) thoroughly mixed in a mortar.

All standardised mixtures contained 5 grams of yeast hydrolysate powder ( i.e. either the leucine or the glutamate enriched material or the commercial yeast extract) , 3 grams of the base mixture and 3 grams of water. After thorough mixing, these three slurries

20 were subjected to different heating regimes i.e. either 65 minutes at 90-95 degrees C in a reaction vial (liquid reaction) or dried at 20 millibar at 120 degrees C in a vacuum oven (vacuum roast reaction) or heated in an open reaction vial at 120 degrees C for 10 minutes after the dissipation of all water (roast reaction).

After the heat treatment all three products had assumed colours ranging from dark

25 brown to almost black. In case of the vacuum roast reaction only the light coloured top layers were used. Taste evaluation of the heated products was carried out by grinding the blackened cakes into fine powders and dissolving these powders to a concentration of 2% (w/w) in water containing 0.6% (w/w) NaCl. The observations of the taste panel are specified in Table 3.

Table 3

	Reference	Leucine	Glutamate
Liquid	Bouillon, slightly roast	Cold tea, slightly flowery, yeasty	More bouillon, meaty, yeasty
Vacuum roast	Burnt, fried potatoes	Astringent, beans, yeasty	Burnt, bouillon, yeasty
Roast	Dark roast, bouillon, umami	Less roast, flowery, umami	Roast, more bouillon, more umami

### 5 Example 11

#### **Non-allergenic whey protein hydrolysates formed with tripeptidylpeptidases.**

The dipeptidylpeptidases encoded by the genes 19 and 55 as well as the tripeptidylpeptidases encoded by the genes 4, 9, 10, 12, 26, 35, 46, and 50 (see Table 1) may be overproduced as described and may be purified according to the methods provided in Example 4. After purification the pH optimum and the temperature stability of each individual enzyme may be established by any of the methods available and known by the skilled person. Furthermore, the specificity of each individual enzyme may be determined using the methods outlined in Example 1. The selectivity exhibited by tripeptidylpeptidases is illustrated in the following experiment.

15 The enzyme encoded by gene 12 was overproduced in an *Aspergillus niger* host cell and purified by procedures described in Example 4. The enzyme thus obtained was incubated at pH 5 and 50 degrees C with different synthetic chromogenic substrates i.e. Ala-Ala-Phe-pNA and Ala-Phe-pNA (both from Bachem, Switzerland). The incubation with the Ala-Ala-Phe-pNA substrate led to a significant increase of the absorbance at 410 nm whereas the incubation with Ala-Phe-pNA did not. This observation clearly demonstrates that tripeptidylpeptidases cleave off tripeptides and do not exhibit aminopeptidase activity that can lead to an undesirable increase of free amino acids.

Moreover, the enzyme encoded by gene 12 shows favourable enzyme stability characteristics as shown in the following experiment. Four samples of the enzyme were incubated at pH 5 for one hour at 0, 40, 50 and 60 degrees C respectively. Then each enzyme sample was incubated with the above mentioned Ala-Ala-Phe-pNA substrate in a citrate buffer at pH5 and the residual activity in each individual sample was

determined by measuring the increase in absorbance at 410 nm. With the 0 degrees C sample showing 100% activity, the 40 degrees sample showed 96% residual activity, the 50 degrees sample 92% residual activity and the 60 degrees sample 88% residual activity.

- 5 In a typical process aimed at producing a hydrolysate with a high proportion of tripeptides, whey protein (WPC 75) may be dissolved/suspended in a concentration of 100 grams of protein/liter, in an aqueous medium having a pH of 8.5. The first enzyme incubation is with the broad spectrum endoprotease subtilisin (Delvolase®, 560 000 DU per gram from DSM). After a predigestion of the whey with this enzyme in a
- 10 concentration of 0.5% enzyme concentrate per gram of protein for 2 hours at 60 degrees C, the mixture is heat-treated to inactivate the endoprotease used. Then the temperature is adjusted to 50 degrees C and the tripeptidylpeptidase is added and the whole mixture is incubated until the desired level of tripeptides is reached. Further processing steps of the hydrolysate thus obtained depend on the specific application
- 15 but may incorporate microfiltration or centrifugation followed by evaporation and spray drying.

CLAIMS

1. An isolated polynucleotide hybridisable to a polynucleotide according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or  
5 a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114
2. An isolated polynucleotide according to claim 1 hybridisable under high stringency conditions to a polynucleotide according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the  
10 group consisting of SEQ ID NO: 58 to SEQ ID NO: 114
3. An isolated polynucleotide according to claims 1 or 2 obtainable from a filamentous fungus.
4. An isolated polynucleotide according to claim 3 obtainable from *A. niger*.
5. An isolated polynucleotide encoding a polypeptide comprising an amino acid  
15 sequence according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.
6. An isolated polynucleotide encoding at least one functional domain of a polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.
- 20 7. An isolated polynucleotide comprising a nucleotide sequence according to a sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114 or functional equivalents thereof
8. An isolated polynucleotide according to a sequence selected from the group  
25 consisting of SEQ ID NO: 1 to SEQ ID NO: 57 or a sequence selected from the group consisting of SEQ ID NO: 58 to SEQ ID NO: 114.
9. A vector comprising a polynucleotide sequence according to claims 1 to 8.
10. A vector according to claim 9 wherein said polynucleotide sequence according to claims 1 to 8 is operatively linked with regulatory sequences suitable for expression  
30 of said polynucleotide sequence in a suitable host cell.

11. A vector according to claim 10 wherein said suitable host cell is a filamentous fungus
12. A method for manufacturing a polynucleotide according to claims 1 – 8 or a vector according to claims 9 to 11 comprising the steps of culturing a host cell transformed with said polynucleotide or said vector and isolating said polynucleotide or said vector from said host cell.
13. An isolated polypeptide according to a sequence selected from the group consisting of SEQ ID NO: 115 to SEQ ID NO: 171 or functional equivalents thereof.
14. An isolated polypeptide according to claim 13 obtainable from *Aspergillus niger*
15. An isolated polypeptide obtainable by expressing a polynucleotide according to claims 1 to 8 or a vector according to claims 9 to 11 in an appropriate host cell, e.g. *Aspergillus niger*.
16. Recombinant protease comprising a functional domain of a protease polypeptide.
17. A method for manufacturing a polypeptide according to claims 13 to 16 comprising the steps of transforming a suitable host cell with an isolated polynucleotide according to claims 1 to 8 or a vector according to claims 9 to 11, culturing said cell under conditions allowing expression of said polynucleotide and optionally purifying the encoded polypeptide from said cell or culture medium.
18. A recombinant host cell comprising a polynucleotide according to claims 1 to 8 or a vector according to claims 9 to 11.
19. A recombinant host cell expressing a polypeptide according to claims 13 to 16.
20. A recombinant host cell comprising a polynucleotide encoding a functionally inactivated protease polypeptide.
21. A recombinant host cell wherein a polynucleotide encoding a protease polypeptide has at least partially been deleted.
22. A recombinant host cell according to claims 18 to 21 wherein said host cell is from an *Aspergillus* species, e.g. *A. niger*.
23. A recombinant host cell functionally deficient in a protease obtainable by a method

comprising said steps of:

- a. In vitro mutagenesis of a polynucleotide according to claims 1 to 11,
  - b. Transformation of a host cell comprising an endogenous gene comprising a polynucleotide sequence hybridisable to said mutagenised polynucleotide obtained in step a),
  - c. Selecting and isolating recombinant host cells in which said endogenous gene is replaced by a mutagenised polynucleotide obtained in step a).
24. Purified antibodies reactive with a polypeptide according to claims 13 to 16.
25. Fusion protein comprising a polypeptide sequence according to claims 13 to 16.
26. Method for diagnosing whether an organism is infected with *Aspergillus* comprising said steps of:
- a. Isolating a biological sample from said organism suspected to be infected with *Aspergillus*,
  - b. Isolating nucleic acid from that sample,
  - c. Determining whether said isolated nucleic acid comprises polynucleotides hybridisable to a polynucleotide according to claims 1 to 8.
27. Method according to claim 26 wherein step c) additionally comprises amplification of said isolated nucleic acid, preferably by polymerase chain reaction.
28. Method for diagnosing whether a certain organism is infected with *Aspergillus* comprising said steps of:
- a. Isolating a biological sample from said organism suspected to be infected with *Aspergillus*,
  - b. reacting said biological sample with an antibody according to claim 24
  - c. determining whether immunocomplexes are formed.

## SEQUENCE LISTING

&lt;110&gt; DSM NV

&lt;120&gt; Novel genes encoding novel proteolytic enzymes.

&lt;130&gt; 20095WO

&lt;160&gt; 171

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2520

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 1

```

cgcagggcgtc cggttgcgccg cgaaaacctg ccgagtgggc cgtttaggct ttgggtctcc      60
ccacgatgta agcataatca ttctgtgcct gagtgtgaat tctcctgttg gaggctgcat      120
cttaattctt aactgcatga aaagcacttg ggtgctatct tctttttcct ttctttcttt      180
tccgtgttca ttccattcc cttgctcttc ttctttgtgt cgacatttac aaatcacatt      240
tttcttatac tttcttttct tcacctcggt tcttcctatt cactctctgt gttcagcatt      300
cgttatcagc actttatctt ttgctcgtct cttttatctt cacttggttg tgcctttcca      360
ctagcaatct atcgtttgat ctttctagag cattgtcttg attgtgtcat tctgtcattg      420
actccggcta tgaaatatta ttctcaatct gcctaaaacc aaattctact ctatcactac      480
acatttgat cacctgatct ggctgagata ggagagtccg gcatctcatc gtctgcatca      540
gacaattgcg ataaattcat tgcttgacc tgttattgat tctccaagt tatgcatctc      600
ccacagcgtc tcgttacagc agcgtgtctt tgcgccagtg ccacggcttt catccatac      660
accatcaaac tcgatacgtc ggacgacatc tcagcccggtg attcattagc tcgtcgtttc      720
ctgccagtac caaaaccaag cgatgctcta gcagacgatt ccacctcatc tgccagcgat      780
gagtcctgt cactgaacat caaaaggatt cccgttcgtc gtgacaatga tttcaagatt      840
gtggtagcgg aaactccctc ttggtctaac accgccgtc tcgatcaaga tggtagcgac      900
atttcataca tctctgtcgt caacattggg tctgatgaga aatctatgta catggtgctc      960
gacacaggcg gctctgatac ctgggttttc ggttccaact gcacgtccac accctgcacg     1020
atgcacaata ccttcgggtc ggacgattct tcgacccttg aaatgacatc ggaagagtgg     1080
agtgtgggct atggaactgg gtctgtcagc ggcttgctag gaaaagaaa gctcacgatt     1140
gcaaattgtca ctgtacgat gactttcgga cttgcttcca acgcatcgga taacttcgag     1200

```



tcgtacccaa	tggacggcat	tctcgggtctc	ggtcgaacca	acgatagttc	ctacgacaac	1260
ccaacattca	tggatgccgt	tgcaaaaagt	aacgttttca	agtcgaatat	cgttggtctc	1320
gccctttcac	gtagcccccgc	caaggatggc	acgggtcagct	ttggcactac	tgacaaggac	1380
aagtacaccg	gcgatatcac	ctacaccgat	accgtcggat	cggacagcta	ttggcgcatt	1440
cccgtaggacg	atgtctatgt	tggcggcact	tcattgcgatt	tctccaacaa	atcagccatc	1500
atcgataaccg	gaactttctta	tgctatgctg	ccttcaagcg	actcgaagac	gctgcacagt	1560
ctcattcccg	gcgccaatac	ttcggggagc	taccacatta	ttccgtgcaa	cacaactact	1620
aagctacaag	tggcattctc	tgggtgtgaat	tacaccatct	cgccgaagga	ctacgtggga	1680
gcaacttcag	gttctggatg	cgtttcgaac	attatcagct	acgacttatt	tgggtgatgac	1740
atctgggtcc	tgggtgacac	gtttctcaaa	aatgtgtatg	ctgtgtttga	ctacgatgag	1800
ttacgggtcg	gatttgcaga	gcgttcctcg	aacaccacct	ctgcgtcgaa	ctctacgagc	1860
tctggaacaa	gcagcacctc	gggatccact	acaacgggca	gctcaacgac	tacgacgagc	1920
tctgctagct	ctagtagttc	atctgatgct	gaatcaggaa	gtagcatgac	cattcccgtc	1980
cctcagtatt	tcttctctgc	tctggcgatt	gcttccttca	tgttttggct	ctagttaacc	2040
gcatcttact	cgacgcctga	acctcgggaa	acatatgcat	tatttacaca	tgctgctgat	2100
ttgtatttgc	atatattctt	cgagcctgga	cggcgtgcgg	gtcatattac	cttacattcg	2160
aagtccttct	ctaataaata	aacatttatt	cttactccac	cagttctggc	tcgcaattaa	2220
ccctgtctaa	gaaaaagttg	gtatagaaca	tggcatccac	tacctggaac	attcaaagaa	2280
ccttgctccg	gatcagtgtg	tatgacttcg	ggtacgattc	tgacatgaca	gttagcgtcc	2340
atcctgagga	ttcatcctga	tctccttacc	tagtatggac	ttatcaaagt	ccttgacgct	2400
attgtaccct	cccacagcca	tcaggatata	gaaatcggcc	aacagcgact	tcattcacatg	2460
gcgaacaccc	tcctcaccca	tgatactgag	gccccagatc	cagagccggc	cgacgaaaac	2520

<210> 2  
 <211> 5001  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 2	
taggaaaatc	agaggcgaca atttgcctcg atactggata agtaccatcg gtcacgaaat 60
tcagcaccga	ctggcttatg tcctgctccg ataccttagc ggacattatg ttagtagttc 120
taagcaagag	cccttggttc ttggtaatcg gcggatcaaa aacgtaaaga agacaaacag 180

aagcgccaca ctaggctctg cctccctctt acagaagatc tgccaggat c gatccacaa	240
agatatacca aggactccaa tgcagcagat cgcaaccgaa agggaaggcg agctgtcaac	300
accgccatgt gacttcaccg ctcaccgcct tagctgcgat gggcaagacc acgaacgatc	360
tcgctcttcc ccagggccag actgaggccg attatatgat ttttttcttt cttttccgtg	420
tgtctcgtct gctgctatat tcttatTTTT ctgttcggta aagatactc ctaagaatag	480
acacggggtg tttttttgtg aattatctgt tgggtgtggtg ctctctatcg aaccggaaac	540
ctgaactcca ctctgaaccg ttacagttgg aggtaacct tcgttcagcg gccaaactgtg	600
tgacctcaaa attcctgaaa catcataatc ggcgtcaagc agagcccatc gtgttgtctc	660
agttactatt gagaagcctg attcgggcaa acgcttctcg atccatgtga gtcattgctt	720
taccagccct gaactccatt gaataaaaaa aaagcaagaa aagagattgc cctccgctcg	780
ttttctgtat taaacatcca atcctcaacc ggcagcctta cattggctgc cacagatttg	840
tgccctcata cagcatgctt cgtggctctc gtgatgtcgt attattacaa tttgcaatcc	900
ccttgttctt gctattggta tttcaaacat ggaatgggtg cttttcccg tttcaattccc	960
cgcaccctga acctcaagca ttgctagctt ctctaaaatg aataaaactg ttatacttgc	1020
ttcctaaaag tttgcgcttc tggcctatgg attactaaca gcattttaga ttatcgctac	1080
ggggtgtgat cacaggattt ggttctaaat cacatttcca gagaccattg agcaaaatgt	1140
catctactca aaagagccat ttcaagctac tccagaagtt caaaccggag tactcgccta	1200
gcgagtttgc tcagtatgag tcggagagaa caggcatgag ggtagtggtc attgacaaa	1260
aaggacccaa agtcacaggt tattttgttc tagccacaga gattctcgat gattcagggtg	1320
ctcctcacac gttggagcac ttgtgcttta tgggctcgcg gaactataga tataagggtc	1380
tccttgacaa gctagcaaca cgtgtttatt cgagcaccaa tgcttgacg gccacagacc	1440
acacggccta caccttggac acagcaggct ggggaagggt cgctcaaatc ttgcccgtgt	1500
acctagagca tggtatagct ccaacactga cagatgaagg gtgctatacc gaagtgcac	1560
atattgatgg cgctggagac gacgctggag tcgtctactc ggagatgcag ggtgtgcaga	1620
ataactctgc agagttaatc gatctaaccg ctctcgatg gacttaccg catgggtgtag	1680
gttttcgcta cgagacaggc ggtatgatgg agcagctccg cgtcctcacc gcggaccgta	1740
tcgagcgtt ccatcgtag atgtaccagc ccaagaactt atgcctaac atcacaggcg	1800
aagtagatca ccagaacatg ctggagacct tggacaagtt cgaagatact attctagatg	1860

tcattcccag	tccctgattca	cctttcaaga	ggccgtgggt	agattccaag	caggcgccgc	1920
cattggagaa	gtccattgtc	cagactgtgg	aatttccgga	agaagatgaa	tctttcgggg	1980
agatagaaat	tagattcctc	ggtcgcgact	gtaccgacct	tgttcaaagt	gagtgttccg	2040
ctgtcctcat	ttcgaagata	tacttactct	gttatagccg	gggctgtcaa	tggtgcattg	2100
ctgtatctgg	ccggttcata	tgcttctcta	ttggataaca	tcctgggtga	gaaggagcag	2160
ctcgccagtg	ctgtctatta	tgctaccgaa	gatcatccca	gcattgagat	ccgcttcaca	2220
ttaaccagtg	tggagacaga	gaaactcgcg	aaggtagagc	aacggttttt	cgaagtgtct	2280
aaggacgcta	tggagaaaaga	tttagacatg	aggtatatca	aggagtgcac	tgaccggcaa	2340
agacggacct	ggaagttctc	taccgaaagc	tccgcctctt	cctttgcgga	gtacgtgatc	2400
tcggattttc	ttttcggaaa	gagagacgga	tcgactatgc	ttgatgttgc	gaccttgcaa	2460
gagtacgacg	tgctggagaa	gtggagtgaa	gaacagtggc	gcagttttat	caaaacatgg	2520
atctctgatg	ccaaccatgt	cactatcctt	ggtgttccgt	ccgttaagat	gtctgacaca	2580
ttaaagaagg	aggaggaagc	tagagtcgca	gagcaaaaga	agcgcttggg	tgatgagggg	2640
ctgaagaagt	tggccgacaa	gctggaaaaa	gctaaagctg	aaaatgacaa	ggagatcccc	2700
aaggagatgc	tggagaggtt	ccaaatccct	ggaatagagt	ctatccattt	cgtggacact	2760
actacagcca	ggtctgggtg	agccctcgat	gccgggcgcc	catcccacaa	ggcgcaaaaa	2820
ctggtggatg	ctgatggctc	tgatctgccc	ttgttcatcc	atttcgagca	tatccccagt	2880
agcttcgtgc	agctctccct	cctcatctcg	gcacaggccg	tacctgtgca	gcttcgtcca	2940
ctgtgtctg	tgtatactga	ggcattcttc	aacctgcctg	tcaaccggaa	cggggaaacc	3000
atcaactttg	agcaggtggt	tgctcgagtt	gaaagggata	ctgttggtta	ctccatggaa	3060
ggagctagaa	gcctaggaaa	ctcgagatg	ttgcggatct	cattccaggt	ggagcttgag	3120
aagtatcaca	cggcgatcgc	atggatccag	gaactttcct	ggaactcgat	tttcgatgtc	3180
gagcgactcc	gagcgattac	cagtcgactg	ctctccgatg	tgccccgattc	caagcgtagt	3240
ggcgacgaca	tgctcgcggc	tgttcatgtg	atggtccact	atgcagcaga	gtctattggt	3300
cgggctcgga	gcaccttggg	gaaggcgcg	tatttgaaac	ggatcaagaa	gcaattagca	3360
gaagagccga	agtctgtcgt	tgcgcggatg	gaagaaatca	gagatgcgct	tttccgtttc	3420
gagaacatgc	gagtcttagt	tatcgctgac	ctggagaaac	ttcaaaaccc	tgtgtcagca	3480
tggaaaccat	ttgctgagcg	tttgggtgca	ggtgcccctc	tacagcctat	cacgactaga	3540
agaccgttgc	tcagtgaggc	aggccagaag	ttgggcggtg	agtcgtatgt	ggttcctatg	3600

```

ccgacgattg attcatcggt cgcatatgct accgcaogtg gtttgattc ttatgatgat 3660
ccaagacttc ctgccttaat ggttgcaatt gcatacatga acgcggttga gggccccctc 3720
tgggttgacag ttcgaggcaa ggggttgcca tatggcacga actttgccta taacattgat 3780
accggattcg tcaacttcga cgtttaccgc tcccccaacg cccataaagc cttcgactcc 3840
agcaagcaga ttgttgagga tcacctctct ggtgcgatgc ctttcgatcc cttgatgctg 3900
gagggttcca ttagcagcat tgtggaagc tttgcgaatg aacagtcgac aattggtagc 3960
gcagcctcag gcagtttcat ccgacaggtg attcggcgcc tgcctagcga ctacaaggag 4020
cgggtgctca agcaggtgag ggctactagc gttgatgacg tgaaaggcgc tctgaaggac 4080
atcattctgc ctttgtttta cccgtccacg gccaatatcg tggttacctg cgctacagtg 4140
cttgaggagg tttgtcattc catgaagaaa ttatgatctt cttgtgtatc atttactaac 4200
tgtcggttta gactatcaag gaaggtctcc aggcacggg attcacgcct gcggtgcagc 4260
cactcaaaga attcgaagat gactatgggc tgaaggctcg cgatgacgag gacgaggagt 4320
ccgacgatga cgacgatgag tatgaaaccg gatctgaaga tgaagatgac agtgatgaag 4380
acatggagga tgacgaagat gatgagtgat gcaatctata cgacaacctc tagacatgac 4440
aagattttatc tgagccagtt cctggataac acctaggctg aaagaccagc taccctggg 4500
ggcccagata tgccgacccg tgtgatctgt attgttagag atgtctcaa ctagcagacg 4560
cgcaatgatt tttgatgtta atgatataat gtacaacata agtgggttaac caccacaaat 4620
ctgcacctaa atcttagttg tgattatcgg tacctaccaa acccgagtaa acgttgccag 4680
aagtttatga aaaagctctc gttcttctta ttctattgaa tgttgtaata aaaagtgtc 4740
gcagatgctt tcgctatcgg gccactact atgattaacc tgaagcttag tctcttaggt 4800
gacataacct gttctacaca ggctgccatt atatttgcaa cacacagctt ctatctctga 4860
cctttgtgag aataatacaa ttactagaaa ccccgaggaga tataaatata ctctactcct 4920
accgaactaa caccagatc gacaaattat aaaccaaacc acgtgacaat atgatatcta 4980
tatatgaata tgtataaggt a 5001

```

```

<210> 3
<211> 3850
<212> DNA
<213> Aspergillus niger

```

```

<400> 3
gcgcgggggt cctgcatgtc ttcatgggtt gggagggtata tgtacatgta atgccgttgg 60

```

gttctggata cccacaataa agtgtttcta ctattacttt tgcattgtta gactttgaag	120
gctgctctgt aagggtccat tccgttggag tcaaacaacc gtctgtccgc gggcatatgt	180
ctcagtctga ggtgagaact gcaatatata ctccaagctt tctcaatctg atgcacagat	240
tgcaaacatc tcccttgctg tgtggtaaag tctccctttc tcggtgaacc ttcttcgggg	300
tcgcaactga ttccattgac cctcaccatc tgtcgaattg ttcccgaag ctgcggtcca	360
aataggcttt acggacgcca cagctgctcg aggccatctc caagggggaa tgaacaatgg	420
aatggtaagc cgctaagaaa ggggaactgt cggttctggt cgattggcag ggtcagggca	480
gtgcttgggc tgttctctg gccctccctt gcttcaagct ggccccgatt tggcagctcg	540
tgaagctcac cagacattca gccagccaga tgactggcac ctttccgctg ggcataaatt	600
ggccctggca gccatgtcat gccaatcttg gctccaggac cagtcattcc ttttcttgtt	660
cctgtcaaac agatcaagtc ctcgaggatg ggagctcttc agtggctgtc catcacggct	720
gctgcggcct ccgcagtgtc agccttgacc ccggagtaag tatctccaat catttggaac	780
tggcccatat tgtgcatagc taaccagctt acctgcatag gcagatgatc ggtgccccac	840
ggagaaccga agttatacca aaccctccg gtgtatgccc attgccaggt ccagccttac	900
aaagaagcgt cgtctgctga cacgagaagg acaccggtct attctcgacc tcccaatggt	960
cgtttgacac tcattctgag agcacctggt ggagcttgat cgacctcaa tcgggcaaga	1020
ccaccactct caccgatgat agcgatatcg aggagatcat ctggcttggc tctgacaatt	1080
ctacgctcct ctacatcaac agcaccaacg cgcaggttcc cggtggcgtg gagctgtgga	1140
ttgcccactc ttctgacttt gcaaatgcgt tggttcaggc ctttaacgat gcctctgcag	1200
actagtgtta atcctacttg gtgcagttac aaggcagcct ctctctccgc cggttttctc	1260
ggcatcaaat caaccgtgac agattccggc gacgtgcatt tcaccttcg tggaaagtcc	1320
tatcccaacg gaacggcata caatgatcag ctccgcgaga cctatcccag tacagcccgc	1380
atctacgaca gcatctttgt ggggcactgg gacacttacc tgaccacgc ctcccacgct	1440
gtattctccg gtaccctgca aagctcgacc agcgacgacg gcaatgttca atatactct	1500
tcagggggat tgaccaacct ggttaaccca gtcaagggtg ccgaaagccc attccctcct	1560
tttgagggca acgacgacta tgacctctcg cctgacggca aatgggttac cttcaagagc	1620
aaagcgccag agctgcctct tgctaacaac acggctgcct atgtctatct cgtcccacac	1680
gacggctctg cgactgcctt tgccgtcaac ggccctgata gtccctgcaac cccggaggga	1740

gttgaaggag aatccaacaa tcccgtgttc tcccctgata gcgacaaaat agcgtacttc	1800
caaatggcta ctaatacata cgagtcggac cgcaacgtgc tatacgtata ctccatcgcc	1860
gatgacacca tcaactcccct tgcaaaggac tgggaccgat cgcctagctc cgtgacatgg	1920
gtc gatggag acaacctcgt cgtggcaagc caagatctag gacgaaccag acttttcgcc	1980
atcccaggcg atgcagggga cgacttcaag cccacgaact tcaccgacgg cggtccgtg	2040
tcggctcaat acgtcctatc caactctacc ctccctgtca cgtccagcgc cttctggaca	2100
agctggagcg tctacaccgc cagccctgac gagggcgtga tcaacacact ggcctcagcc	2160
aacgagatcg accccgagct tagcggcctt agttcctccg actttgaaga gttctacttt	2220
gacggcaact ggactaccgt aagtctatcc ctccctgccc ccaccaccac atcacaaaca	2280
tactaaactc accgcagctc caaggatgga tcacctaccc ccaagacttc gactcatcca	2340
agaaataccc cctcgccttc ctcatccacg ggggccccga agacgcctgg gcggatgaat	2400
ggaacctgaa atggcactcc aaggctctcg ccgaccaggg atacgtcgtc gtccagccaa	2460
acccacaggg aagcaccggg ttcgccagc agctcacaga cgctatccaa cttaactgga	2520
gtacgccatt ccctatcccc aaactcccct cttaaacata eagctaacaa atgaaataac	2580
agccggcgcc gcctacgacg acctaaccaa agcctggcaa tacgtgcacg atacctacga	2640
cttcatcgac acggacaacg gcgtcgcgc ggggtcccagc ttcggcgcgt tcatgatcac	2700
ctggatccag ggcgatgact ttggacgcaa gttcaaggcg ctggttagcc atgatggtcc	2760
gttcattggc gatgcgtggg tcgagacgga tgagttatgg ttgttgagc atgaggtgag	2820
tggaccaagc caaaccccc ttttctcccc ttacaccatt acccctatac aaatatgatg	2880
attctgaccg tgtatagttc aacggcacct tctggcaagc gcgcgacgca ttccacaaca	2940
cggatccatc cggccccagc cgcgtcctcg catacagcac cccccagctc gtcattcaca	3000
gtgacaagga ttatcgcata cctgtggcaa atgggattgg actgtttaat acgctgcagg	3060
agaggggctg gccagtcgg tttttgaatt tcccggatga ggatcattgg tatgttcata	3120
cccttttctt ccccttttt tctcccatga ttatgggtgt tgtggatgct gatgtagcta	3180
tgtgtgtgtt tagggtcacc gggcaagaaa acagcctcgt ctggtatcag cagggtgctgg	3240
gatggattaa tcggtattct ggggtgggag ggtcgaatcc tgatgcgatt gctttggagg	3300
atacggtgaa tccggtggtg gatttgaatc cttgatcatt ccctgttgct cgttactact	3360
agtcagttat gatcatgttc tggctgggtc ccaggataga tggacggta ttactggctg	3420
ttatattctg ttgcagtggt ttactagttg gtagatcagt tacgagatga tgtatgagac	3480

gacagaaaga cttatgctta tgttgggagc tgcttcattt gtatatcaat ttattcttgt 3540  
 agtgattgat aactaactac tgtctgactg tctgtcaacc gctatactaa cattatacca 3600  
 accaaccaac caatcaaatac aatttctggg tctttcttct cttctgtttc ttcacctcgc 3660  
 aactagacca attcatcaag gacagggcag gacaggatct ggtatctgaa cggaacaacc 3720  
 gaaggaaaaa caaatcatatc acaagctttt gtacaatcaa accataagaa tcagtacagc 3780  
 tttctctttc agcctttcca aatgagagga aggacagaga aaatacaaag atgataccct 3840  
 agaaacgaaa 3850

<210> 4  
 <211> 3139  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 4  
 attgagtagg ctgcgctctt tgattctttg cgaggacta aaccacaaca ggcaattgag 60  
 atgttcggga gagaatatgc ggggatgcta tgcctgttgc agggatgatt atctccacac 120  
 tagcgcgtta aaggtttagt agcctgagat ggattgccga tctccgaccg ggccctgcct 180  
 cagccccagt acttgtggaa cgcgtcgaag atttacaaca ccatgccaga cctaactagg 240  
 taataaagtt gcgatgatgg ggactgccgc aaggctgtca atttgggggc cgaactcagc 300  
 ctcaacctgg aaaaattaac tccgattgtt ttgatttgat catgggagat tacagtctac 360  
 gtgaaatgag cttataaaga acgttggagt accggctctc aacctgtctt gtacctgcaa 420  
 gctttctctc attccttct atctttctta aaatcctctc attagacatc atgacgaggc 480  
 agacttctct cgttcccagg ctactaacgc tagcctcaet agctgcactt tcacaagcag 540  
 agctaggcaa gatccaatgg aaaggatctt gcaacttgac cacttatccg gcattgatct 600  
 gtggaacact agacgtgcca tacgactaca cggagtcaaa ttccagcaag aactgactc 660  
 tcgacatcgc caagtggcca gcgaccaaga aaccagtctc ggagcccatc atatttaact 720  
 ttggaggacc tgggtgcaat tcgttcgagg gccttgggct ttatggagag gaatttcagg 780  
 cgtaggttgc agttctgctt tgataccgca tcttatgctg actgacattg ttctctagta 840  
 ttcttggagg tcacaatgat ttgatagctt ttaacaaccg gtttgtcgtc cttctttctt 900  
 gagctagaaa catctactaa cgttgtacct ttatatagag gcgttggaaa caccatcccg 960  
 ttctctgctc acagcgatga cgccaccgt gaactcgtcg cccttcaagc tcctaacgac 1020  
 ggcagagcgt ccagcacggc tttgggagaa atctggggcc agaacgaaa catcgcacag 1080

gcatgctatg ctacgaacaa tcaaactggg agtcttattg gaactagctt tgctgcaagg	1140
gacatcatgc aggtcgctga tgcgctcagt ggaaaggata gtttgggtcaa ctactgggggt	1200
aaatatcacg gctgaaccga gtttatactt ttgctgacaa tctacacttt aggattctca	1260
tacggcacta caatcgggtgc tgttctcgcg gccatgttcc cggatcgaaat ggggaatgtc	1320
gcgcttgacg gagtggacaa cccagagag gctctttatg gatagtgagt ggcccttgaa	1380
gtttgcccg tctggtatga ttcagacagc taattccttc cgaaaagcaa cgcacaagcg	1440
gttgtggacg tcgacaaagt tttcgaagga ttctgcacgg gctgcatggc cgcaccggac	1500
ctctgccta tcgccaagga gtacaccagc gccgccaact tggagccgc aatttacctg	1560
atgctggaaa acctcaagta caaccgatt gccattcccg aaaccgggtg aatcgtaact	1620
tggagcgacg tcaagtcgac cttttttgag gccatgtacc tgccaagctc ttggcccttg	1680
acctctgagc ttctttacta cgtgcaaacc cgcaacacaa cgatccttgg caactctgaa	1740
gtatacgaca ccatcaaata ctacgggtcaa tcggcttctt tgacttcggc ttccgatgag	1800
gtcggcacgg ccattacatg ctccgacaag catcgatctg ccaccattaa agaggtcctc	1860
ccgtacgtca aagccagaca ggctctgacc aagatcgga gtgatggctc ggacggcgac	1920
atgagatgag cgcagtggaa tccgaagatg ttcgccaagg agcgctactc cggtgacttt	1980
gaagtcaaga cagccaaccc ggtgttgatt ctgagcaaca cttacgatcc agcgactcct	2040
cttcccgcag cgaagaacct gacagagacc tttgaggga gtgtcttgct cgagcagaac	2100
ggatacgggt tatgtttata cttccccttc tcatcatatc aaaagtgagc aagcagctaa	2160
cctactgatg atagcatact accctgtcta tgccatctct ttgcaactgc aaggccgtcc	2220
gggcttactt caccaatggc acattgcccg ctgacggaac gatctgccag gtggacgtgc	2280
ctctgttcac gaacttgacc tacaaggatg tgtggccgaa gagtttcaa cggagcgttg	2340
agtcgaggga tgatgcgact atcctcaagg ctttgatgtc ggtccgtgat aagatgtcgc	2400
gacgcaggat gtggtaagcg catgctatag atggggatgt tgaaaacca aagcgatgac	2460
tggataatgt tcttcatata atttattctg tgccgattcc ggcatacgct cgtcatgtaa	2520
tagagtttag ttaatgttgc aagggttgt atagtattta tttgtacacc aacagcgctt	2580
catggagacc ggaacttccc tgagtacaga atttccatc taggctttta tttaactttg	2640
acaatactca gtagtttga tgtcgatagc attgaggcaa gtaccggttg ttgttttggt	2700
agtggagtga atcaggactg tcccacaaca atccgctgat ctgaatgttt gatgtttcga	2760



tctgaggtat ctgagctgcg agcctccaaa tcggcaaccc catacttcag ggatattcca 2820  
 gaacattact agccttgag gctttgaggt ttagctgcag ggcggtcaaa ctaattgatt 2880  
 tctctcaatt gtcctaccgc tattgagtga tcttttagtg atgagtggaa cggagaattc 2940  
 ccggtcggat aatgcctgca ttagtattgg ccaacagagt attccatcaa cgactcccg 3000  
 gctgacattt aatccatgca caccctgaat tacctcgagc ttattctcgg tcctacattt 3060  
 gatcctctca tactttccct tatgtccttg cccacttgct ttacagattg aatccggatc 3120  
 cttcagcact cggcagaca 3139

<210> 5  
 <211> 2940  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 5  
 atagcagaac agaacatgta tcttgtaac gaattgattg atttcagcac ggaaatgttc 60  
 aaggcatgga acaattgctt ctgacccgga accgcggatt gcaaggatgg atatgtggat 120  
 cagatgggtg gaagaagatc tgtctgttag catacttcat aagttccaag gaggagtaaa 180  
 tgtggagtca taagagtaat atcgaatata atagaatggg gttgtcttgc taacggtgaa 240  
 tcggactccg tcggctctgc cagcgatcgg caggtcacgc gtctgcgtaa cttggtactt 300  
 atcttcccag tcacctaagc actgttactc cactcttctc tctttgacga taagaagata 360  
 gcagagactc ttgataaaaa gggttgggag catgctttga atttcttcac tccgagagct 420  
 ttctgtcccc atctggtctc ttgttgctcc cgatgtacta ctctctctgg gttgctgcct 480  
 tgggtggccgc gctgcccgtc tcccgggccc agtttggtggc tccgcccacg gatctcatc 540  
 ccaccaaggg atatctcgac atccccgtcc gctacaaaca ggtccccacc ggcatttggt 600  
 agactgatcc cagtgtcaag agcttctccg gttacgtcga tgctgctgag catgagcaca 660  
 tcttctcttg gttcttcgag gcgcgcaacc aagatccac cgaggctccc ttgaccgtct 720  
 ggatcaatgg aggcattgtc gaccccggtc attatttcct tccaattgct aaccgttcgt 780  
 aggtcctggg tcctcctcca tgatcggtt gtccaagag cacggcccat gcggcattga 840  
 cgccaatggc tccgtctaca acaaccctca ctccctggaac aacgccagca acatgctcta 900  
 catcgaccag cccgtgcaga ccggttctc ctacagcatt ccggttcccg gctatgtgga 960  
 ttcttcaca gacaatgtta ttgctctgcc ctccccgcc tgccccgact atgcagcgga 1020  
 tatgttctgt ggcacttact cctaccccaa cgtgagcctt acggctaatt ccaccgacaa 1080

cgccgcccc	aacttctacc	gcgccctaca	gggttttatg	ggcgcatctc	ctcagtactc	1140
gcgcgaaacc	ttccacttca	ccacggagag	ttatggcggc	cactacgggc	ccgtcttcaa	1200
cgagtagatc	gaggagcaga	acgcccattc	ccagccggga	gccaagaaga	tccaactggg	1260
cagtgtgatg	atcggcaatg	gctggtatga	cccgattatt	caataccagg	cctactacaa	1320
ctttacggta	cactacctgg	tttctgatcc	ttatccttac	agcctggaca	ctaattctatc	1380
tacaggtata	tccgggcaac	acatacgact	acctgccatt	caacaagtcc	atcagctcgc	1440
tgatgtacaa	caacctctat	ggccccggaa	actgcctcga	ccagctctac	gactgcgccg	1500
cccgagggcat	cgacgagatc	tgcagcactg	ccgacgattt	ttgcgccaac	gaggctcga	1560
acgtctacga	catttactcc	ggtcgggatg	agtatgactt	tcgtgaactc	actccggacc	1620
cgttccctta	cgagttctac	gttgactacc	tgaacaaagc	gtccgtgcag	gccgccatcg	1680
gcgcatacat	caattacacg	gagagcaaca	acgtgttg	actcgccttt	tcgtccaccg	1740
gtgacgacgg	gcgactcatg	aacaccatcc	aggatgtggg	caagctgctc	aaacaggggtg	1800
tcacggtggt	catgtacgcc	ggggatgccg	actataactg	caactggctg	ggtggggaag	1860
ccgtgtcggt	gcaggtcaag	gccgccaaact	tcagtagtgc	gggttacacc	aacattgtca	1920
cctcggatgg	agtgacacac	ggccagggtgc	gccaggcggg	gcaatttgcc	tttgtgcgag	1980
tgtatgagag	tggacatgag	gttcccttct	atcaaccctt	gcttgcgctg	gagatgtttg	2040
agcgcgtcat	tggcggcaag	gatgtggcga	cgggaaagat	tcccatctcg	tcgagtttac	2100
agacggtggg	cacgccaag	agttactacc	gggagggcaa	cagcacgatt	cagtgggagg	2160
tggttgattc	tctggcgacg	tacaacacaa	ccacgaatgc	tccgaaccgg	gtgagccgga	2220
ggctgaagcg	gatgggacca	gctttgcggg	ttcagatgta	gatctgaagt	acctgcgatt	2280
gtgcattgaa	gtacattggt	cagtgcattt	accgatcatg	gctagctgtg	ccgccccaaag	2340
ggggaagcta	caatctaaac	gccatatctt	tcgatgcaga	caccttacga	gccatgaaat	2400
gccattttat	gatcaggcta	tctactgccg	gtgattttat	gtagtggttg	aaattttctg	2460
ttcaatcgca	acccaaagga	accaactggc	tgtaaaagac	acaacataac	tcgccagagc	2520
caaactgtgc	gaagatatga	gaagcaaagt	ttaaagcgtc	ccaagccatg	gtttccctgt	2580
caagcctcat	tcactctatt	ggcttcagct	gaaagaagag	gataaacatt	caggggtaga	2640
accagacaaa	atctggtctg	gcggggatct	ggtggggacc	cgaatccaag	ttgcgttagt	2700
ttgagggcatg	gatcgacacg	cgacgaacat	gcagtgaggg	gccgctatcg	ctgttttgac	2760
tcgacatcgg	acaaaaacca	aggaaattcg	tattcatcga	tcgatagtcc	ttctcatctg	2820

gcaaggcatg gatccgtctc cccacttcag ccggtacctc ccggcacaac aaaaggagca 2880

tggcagcctg atttcctgcg ttccaactgt tcgtcggttg atctccctga tcaagtccag 2940

<210> 6

<211> 4550

<212> DNA

<213> *Aspergillus niger*

<400> 6

tgaaccatca ggtgggacca cagagcccac cgtccagctc aaggcagctc tctattcgaa 60

gaaagaggta ctggatatat cgggtacttc tagctccagg tcgtgaagcg ttgcgagata 120

cacaaatact gttggcgatc gaatgggacg aacatgtgaa tgtagcacc agaagtggat 180

ggtagctacg aacgatggga ggcggaggct cgagtgtacg atagagctgt ggagatagat 240

tcgtatataa tagagatata tattcattgc attgcattgc tgtggtagaa aacttgtttt 300

ggatcgcatg aattgctggc ctgaatgac aggtcagaag acgccgcagc tccgccggac 360

aagagccaat cagagggcgc caatcggggg gtccgcccggt ttcccttttc agtgtctgtc 420

actgcagctc gcctgacttc agttcctttt ctccttcctc acggtcctcg tcattcgccc 480

ctctctgttg cagtctctct tgttgggggg tcttgtgaat gtcttgctgc tggctccaca 540

tccacaaaag gagcctactg tctgtcgcta cgaacaattc tgttgcgagg gccgctgcct 600

ctacctccgc cgcgccgcgc cgcgcgtcat cgcgccgcgc tggttctaata acttattcgc 660

ctctttatcg ccccatcacc aatcccatcg gatttacttt gtgcctgcg aggtcactag 720

tttctcgcaa tcttaaattt cctgcctatc ggcgtcttag tcgacacttt tctttgtgcc 780

cggccgctgc aacgcccggg gtcaccacga gcatctgac tggtcaggcg cccgtccgct 840

ctctcagctc gctcattata cactctacga gaccccgctc tatacgtatc cgtaccgacc 900

agatggattt gaatggagac gcaggcgcca agcgcaagcg cagctccatc accacacccg 960

ccgaacggcc cgtaaagcac cttcgccccg aatcgagcgc attgacaccc ggggattcga 1020

cgcctgccaa tgggactgta tacgatgtgg aggatgatga agatgcgagt cgtctgctgc 1080

ctgtagggcc tgctcaggcc gactcaccgg aatggcaagc taccatagag gaggttgtga 1140

aaagcgtagt gtctatccac ttctgtcaga cctgctcctt cgacacggag ctgtccatga 1200

gtagtcaggc tactgggttt gtggtagatg cagagaatgg gtacatattg acaaaccgac 1260

acgtgggttg cccgggacct ttctggggat actgcatcct tgataacat gaggaagtat 1320

gttgtagatt ccacatgtgg atcgcccttat gacagtgatg ctgatttgaa ttggttacta 1380

gtgcgacgtt cgtcctgtgt atcgggaccc tgttcacgac tttggaattt tgaaattcga	1440
cccgaaggct attcgatata tgaaattgag ggaactgaaa ctgcagccgg atgcagctaa	1500
agtgggatca gaaattcgcg ttgtgggttaa tgatgcagga gaaaaactga gtattctgtc	1560
tgggtgtcatt agtcggctgg atagaaacgc gccgaatac ggcgatggct acagtgactt	1620
caatacgaat tacatccagg cgcgcgcagc agctagcggg ggaagtcccg gcagtcctgt	1680
agttaacatt gatggccatg cgattgctct gcaggccggg ggtcgtgcag acgggtgcagc	1740
gacggattac ttcctccctc tggaccgacc gctacgcgca ctggaatgca tccgtcgcgg	1800
agagcctgtc acgcgtggaa cgattcagac gcagtggatc ttgaagccgt tcgacgagtg	1860
tcgtcggttg ggcttgacgc ctgagtggga ggcgaccgtg cgtaaagcag cgcccacgga	1920
aaccagcatg ctggtggccg agatcatcct gcctgaaggc ccggcggacg gaaagctcga	1980
ggaaggagac gtgctcctgc aggtcaacgg ggtgcttctc acccaattca tccggttggga	2040
tgacatcctg gattcgagtg ttgggcagac agtgcgctctg cttgtccaaa gaggcgggtca	2100
gaatgtggag attgagtgcc aggttggcga cctgcattgc atcacgcccg accggttcgt	2160
gacggtggct ggaggcacgt tccataacct gtcttaccag cagtcgcggc tgtatgccat	2220
cgctactcgc ggtgtctacg tctgcgaggc tgccggctcc ttcaaactgg aaaacacact	2280
gtcaggatgg atcatcgact cggtggacaa gcggcccact cgcaatctgg atgagttcgt	2340
ggaggtgatg cgaacgatcc ccgatcgctc gcgcgtggc atctcgtatc ggcatattcg	2400
cgatctccac acccgaggca ccagcatcgt ctatatcgat cgacactggc accccaagat	2460
gcgactggct gtgcgcaacg acgacaccgg tctgtgggac ttttcggacc tcgcggaccc	2520
tatcccagct cttcctccgg ttccgaggaa agccgatttc attcaactcg atgggtgttag	2580
ccagcctgct gcggccgaca ttgtgcgcag cttegtacga gtatcctgta cgatgccct	2640
gaagctggac ggctaccccc aggccaagaa gactgggttc ggattggctc tcgatgcaga	2700
gaagggtttg gtggttgtgt cgcgagcgat cgtgccgtac gacctctgcg acatcaacgt	2760
cacggtggcc gactccatca tcgtgaacgc taaagtagtt ttctgcacg cgctccaaaa	2820
ctacagcatc atccagtacg acccaagcct ggtgcaggcg ccggttcaga gtgccaaact	2880
cgccaccgac tacatcaagc agggacagga cacgatcttt gtgggattca accagaactt	2940
ccggattgtc gtggccaaga ccgccgtaac cgacatcacc actgtttcta ttccagccaa	3000
cgcgctccgca ccgcgctacc gcgcgatcaa cctggacgcc atcactgtgg acaccggact	3060

```

cagcgggcag tgttctaacy gtgtcctgat tggcgaggac ggagtgggtg aggcattgtg 3120
gttgaactat cttggagaac gcacatctaa ttcgcataag gatgtggaat accatctagg 3180
atttgcgact ccatctcttc ttcctgtcct gtcgaagggtg cagcagggag agatgccgga 3240
attgcggatt ctgaacatgg agagctacgt ggtccagatg agtcaagctc gtatcatggg 3300
cgtgtcggag gaatggatcg agaagggtgac gcaagctaac ccatcgcggc atcagctctt 3360
catgggtgcgc aagggtcgatt gcccaccgcc tgggttcaac tcagcggccg acacgttcga 3420
ggaggggtgat atcatcctga ccttggacgg acagctgacg acccgctct cggagttgga 3480
tatcatgtac gagaaggata cgctggaagc cctgattgtt cgaaatggac aagaaatgcg 3540
gatccagggtg ccgactgttc caacagagga cctagagact gaccgtgcgg tcgtgttctg 3600
tgggtgctgtg ttgcagaaac cacaccatgc ggtccgtcag cagatttcta agctacacag 3660
cgaagtctac gtcagcgcaa gagtatgtc ctcaccctt aaccactgcc atcaagtaac 3720
taaccaccct atcccttcaa cagagtcgcg gatccccctc ctaccaatac ggcttggccc 3780
caaccaatth catcaccgcc gtaaacggcg ttccaacccc gaacctggac cgcttctccg 3840
aagaagtgag caaaatcccc gacaacacat atttccgct acgggcgggtg acattcgaca 3900
atgtgccgtg ggtagtgacc gtgaagaaga acgatcatta cgtatgccac aaccctccc 3960
tctttacctc caccaaattc agagaatgtg gagactaaca caataatctc cagttcccca 4020
tgtccgagta tatcaaagac cagtcccagc cttccggttg gcggaccgtg tctcagaca 4080
aggataaata taaagacggc attgcaccgg atgctgcgaa cttgaaccg gatgctatgg 4140
acgaaggggt tgatggagtc agtgatattg agccggattt ggagtgattg aaggcggact 4200
gtatagtatt ctgtgatgag catggctgtg ttagatgtgt atagcagaca tggcttgga 4260
tagtagaaaa agtgaaaaat gggaaaatga tagagattaa atcggttcgc atatacgaag 4320
ttgtagatgg atgtattgtt tcggatgttt acgtagtacg tagtggctac tctatcgagg 4380
tgtgatgata gcattagtct ttgatttgtt ttcgtcccat ctgcacatgt actccgtata 4440
tgagaagtat gttgctcgac aaccaagtc tgaaagtatg aatgaacgaa tcgacaacac 4500
acatgaagat aattttatcc aagcaaaaga agccccattt catcttattt 4550

```

<210> 7

<211> 2660

<212> DNA

<213> *Aspergillus niger*

<400> 7

gaatgcgctg aaaaaaatgc tgttgatagc ctaaggtagt caccgcacgg gcttgtgatt	60
ggaggaaacc gcaatgacgc tgggtcccgctg ccatgagctg actcagctgg ctgactcaac	120
gcgtgacttt ctgcaaaggg aaggcacccg catgtgattg gtgccttcc gttcctgcta	180
tcgaggcgctc atcgccctaca gcccacgcag tacacctcct cttctctcct ctctccttcc	240
ttccttctctc tccatcctct tctgggtttc cattgatcac ccagtagctg gtattttctg	300
agctacttgc tttttctatt ttgatacttt tgtgtccgta agttcacttt atgccctctg	360
acccccccct tgataaccgc tgctgataag ctccctgccc aggtaccgta ccttcagac	420
cgcaaggtag ccatcctctg cctactcatc ccatcaccat ctcaattcat accggccccg	480
tagggtttca gcaacaatga gagtccttcc agctgctatg ctggttggag cggccacggc	540
ggcgttctct ccttccagc aggtccttgg aggtaacggt gccaaacacg gtgccgacca	600
tgcggccgag gtccctgcgg atcacagtgc cgacgggttc tccaagccgc tgcacgcatt	660
ccaggaggaa ctgaagtctc tctctgacga ggctcgtaag ctttgggatg aggtggccag	720
cttcttcccg gagagcatgg atcagaacct tctcttttcc ctcccaaga agcacaaccg	780
ccgtcccgac tcgcactggg accacatcgt ccgcgggtcc gacgttcaga gcgtctgggt	840
cactggtgag aacggtgaga aggagcgaga ggctgatggc aagctggaag cctatgatct	900
cagggtcaag aagaccgatc ctggctctct tggcatcgac cccggcgatga agcagtagac	960
cggttatctc gatgacaacg agaatgataa gcatttgttc tactgtaagc acaccttgggt	1020
tcaagatcac gctttttata tgctctggat atctaacgca acttaggggt cttcgagtct	1080
cgcaatgacc ccgagaatga tcccgttggt ctgtggctga acgggtggccc tgggtgctct	1140
tccctcacgc gtctcttcat ggagcttggc cctagcagca tcaacaagaa gatccagccg	1200
gtctacaatg actacgcttg gaactccaac gcgtccgtga tcttccttga ccagcctgtc	1260
aatgtcgggt actcctacag taactctgct gtcagcgaca cggtcgctgc tggcaaggac	1320
gtctatgcct tgcttacct cttcttcaaa caattcccc agtatgctaa gcaggacttc	1380
cacattgccg gtgaatctta tgctggtcac tatatcccc tcttcgcttc ggagatcctg	1440
tctcacaaga agcgcaacat caacctgcag tccgttctca ttggcaacgg tctcaccgac	1500
ggatacaccc agtacgagta ctaccgtccc atggcctgcg gtgacggcgg ttaccagct	1560
gtcttggacg agagctcctg ccagtccatg gacaacgctc ttcctcgtg ccagtctatg	1620
attgagtctt gctacagttc cgagagcgct tgggtttgtg tcccgccctc catctactgt	1680
aacaacgccc tccttgcccc ttaccagcgc actgggcaga acgtctatga tgtccgtgggt	1740

```

aagtgcgagg atagctctaa cctttgctac tcggctatgg gctacgtcag cgactacctg 1800
aacaagcccc aagtcacga ggctgttggc gctgaggta acggctacga ctggtgcaac 1860
tttgacatca accgcaactt cctcttccac ggtgactgga tgaagcccta ccaccgcctc 1920
gttccgggac tcctggagca gatecctgtc ttgatctatg ccggtgatgc tgatttcatt 1980
tgcaactggc tgggcaacaa ggcctggact gaagccctgg agtggcccg acaggctgaa 2040
tatgcctccg ctgagctgga ggatctggc attgtcgaca atgagcacac gggcaagaag 2100
attggccagg ttaagtcca tggcaacttc accttcatgc gtctctatgg tggtgccac 2160
atggtcccga tggaccagcc cgagtcgagt ctcgagttct tcaaccgctg gttgggaggt 2220
gaatggttct aaagacgtgc taccaccgca tatagacttt ctggtcattt cggtgacact 2280
gcagatatgt ttcttaacga tagtttgagc atgcttgta atgcccacta gtcccgatcc 2340
ttatatgttg catggtatct atgagttttg tcactatagt gcattataca tttgtacttc 2400
gtatgagaat gaatcgatcg catttacacg catataaata gtacccaaac cgtctggaca 2460
tgaataaggc ccggccagta gtttacatac agtgtagaaa actaggcgta cagacgtctc 2520
agtacgtaat caatggttaa aaaaaccact cccatagaag ccaagccata agagcctact 2580
catgtagttc gccactgaac gcaccggtat atcgtaaacc agcagaaaga gaaaaggaaa 2640
attgaggaaa ggacgatttg 2660

```

```

<210> 8
<211> 1680
<212> DNA
<213> Aspergillus niger

```

```

<400> 8
aaaacgtgcg cactgcaccc actcgttccg gctggggctc agaaatctgg acgggtcccag 60
gcagatcggg gcctgggcaa aaccttgata aaaatagctt gttcgatctt gagttagaca 120
gccaattgta tactcactag agacacttga tgattcagtc tgtgacgtac gtgcacctcc 180
acactccgtc gatggattat gtgtccccgt gggcacgcgg agatcgggga catcagtcga 240
gaaacttgcc taatctagtg acaagcagaa aagtcaaagt catccgcatg cgacttgcat 300
atcatctaga gggatataat aaagtcgtgc gtttatgacc ttgcaggaaa cgaccgcct 360
cctcctgcct ctttattatc gataccctct gccactagcg tcgtacatca cacttcacaa 420
tccattctcc tctcattcat catgaagttc acaaattatc tcttgacgac tgcaacgctc 480
gcaagcagtg tcctagcggc tcctgctccc cgcaccgggt tggaggacag actccgtgcc 540

```

cgggtcattgc agcgtcaatc acatcctctg gcacctattc cacttgacac atccaccaaa 600  
 gagaattcca gactcctcga agccgacgag aataccaccc atgttacata cagcagtaac 660  
 tggggcgggcg cagtgcgcga gcaaccacct ccgcaaggca cgtattctgc cgtgtcggca 720  
 acctttctgtg taccagaacc cacggcgcaa ggggggagcg gaacgcaggc tgggtcggcc 780  
 tgggtcggga tagatggcga cacatacagc aacgccattc tacagacagg agtcgacttc 840  
 tacgtggaaa acgggcagac gtacaacgat gcctgggtatg agtggtagcc agactatgca 900  
 tatgacttcg acctagatgt aagcacaggg gacacgatcg tcgccaaggt ggaagccatc 960  
 tcgccaagtc aaggtgtagc cactattgag aacatatcga cggggaagaa ggccacgcag 1020  
 acgatcagag cccagctgc gacagctacc cttgccggcc agaattgccga ctggatcgtg 1080  
 gaggatttcc agtctggcga ctcaatggtc gatctggctg gctttggcga gatcagcttc 1140  
 tggggcgtgc aagcacaagg aggagggtct acatggggtg tagatgatgc gactattgtc 1200  
 gaactgaagc agggcaacga agtggtgaca gacgtggagg tgcaaagtga ttcggccttt 1260  
 acggtgaaat atacgagctg atgtgatggt atatggctgc atattctcat ccttcgacta 1320  
 atctttctcc ttttggacgg tgacataatt tttctggttg attttgaata tgccttgatg 1380  
 tatttcggta gtagttttaa gggtgatact tccagcatgc gggctcggct attgggagga 1440  
 accaagaagg ctatatggcc ctcggtatt cgccgcatc taaggtagca tgccttctcg 1500  
 gctttcctta tatatatcta ctttccattt ccccaacctc attcttgatg cgagaatcta 1560  
 cccacacata cagttaatca tgtcccgat ataccaacta agccgagcat ttcagcgag 1620  
 ccaagttggc gcgctccggc cgcgctctct actaccgct cggatcatcc gctcgggctt 1680

<210> 9

<211> 2590

<212> DNA

<213> *Aspergillus niger*

<400> 9

ttacatgctc tgtgtgttgg taaacacgct gtcacattct tcatgtctc tggattgcac 60  
 gataacttta ccggtctct ccaaccggat tgatgaaact atcaacaggg ccccgcat 120  
 ttggcataac cgacattttg aaaaagtatc gcgggcgaga agagagcctt ttcgacaac 180  
 aaacgtcggc ctctttggtt tgcctcgaga gacatagata cagttgaccg cggcgcgaca 240  
 ctttttagga gcgcagagga cggtttctgc ggcgatttga tccgcaggcg agcaaaggct 300  
 taagacacct ctgtttggaa ctgcgcagg accagaactc gaaactaatg cgacattcga 360



gcgacgatga tatatgtcaa ctatatcctg ggacttctgt ccctcttaca caccgctgta	420
gccacagctc ctgattatgt cgtggtagac caactgaaca gcatccccga cggatggaca	480
aaaggcgcag ctccccgcc atttactccg atgaagttct ggttgctgat gcatcacgag	540
tacaaggcgg acttcgagca gaaagtcac gatatctcga caccgggtca ccgggattat	600
ggacggcata tgaaacgcaa cgatgtcatg gcctttatgc gcccatccga tcaggtctca	660
aagatcatct tctcttggtt tgagtcggag catgttccac caaatgccat cgaagatcgc	720
ggggattggg tcgccttcac agtcccgttg gcccaagcac aatcaatgat gaagaccgat	780
ttttacaact tccaccacct ggaaacaaac acaacccaaa ttaggaccct caagtactcc	840
gttccccgagc aagtcgatgc tcatctgcaa atgatccage caacgactcg cttcggccga	900
cctaagacac aaaccagcct accgagcctc atgccagtgt cggttaacat tgatgaaata	960
agcgaagact gcttgacagg cgtgacgccc atttgccttc gccagctcta tggtttacct	1020
agcaccaagg caagccccga ctcgagaaac gtcctcgga tttccggcta tctggaccag	1080
tacgcgcgct acagtgcct cgacgagttt ctagccgtat actctccaaa cagcgtagac	1140
gccgacttct ccgtagtata gatcaacgga ggccaaaacc cacaaaactc acaagagggga	1200
agcacagagg ccagtctcga catccaatac gccctctcca tggcatttga cgctaacgcg	1260
actttctaca ctaccgccgg acgtgcgcca tccgtctcag actcgggtac ggtgagcacc	1320
gacggctcga ccaacgagcc gtatctcgaa cagctccagt atctgggtgg tcttccggac	1380
gaggatcttc ctgcagtgt tagcacgtct tacggcgagg atgagcaaag tctgccggag	1440
gaatacacag aagccacgtg caatttattt gcccaattag gtgcacgcgg ggtctcgggtg	1500
atcttcagca gcggagactc gggcgctcga ggatcgtgtg tatctaacga cggaagccag	1560
aggacccgct ttcagcctat cttcccggcg tcgtgccgtt ttgttacatc cgtgggtggg	1620
actgagggcg tcgggccgga aaaggctgtg gacttttcga gtggaggggt ctccgagcgc	1680
tttgctcgcc cgctgtacca gaatgcgagt gtggaagcat accttgcccg cttaggagat	1740
aaatgggatg gattgtataa tccagacgga cggggtatct ctgatgtgtc ggcccaggct	1800
agcaactatg taatcaggga ccatgggcaa tggctacaaa ctgcgggaac aagggttagtg	1860
gccctaccaa gtcaacaatt gaaaatcaaa cgagctgata atattacagt gctgccgccc	1920
ctgtctttgc agcagtcac tctcgactga acgctgcacg tctcgagcag ggtaaaccta	1980
cactaggggt tctgaatcct tggctgtact cactcgacca gcaaggattt acggatattg	2040

```

tagacggcgg atcagtgggt tgtgacgggt caaatggagg agctcttggt ccgtatgcc 2100
gttggaatgc caccaaggga tgggatccgg ttactgggct ggggacacct ctgtatcaga 2160
ctctggagca gttggcgag tctgcttagt actgcggcgg gatggcctat tttgtgtcgt 2220
tgatgttttt gtcccctaaa tgtcaacgcc attaatctct ctcaagtgcg attagatttc 2280
gtaaaacaga agctggacaa tatgcagaaa ttagagtaca aagctggaga cagaaggtcg 2340
atctccagaa tttgctaatt gttgtgtgtac tcacgtcagg gtgctcgagc acaccagcta 2400
actaccaact ttaccggtta attctaccgc agtagtaatc tagaaaatac tagataagct 2460
gatcaagctt gaaacaaata agcttaccga ccgagaccca tacagcctcg cagtacaaca 2520
acttactacg ggtgagacat cctcaccggt ccgtaagatc gaaaggatta ctatacacgg 2580
agtaagcact 2590

```

```

<210> 10
<211> 3080
<212> DNA
<213> Aspergillus niger

```

```

<400> 10
ggtacagtag tgggttttag tttggatgta tctggagaca tcgatgcttg ttccgaggcg 60
ctaatttggg gccatcgctt agggaagaaa aagaaaggaa ggatttcac tgccgaggca 120
tttttgggtca ggcattggca atactccaag cagcttgcca aagtgagaaa tgtgcttatg 180
aataatattg agtaatagtt aatcaattgt cttacaggat aatatgggaa tagcattggc 240
attgcgtgggt tggcaggcag catgttgcaa attgcaacaa cgcgatcccg gcgatcgccg 300
tcggactccg ggtgggaatc aggggtggag acccattgct tatcaacaac agccgacgcc 360
agtcgttctg ggggtgcattt gcagaatctt tggacgaatc agccttttgt cagtatcggc 420
cggtcgcaat tgaccagct tgctagccgt tggagacatg caatgatgcc attgtctcgt 480
ccgataagca agtgcgcca atccctcggt cctctcgggt gtctcagaaa agttataatg 540
tccgtctcgc ctgcctagcg aacaattcga actctgtgtg tgttgctcct ctcaaggctc 600
ccagcatgcg ttcttccggt ctctacacag cactcctgtg ctccctggcc gcctcgacca 660
acgcgattgt ccatgaaaag ctgcgcggcg tcccctccgg ctggcatcat gtcgaagatg 720
ctggctccga ccaccagata agcttgctga tcgcgctggc acgcaagaac ctcgatcagc 780
ttgaatccaa gctgaaagac ttgtcaacac ctggcgaatc gcaatacggc cagtggctgg 840
accaggagga tgtcgacacg ctgttcccg tggccagcga caaggctgtg attactggc 900

```

tgcgagcgc caacatcacc catatttccc gccagggcag cttggtgaac tttgcgacca	960
cggtcgataa ggtgaacaag cttctcaacg ccacctttgc ctactaccaa agcggctctt	1020
cccagagatt ggcacacaaca gactactcca tcccggatga tctggtcgac tcaatcgacc	1080
tcattctccc aacgaccttc ttccggcaagg aaaagaccac tgctggctctg aaccagcggg	1140
cgcaaaagat tgacacccat gtggccaaac gctccaacag ctggtcctgt gccgatgtca	1200
tcacgctgtc ctgcctgaag gagatgtaca attttggcaa ctacactccc agcgcctcgt	1260
cgggcagcaa gctgggcttc ggcagcttcc tgaacgaatc cgctcgtat tctgaccttg	1320
ccaagttcga gaagctgttt aacctgccct cccagagctt ttccgtggag ttggtcaacg	1380
gcggtgtcaa tgatcagaat caatcgacgg cttccttgac cgaggcggac ctcgatgtgg	1440
aattgctcgt cggagttgct catccccctc cggtgactga gttcatcact tctggcgaac	1500
cgtgagtatt gaattcctag acagagcttg aatcgaagct aattgtgtag tcctttcatt	1560
cccgaccccg atgagccgag tgccgccgac aacgagaacg agccttacct ccagtactat	1620
gagtaccttc tctcaaagcc caactcggct ctgccccaa tgattttcaa ctctatggt	1680
gacgacgaac aggtacgacc ccacattccc ctttcctgt atgtagatac taaccggacc	1740
agaccgttcc agagtactac gccaagcgag tctgcaacct gatcggactt gttggcctgc	1800
gcggcatcag tgtcctcgag tcgtccgggtg acgaaggtac acttacttcc cctgtcctat	1860
tccttgcatc gaaaataccc taacagcagc acaggtatcg gatctggctg ccgaaccacc	1920
gacggcacca accgaaccca attcaacccc atcttcccgg ccacctgtcc ctacgtgact	1980
gccgtgggag gaacaatgtc ctatgcccc gaaatcgctt gggaagccag ttccggcgga	2040
ttcagcaact acttcgagcg ggcgtgggtc cagaaggag ctgtgcagaa ctacctggcg	2100
caccacatca ccaacgagac caagcagtac tactcgcaat tcgccaaact tagcggtcgc	2160
ggatttcctg acgttgctgc ccatagcttt gagccttcgt gagtccattc ccagcatcat	2220
gataatacga aatagggctt aatgacatct gcagatatga gggtatcttc tacggcgccc	2280
gctacggctc cggcgggtacc tcagccgctt gtcccccttt ctctgcgcta gtgggcatgc	2340
tgaacgatgc tcgtctcgcg gcgggcaagt ccacgctggg tttcttgaac cccctgctct	2400
atagcaaggg gtacagagcg ttgactgatg tgacgggggg ccagtcgatc ggatgcaatg	2460
gcattgatcc gcagaatgat gagactgttg ccggcgcggg cattatcccg tgggcgcact	2520
ggaatgccac ggtcggatgg gatccggtga ctggattggg acttcctgac tttgagaagt	2580
tgaggcagtt ggtgctgtcg ttgtagatgt atactatata tatggtatga gattatgtat	2640

gtgatatgtg atattatgtg agagagaatg gtttagactg tgcgtcatat acatggacag 2700  
 ttcattttct cattaaacga gcaccttcat acggttaagga cctcagaggt tcctcccatt 2760  
 gttatgaccg cttcccttct ttctagagat acatgcttcc ccaccccgcc tcaacgcgac 2820  
 cgtctacgga caccagtcag aagaccccaa caaccacta ttagtggcta gtaaggacga 2880  
 catgcataat tactccgtga aacccccgaa attaagcccg acaggggcat agagaaaccg 2940  
 atccaatcac ttaacttacc ccgcttctag cacggcatag ggctgagcga tgcgatgggtg 3000  
 caatggccac gccgttgccg attagccgta gggccagttg tgaatttccg ggatcaccct 3060  
 acaacacatg cttcatgcgt 3080

<210> 11  
 <211> 1890  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 11  
 gaggatgata gtctgatggc cattccgctt gaggcaaagt gtgcccgaat gtcacgcggg 60  
 cagctagtct tctgcaggtc tgcagttgga caggggaact tgagtgtat tatcgccaag 120  
 gtgaatgttc tctaccgctt tgataccaga gtgatcgctc cttttgccgt cactcttggg 180  
 gttgcaagc agatgtcgtt cgtttgcata tgggagccga agatccacgc aggggtgcttg 240  
 aaaagacata ctgcgatcct cccgtttcca agaatgcttg tacacttgaa gtttttgtca 300  
 agatccccc gcctggccag tcccagccta agcgaaatga gctttccctc aatgctgcag 360  
 acaggagaca ccacgctttt ggcgccttgg caccatcagc caccgtcggg cctatcatca 420  
 tcgccctggg caatagggaa cgcgtcaatt gcgtatctgg gtagtggtat ctgctcgata 480  
 ttgcaccggc agagcaggaa tcgggattgg cggatgtaga gaaaattcag cttcaaggag 540  
 gggggaaggg agacgctgaa atggtataaa accacgtcca attccctacc agatagccct 600  
 catccagcag catcaaaagc atcttccact cagactccaa gcagctccca gtccctcttc 660  
 aattcattac cttccaaaca tcatcccatc aagatgaaga ctactgctct cttgaccgcc 720  
 ggctgctgg ccaccactgc tatggccgct cctctgacgg ccaagcgcca ggctgctcgg 780  
 gccaagcgct ccacgaaccg ccagagcaac cctcccttca agcctggcac caacgaggtc 840  
 ctgccctta acggcaccaa gaatgtggag tacagctcca actgggcccg tgccgtcctc 900  
 attggcactg gttacactgc cgtgaccgcc gagttcgtcg tgcccacccc ctccgtgccc 960  
 tccggtggct cgagccgcga ggagtactgt gcctccgcct ggggtgggcat tgacgggtgac 1020

```

acctgtgaca ctgctatcct ccagaccggt gtggactttt gtgtccaggg cagcgagggtg 1080
agcttcgatg cctggtacga gtggtacccc gactacgcct acgacttcag cggcatctcc 1140
atctcgcccg gtgataccat caaggtcacc gtcgatgcc a gcagcgacac caccgggtact 1200
gccacgattg agaacgtgag cactggtacc acggtcaccc acagcttcac gggcgggtgtt 1260
gatggtgatc tgtgtgagta caacgtgag tggatcgtcg aggacttcga ggaggatgac 1320
tccctcgttc cctttgccga ctttggcacc gtgactttca ccagctgctc cgctaccaag 1380
gatggttcct ctggtggccc tgaggatgct accatcatcg acatcgagca gaatgagggtg 1440
ctgacctccg tttccgtctc cagtagcgag gtcgttgtca agtacgtcta agacgttgga 1500
tgtatggggg tggggattgt tgatgccccg atgggtgtgc tttcgacggc aatgggtgaga 1560
tgagtgatgg aaatgagagg ttggtctttt ggccccggggc tagttttctc ttggtactcc 1620
tgaaaagcca atagttcaaa tgtctttatc ttgttagttt gatgttatag tttgccttga 1680
gttgatttaa ttgaaccaac gttggatcat cgtatccctt agcgcaaata aaatattacg 1740
tacgcctttt aaaatattat gtatgtctgt taaggttctg actgttcaga tttatgtcaa 1800
acaacagcaa atcattggta atccaggact cggggatatg agcttcagac attcacccca 1860
ttactgcatg actatgaccg tgtcttttagc 1890

```

```

<210> 12
<211> 3080
<212> DNA
<213> Aspergillus niger

```

```

<400> 12
ttgttgtgat tgctaagaga catcacattg ctcatatgag tttgattgcy actgttaata 60
ttaatgtccg actgggagga aatgagtggc gttatccagg cagctgcatg caatactaca 120
ttccctcac gagggaaatc tggccatctc ggaaatcaat ggtgtcatcc gagttgattc 180
ccctcaataa tggctctgat aagccactat tgctgcagaa cgcctatctg tgccgttagt 240
gcatgcatag tgtccccagt tctttttctg ccgattaatc tattgccaga cggactccgt 300
cgcgcttccg aatgccggga accgcggcta agctttgctg tagctttgct gcaggaacat 360
ctgcatcttt caaaatatct tcagaggagc cgatcgctga gtttctcaag agattagatg 420
aatgttcgta cttggccgca atataagctt catggcggct tcaaccttcc atgagaaata 480
agaataaggc tgccggggat ggcctcaccg tgtccctgca tgcaagggat gcataatgca 540
ccgtgacctg ttccaccacg ccggagcccc cccgccctcc gacggcccaa acccactgca 600

```

gaatggcttg attaatgtcc ccttctataa ctaaccgggtt gttcctcgtc gttgtctgct	660
ctgctctcca cccagggctcg tttttgcttt tgcctcctta accatggctcg ccttttcccg	720
catctcggca ggcttcgccc ttgccgcccc tgcctgggcc agcgtcgctc tggagaccgt	780
caagtctggt cccagcgact ggaagctcgt ggaggtctgt gataccagct ccacaatttc	840
tttgtccggt gctctggcgc gtcagaacct ggaccagttg gaggagaagc tcctggccgt	900
gtccaccctt ggcaaggaca cctacggcca gttcttggat ctggacgaca tcaatgagca	960
gtttcctctc gcagatgacg ctgctgttgt ggcttggctg aagaaggcag gcgtcaccca	1020
gatccataag gaggggtggc tgctgaactt tgcgaccact gtgggcacag ccaaccagct	1080
tctcaacacc accttctcgg tgtacaagag cggatctacc cagaagctgc gcacaacgca	1140
atactctggt ccgatgagc tgaccgggtc cattgatctc atctcgccga ctgttttctt	1200
tggaaagtcc aacgctgcgc gctcggcggc cgtgcgtgct tcgcagacta ccaaggagac	1260
cagcagaaag aagagcagta atgtgtgcca gtacatcact ccggattgcc tcaaagagca	1320
gtatagcatt gactatacgc ccgaggcatc gtcgggaagt cgtgttgggt ttggcagttt	1380
cttgaacgag tcggccttgt actcggattt ggatctgttc acccagtact ttgacattcc	1440
ccagcagagt ttactgttg agactatcaa cgggggaatc aacaaccagg agaatgatcc	1500
ggatggtgaa gccgatctcg atgtccagaa catcgtgggc atctcgcatc ccttgccggt	1560
gacggagtac attaccggag gatctccgtg agtgttccca aagatgcaat tgaattaaag	1620
ctaattgggtc agtccattca ttcccagcgt cgagactact accgacgaga acgagcctta	1680
cctgcagtac tacgagtatc tgctggccaa gaccaacgac gagctgccac tggttatcag	1740
caactcgtac ggcatgacg aagatgtaag catccctgcc tcccacacaa atcgccctgct	1800
gacagaatag accgttccca ttgcctacgc caccgcgta tgcaacctca tcggcctgat	1860
gggcacacgt ggtatctcca tcctcgagtc ttccggcgac tctggtacgt tgtaccccat	1920
atatattgca tcaagtcccg actgacaaat acaggtgtgg gcggcgcatg catgtccaac	1980
gacggcaccg acaagaccga attcaccctc atgttcccag gaacatgcc gtacatcacc	2040
gcggtcggcg gcacccaaga cgtgcccga gtcgcctggg tggacagctc cggcggcttc	2100
agcaactact tctcgagcc gtcgtaccag tcggatcagg tggagacct cctggacaag	2160
tacatctctg cctcgacgaa gaagtactac gagcagtaca ccaacttcag cggtcgcgcg	2220
ttccctgacg tgtctgcgtt tgcaggttct ccttagtatg tatccatccc agatgattgt	2280

atggacatct gctaattgtcc gacagctacg aaacttatat tgatggtcag ctcggccttg 2340  
 tggcggttac ttctggcgct agccctgtgt ttgcggggat cgtcgcgctg ctgaacgatg 2400  
 cccgtctgcg ggccaacaag acatccttgg gcttcttgaa cccttggctg tactcgagcg 2460  
 gctacaagag cctgaatgac attaccagtg gcgaggcagt gggctgcca ggcatgtgg 2520  
 agggcgctgg agtcattcct tgggcgagct ggaatgccac gacgggatgg gatccggcga 2580  
 cagggtctggg aacgcctaatt tttgccaagc tgaaggaggc ggttcttgcg ttgtaagcag 2640  
 gaggatactg agtggacgtg cggagtgaag gatatgtgca aggcgttaac ttataatagc 2700  
 ctgtgtgtgg actatagaat catctacagc ccacaaccaa ttagcttctg catagtcacc 2760  
 acccttaaac taaggataat caattgttta ccgctgtcag tctcaaatec gtcatgtcat 2820  
 ggacctgtt cgatcaactt gaaacaagct taatctacca gggcggtga tgaaccgcc 2880  
 agcggacact tgtttcagtt acccgcaagc ctgtatccag tatgcaagcc ctacttaaac 2940  
 ccttcaccac cctgattatt ctactctctc tctctctcca accacaccat tcttttcttc 3000  
 attgtgccgg tcacatccat tctttacttt cattctctc ccttctcttc tcttctctac 3060  
 ttccccaagt cactcattat 3080

<210> 13  
 <211> 3598  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 13  
 accggagcag aggaacaagc ggagaagctg aaacgtatga atgctgagta cgagcaaaag 60  
 ttccctggct tgcggtttgt gtatgttctc tcagtatacc caacgacttg tgttggctg 120  
 acatatctcc ctggcatagt acttttgtaa acggtcgcaa ccgggatgtc atcatggagg 180  
 agatgcgtga gaggattgac cggggcaatg ccgatcgtga ggtggaggag attatacagg 240  
 tgagatggct gtctacccaa acacggagca gtgctgacag ttcgctcctt taaaggcaat 300  
 gtgcgatatt gcaaaggatc gggcgcgga actggagcag tccgctaaga tatagttcac 360  
 atactgcaag catatattta aacaatgaat acccttcgat ttcagcaggc gctgcgacat 420  
 ctcttgctg aatcgtgct ttacaagcca tatttcggtc catgcgattc atctatggag 480  
 cactctgcct ctgtccgga acaatggctg gtaatctgca tggaaacttg tgattccgtt 540  
 agtataaagt gaccaactag tgccggcgaa ttatgggaag cctgccttgt cttacgacgg 600  
 gacgatcttc cgtcgaacgc gtgctaccag cattttcata gtatgacggg tccgtatttg 660

atttactatc gatggtaaaa cgcctcctct atgggggtccc ctagcactcg gcaggccagc	720
ttgtgagaca acccgggagg tcagccatta ttaggccaat gagagctggc aggttgagaga	780
ggttgtactt cgacaatgtt ggacagccat gcaacgtcgg acaatagctt tgatagggaa	840
tatcctaagg gcgaaccagg agggataggg gtaggtatgg ctgtatcgat tagtagtccc	900
tctttcacc cagaacaaact ctagtatata tagtagtaaa tgttccgcgg atggccaatg	960
accccaaata atctttcatc ccatccacgc atgagcaaac atgcatggtc tgcgcctagt	1020
atgcagcata gggacattgc ctttggttat cctggcatat ccggcggtt cattgcatac	1080
aacttcagca gccgtggact tggactccct tcgtctgacc tctaactccg aatacgtcaa	1140
ttctgtccat gtagacacga atcgatcagt cgcagtgtcc gctgaagaac attataccga	1200
tacagcagct cgactgggtc agaacattgt tcctggagcg agctttcgtc tcatcgatga	1260
ccactttgtc ggcgacaatg gagttgcaca tgtatacttc cgccaaacgc tccatggtat	1320
tgacattgac aatgcggatt tcaatgttaa tgtctgtccc ccaattactc tgttcggaag	1380
gaagcttact gttacagatt ggaaaagatg gactgggtctt gtctttcggc cattcgttct	1440
tcacaggcgc gttgccgagc agccatctgg acaataccaa egttttgagt ccggaggctg	1500
cacttagagg agcaagggac gctatacagc ttccactgac tattgacaat gtttctactg	1560
aagctgcaga ggggcggaac gagtacatat tcagagagggc agtgggagcg gtatctgacc	1620
ccaaagctaa gctagtctac cttgtcaagc cagaagggac tctggcgctc acctggagga	1680
tagaaacaga catgtatgag cactggctac tgacatacat tgatgcagag actaccactg	1740
tccacggcgt ggttgactat gtcgcagacg cgacatatca agtttagtga gtggctctcc	1800
ccatcgaata acgaagctaa gacaacagtc cctgggggac aaacgatcca gcagaaggac	1860
atcgcaccat tgtcaccgac ccctgggacc tatccgcac cgcatacacc tggataagcg	1920
atggacggga caactacacc acaaccagag gcaacaatgc catcgcacac tggaaatccga	1980
ccggcggtgg ctctatctc tacaacctac gtccatccga cccaacttg aatttccaat	2040
ggccatactc cccaacatg tccccacccc gatcatacat caacgcctcc atcgtccaac	2100
tcttctacac agcaaacgcc taccacgacc tcctctatac actcgggttc accgaatccg	2160
ctggcaactt ccaatggaat aacagcgccc acggcgccg agacaaagac tacgtgatcc	2220
tcaacgcaca agacgggtcc gggttcagca acgcaactt tgcaaccca cccgatggta	2280
tccccggccg tatgcgcatg tacatctgga tcgagtctac tccgtcgcgt gatggaagtt	2340
ttgacgcggg cattgtaatt cacgaatata ctacgggtgg taagcatctc cccagaagat	2400



ggaagtccta atctaacaaa ccagtatcca atcgtctcac cggcggtccc cacaacgccg 2460  
 gatgcctcag cgccctcgaa tcgggtggca tgggcgaagg ctggggcgac tttatggcga 2520  
 cggccatccg aatcaagccc aacgatacac gcacaacgtc ttacactatg ggtgcatggg 2580  
 cagataatga taaatgtggt gtccgggact atccttattc tacctccttt actgagaacc 2640  
 ctttgaacta tacgagcgtg aataccatga acggcgtgca cgccatcgga actgtctggg 2700  
 caaccatgct atacgaggtc ttgtggaacc tcatcgacaa gtacgggaag aatgatgggt 2760  
 cgaggccggt gtttagaaac ggggtgccta cagatggaaa gtacttgatg atgaagttgg 2820  
 tgggtgatgg gatggcactg taagtgatgc acagaatagc ttctttcacc tttgtaatgt 2880  
 ccgtgggtatc ctgactaatg gactgaaggc aaccatgtaa tccgaacttc gtgcaagcca 2940  
 gggacgcgat ccttgacgca gacattgtgt tgactggcgg gaagaatcgc tgtgagatct 3000  
 ggaggggggtt tgcaagaga ggattggggc aaggagcggc tcatagtagt ttaaattgga 3060  
 tgcggagggg gagtacactt ctctctacgg gatgttagtc ttgcacaggt cgttcttggg 3120  
 gagagatgag tggagatgcc tgggttatta gaataggact aattatctag cactaataca 3180  
 atatcgacag atctaaacag taagtataaa tctataagtt atcacacgca taaaccccat 3240  
 caccctctag tctacttcga aacaaacacc acaccaccaa catcctcacc ctcaccaaac 3300  
 acccctcccc cgcataagaa cctaaacaac agccctcaac tccatactct gcgccccct 3360  
 cgccacacac aacaacaacc caccacgag cagactcacc cccgcgtata tcgacagcgc 3420  
 cagaaacca tacttctgca ccagcgcccc ggaaataggt atcccagcca tagcactaca 3480  
 ctcccagata agatattgatt agcaaaatcc acccttactc cccaagaaga tcaattcaaa 3540  
 ataaatctaa tgtgcatacc tcaaagccgt agccccata acaaccccca ccgccaac 3598

<210> 14

<211> 2847

<212> DNA

<213> *Aspergillus niger*

<400> 14

cttttggctt gtgatcttga ttgctagaga tgtatatcct cacggatacc gccggagtgc 60  
 gccatttctg gttaccttct ctttcccttt ttgtctcgat cgtgaggcgg aacgcaggat 120  
 gaagacacgg cttctccacc gcggcccacc aaccaacaat gtccttgagc gcccaactct 180  
 ccatctactg gtcattgggc caatgcagag actccgtcga gctcaaatgg gccggccaac 240  
 cccgagtcgt caggggcagc ggacgcgacg agctaaatta gaccactgat aagacgcgat 300

```

agtccaaagt ctgaccgtca cattgtgcca ggcagataag ttgaatcgtg tgactggatg 360
ttggctaacg tatggcgtct ccggaggccc gacggaccct gcgcgatcgg cggaggagcg 420
caatctaagg acatccgcgc ctaagatata tacccttcag cagttcagcc tagccctgca 480
gacttgtcgg accagtgcta tcgtgatcgg cccccacggc cgaatgagct cttgtctctt 540
tccgtcagac cctgccagtt aatctgctat ctactccgcg gtaacatcgt gcctgtctcc 600
actaaggcag ggtccagggc tgtatgtctt actttgcacc gagtcggccg ccggttggtc 660
ctgtcttggc aattgcgaat atcctcacgg gcgacggacg acacggattt ggacggacat 720
gcggagatct tcgtcggttt attcctggaa gggacatcat ctccctccat catgacggct 780
gccatagcgg ggactctgag acatttttgc tctgaagagc atggtcgact tggatgatgg 840
aggagttagt cgagggtcaat gaggagaggc ttgcaagtat aagaagagac tgctcgacca 900
gcagaatgga tcttcttggt catcaaccaa gagtccaagg cttctttgtc tggttctatc 960
tcttctccga actctcttgc ttgacattct cgtggtcaaa atggtcgtct tcagcaaaac 1020
cgctgccttc gttctgggtc tgtcctccgc cgtctctgcg gcgccggctc ctactcgcaa 1080
gggcttcacc atcaaccaga ttgcccggcc tgccaacaag acccgcacca tcaacctgcc 1140
aggcatgtac gcccggtccc tggccaagtt tggcggtagc gtgcccaga gcgtgaagga 1200
ggctgccagc aagggtagtg ccgtgaccac gcccagaac aatgacgagg agtacctgac 1260
tcccgtcact gtcggaaagt ccaccctcca tctggacttt gacaccggat ctgcagatct 1320
gtaagcttcc ctgctcgggt gttcgggcaa atcgtgacta acctggacta gctgggtctt 1380
ctcggacgag ctcccttctt cggagcagac cgttcacgat ctgtacacgc ctagctccag 1440
cgcgaccaag ctgagcggct acacttgga catctctac ggtgacggca gctcggccag 1500
cggagacgtg taccgggata ctgtcactgt cggcgggtgc accaccaaca agcaggctgt 1560
tgaagcagcc agcaagatca gctccgagtt cgttcagaac acggccaatg acggcctttt 1620
gggactggcc tttagctcca tcaacactgg tgagtcaatc ctacatcagc cgggttgacc 1680
tacctgctga ccgatacaca gtccagccca aggcgcagac caccttcttc gacaccgtca 1740
agtcccagct ggactctccc cttttcgccg tgcagctgaa gcacgacgcc cccggtgttt 1800
acgacttttg ctacatcgat gactccaagt acaccggttc taccacctac acggatgccg 1860
atagctccca gggttactgg ggcttcagca ccgacggcta cagtatcggg gacggcagct 1920
ccagctccag cggcttcagc gccattgctg gtaagaaccg ccttcattta acacacaact 1980

```

```

tgtccacctc tttactaact agtgtataga caccggtacc accctcatcc tcctcgatga 2040
cgaaatcgtc tccgectact acgagcaggt ttctggcgct caggagagcg aggaagccgg 2100
tggctacggt ttctcttgct cgaccaaccc ccctgacttc actgtcgtga ttggcgacta 2160
caaggccggt gttccgggca agtacatcaa ctacgctccc atctcgactg gcagctccac 2220
ctgctttggc ggtatccaga gcaacagcgg tctgggactg tccatcctgg gtgatgtttt 2280
cttgaagagc cagtacgtgg tcttcaactc tgagggccct aagctgggat tcgccgctca 2340
ggcttagatt atccactgaa gtggagtcta tgatctgctg attgatccct cgacgatgaa 2400
ctacatgtgg aaatgcatag cagacgaggg tgatggtgat gatgttgatt tgatgatgac 2460
ccgtacatac ttgatgaagc tcggtacata tgcaaatgtg actgtatcta tgtgatgaat 2520
atatgtatcc atctcatggc ttttggctat gagtgcagga taaacacctg aaccagtagt 2580
agtactttcc cacctatatc tactgcggtg cctcgccgg cccaacatca cccagaggt 2640
ggccgcagag gagtcttata agatagctac tatcagttac aacacctctc tgacagatgt 2700
gaaggagtac aataaatcac cgaaacacaa attcaactaa agtcggtaag taataataat 2760
ttaagacca atccacgcaa tgttaaacta tctctggtgt tgaaagatct ctcccctggc 2820
aacacctagt tgtgggagaa ctgtgtt 2847

```

```

<210> 15
<211> 2899
<212> DNA
<213> Aspergillus niger

```

```

<400> 15
gcccggtga agaccggaca ggaagcggat aggtacggga cattttctaa tctaccgcg 60
atcgggacat ggctaacc aa gcatatagac tcgaattcta ccggtaaatc aagtatggga 120
cgtgcatcag gctggatatc ggattacgca aggcgaacag ggggaccggt agctgtatta 180
tcaacatcta ggctatttca tattaggaca acgactgacg cattgggtat tccgctgggg 240
tagtcttatac gggtggggcc aagtaccttg tagaactgta acccacgtta ataccgccac 300
ttggctgggg cggtgattta gcatatgtaa gctccagttg gacggctacc cgagcttccc 360
atgatctaca ggagtacgtg tctggctgct tgctgcctac ttggtagaca ggtcagcgat 420
aggtagatag gacctgtccg cagctgttgg ctagtgttgg aaggcgggtg cgctagtttg 480
aagtaggcag gcaccgggaa cctaaggcgg tcttacatca tcaccgcgc tcggattcgc 540
gtgatccgac catcacgata aggcctcagg tagcaaggag accttccaga cagctctgaa 600

```

tgagactcaa aggtagatat aatgatggaa agataggata gctagatcag gcttattgta	660
cctgatcggt aagagcctag agaagatgta cctggaagac ctggcagcta caatcacctg	720
gagcgataac ccgtgacgat ccccttgcca aatgacgcag ccgggctggc caaccattgg	780
ctgcgacctg gcaggctcgct ccgcaaccag cgccgcccgg ctccaagtca cccgcatcac	840
tcttccttac cccagacct cctcttttcc ettgctatcc tccatctctt ctccatcggt	900
ctttgtctct atcatcattt tctattcata cgtgcatcat tcagtcgttt ggcccagtcc	960
atcatatccc gctgggtagc cgtttccgcc gtcgcccata atgaagtcag cctccttgct	1020
cacagcatcc gtgctgttgg gctgtgcctc cgccgaggtt cacaagctca agcttaacaa	1080
ggtgcctctg gaagagcagc ttgtgagtgt ggtctttcac tgctttgttt tttttagcta	1140
gttagcttca aagaagctcc agaaccattc aaagctgatt tcgtggtcta tagtacacgc	1200
ataacatcga cgcccatgtc cgcgctctgg gccagaagta catgggtatc cgcccgcca	1260
tccacaaaga gctggctgag gagaacccta tcaatgacat gagccgtcat gatgttctgg	1320
tggacaactt cctgaacgca cagtgtatgg agataccgtc ttcttatggc tgcaactgct	1380
gacccttctt gccatagact tctctgagat cgagctgggt actcccccc agaagttcaa	1440
ggttgtctct gacactggca gctcgaacct ttgggttctt tcgagcgaat gcagctctat	1500
cgctgtctac ctccacaaca agtatgattc gctcgcctcc agtacgtatc acaagaatgg	1560
cagtgaattc gccatcaagt acggctctgg cagccttagc ggattcattt ctccaggacac	1620
cctgaagatt ggcgacctga aggtcaaggg acaggacttc gctgaggcga ccaatgagcc	1680
tggccttgcc ttgtccttcg gccgggtcga tggcattctc ggcttgggtt atgacaccat	1740
ctccgtgaac aagattgttc ctcccttcta caacatgctt gaccaggac tcctcgacga	1800
gccggtcttt gccttctacc ttggagatac caacaaggag ggtgacgagt ccgtggcgac	1860
cttcggtggt gtcgacaagg accactacac cggcgagctg atcaagattc ccctccgtcg	1920
caaggcttac tgggaggttg agcttgacgc cattgctctt ggcgatgatg ttgctgagat	1980
ggagaacacc ggtgtcattc tggacactgg tacctccctg attgctctgc ctgctgacct	2040
ggctgagatg atgtaagtcg aattcttcgg attcctgggt tgaaaagaaa tgctgctaac	2100
aaccttctag caatgctcag atcgggtgta agaagggtg gaccggccag tacaccgttg	2160
actgcgacaa gcgctcgtcc ctgcccgatg ttactttcac ccttgccggc cacaacttca	2220
ccatctcttc gtatgactac accttgaggg tgcagggtc ttgcgtcagt gccttcatgg	2280
gcatggactt ccctgagccg gttggtccct tggccatttt gggcgatgcg ttcttgcgca	2340

```

agtgggtacag cgtgtatgac ctgggcaaca gcgctgttgg tctggccaag gccaagtaaa 2400
ttagttctgc gggttgatgt ggtatctatg atgcagctgk tgctgtcatt attgcttctt 2460
gtagcttgat ctatgat ttt tgcagacgaa cacacgtgat gttgtgaatg gttttcctca 2520
tgtttgcagc ggttgccgga tagattctag ggatcttcaa tggaaagccg gtgatattat 2580
ttgaccttta tttgggcaact gagaatcttg actgtatgaa atatgatagt aacaccttaa 2640
acatgaatgc aaatggcgta aaccgtgtga tgcagtcaca ataaccagca accgcggtac 2700
cagccgaagt ctgggcccgc gagtctcgcc ccgcacaggc caggcgccaa acccaagcag 2760
cgctcttggc agccaagcct tcttcacac gctctcacca cctcctccat ccaggcttct 2820
tctctgctcg gtctttgttt catcatctc ccaagcctgc ccttctattc aaccgctctt 2880
cgatcttcat atccgatcg 2899

```

```

<210> 16
<211> 2738
<212> DNA
<213> Aspergillus niger

```

```

<400> 16
gaggcatgag gcatttctga ggcccgtac tccgcattct gcagcatatc gtctctgcgt 60
aggggagggtc gaaaccagct gtaggactcg gcttcgggtg atctgtaccg actgactaga 120
aatcgctcaa tcgtgtagta tagctgtctc tttgttcctc acaacatgtc tacgatatgc 180
tattaaaaaa agcagaagat ggagtcagag ccaccgggtt agggccgggc cgcccgggag 240
gagaacaaaa tacgggacag aatctcagtg atgggggaga agagagagtg gcgacctgac 300
aattcacaca cgacacgaat aatagccgaa actaacaaga taaatcacat cacatcatga 360
agaagacctg cgtaatgatg ataagcaatc ccaccaataa tacaatgcca ttgatagtgg 420
ctgacctgaa gcaattcggg gaggagacgc caagctcgac gatcaccgga gcttgaaaga 480
ccaacgagac aagatgacag gcccgtcgca ccacgccact aactgcccta acagaaatcg 540
gcctgaatag tgcgacgagt gtcccgggtc tgggcctcca cgataagata agtcatgggc 600
ttatcgcgtc atcggcgccg atctcgcgat cagctgaaac caatcattca atcaatttgc 660
atcacccgac tgggggagag atttcagggc cagctgaaac ggtcgggtgc cgagattgtc 720
agtggatgat gaatgttatg ctggaagaga gggggagaat gacgtctcaa ttctgggtca 780
cttactagtt gactagccac ctagtattta gctgctagct agggattcgg tttaaaagcc 840
tgggtggttct tctcttcttc tcgtcatttt ctcttcatct cataccatt ctctaaaact 900

```

cctccacttt gatcaattat cctccatcat ggctacaaa atcaagctca tccccaatct	960
caactacaag cgctcaggca ccaagtccta cgtgcacttg atgcgcaagt accgcttcca	1020
tcccaccaag cctggctcct acactctcag cagctccatc caacagaccg gtcgtccgta	1080
cactgaaaag cccatcgggg gtcgggcca tatccggcag ctggtgcgga agaagagcac	1140
caccagcgat gaggttgcg aggttccggc cgaagatgtg cagaacgact ccatgtatct	1200
ggcgaccgtg gggatcggaa cccggcgca gaacctgaag ttggactttg aactgggttc	1260
agctgatctt tgggtacacc ccattatga aagacctaat atggaaacga gcgtcactga	1320
cagatgtagg tctgggtcaa caactcccc tcaacccttc tatccgagaa caagacccat	1380
gcgatcttcg actcgtcaa atcgagcacc ttcaagacct tggaagggtga atcctggcaa	1440
atctcctacg gagatggatc ctccgcatca gggagtgtgg gcaccgacga cgtcaacatt	1500
ggcggcgtag tegtcaagaa ccaagccgtt gagctggcag agaagatgtc cagcacattc	1560
gcccaggcg aaggggacgg attgctcggc ctagcattca gcaacatcaa cacggtacag	1620
ccaaagtccg tgaaaacgcc cgctcgagaa atgatcctgc aggatgacat tccaagtgcg	1680
gctgagctgt tcacggccaa gctggatacc tggcgggaca ctgatgacga gtcgttttac	1740
acctttggct tcattgacca ggatctgggtg aagacggcag gtgaagaggt ctactacacc	1800
cctgtcgata acagtcaagg cttctggcta ttcaactcga cctccgcgac ggtaaatgga	1860
aagaccatta accggtcggg taacaccgcc attgtgata ccggtacgac gctggccttg	1920
gtggacgatg acacgtgtga ggccatttat agtgcaattg acggcgccta ttatgatcag	1980
gaagtacagg gctggatcta tccgaccgat acggcgaggg ataagctacc cactgtgtcg	2040
tttgccgtgg gtgaaaagca gttcgtgggtg cagaaggagg acctggcggt ttcggaggcg	2100
aagacgggct atgtctatgg aggaatccaa agtcgtgggtg atatgacat ggacatcttg	2160
ggagacacat ttttgaagag tatttatgct gtaagtgcac tgctgttggc gttaaggggt	2220
gatatcgaag ctactaact ggattgcaga tctttgatgt cgggaacctg cgctttggag	2280
ccgtccagcg cgaggagttg cgccagagcc tgaagtcgga gtagacgagt ggctgaatct	2340
atcatggttt gatgatgtta tgtatttgca tgtcccgttt ttttgggtta atcctagtgg	2400
cttttgagcc ccgaagtatg tacgcagtaa atagcagtgc aatatagtag tccgtacctt	2460
gttatcagat gctctgggtt gaagcacaaa ggaagccatc agtctcccaa tcagagcttc	2520
cagcccgccc cgtccttcca tttccacaac ctccagcgcca tgaaacatgc catccctgct	2580

cctaccataa cgcgcgcaaa aagctgcccc ttccagaaaa cagcatgttc cagatccaac 2640  
 aacgccccgg caataggatt tccaatgaga atgccaagcc cgcggaacac gaaagacatg 2700  
 cccatccacg tccccacaac agccatgtct ggacacaa 2738

<210> 17

<211> 2349

<212> DNA

<213> *Aspergillus niger*

<400> 17

cgcgcactaa ccctccacgt attccaatat accaaatctg cccaaagcgc cagccagctt 60  
 cctcaagcct tgcggtcaga taaggccctg tacctagcta gttgccgctg ctcccggcgc 120  
 tgggccaagc cgtcggacgt cgtcccccc tctttcccc tcctctcccc tctccactgg 180  
 tggaaacgatg tctggctgtt gccatcgttc tcagaagcaa cgtcccctgg atcgggtggc 240  
 tgtcgtacta ttgcatgttc gtccgcgcta ctaggaaagt ttttttccca cccggagtat 300  
 ccgtgttttag tccgcgggct ggctgaccgg ctagtggcc gtgccagttg ggtaaggttc 360  
 caagggagga ccttactagg tagaaacggg atccaacaat gaggggaaaa gggcggatat 420  
 ggcttgccgg gggttcattg cggcctggac gaagaaaggg agatgatcac taatgcaaca 480  
 caatcttggc ttgcaaggaa ttgcgtcca accagaatgt ctctgcgtag ggatgccaat 540  
 tcgtgcgggc catgctggat ggatagtacg ctgctccact ctgctcgcac cttttgcagt 600  
 ccacaatcgt tccccgtat cgttgggcgg gggcgttttt ctgcagctat gggtgctgct 660  
 gccccgacgg tgaacctttc tgcattcccc gtttttagtcg atttttagttg gcgggcctgg 720  
 agattaaact cgtcggacg aagaggagca gtggtgtcat cgtcggcgga ttgcatgcta 780  
 tcggaagagc atggaagagg gaaaacatca acttcatttg caaacgctc gagcataaat 840  
 agaggcctgg attccgccgt tctggtgtct tttcttcttc atccagcatc gcaagtctct 900  
 caagcatcgc ctggttcgtt cttctcactc tccaccacc agccttgta ataagttagc 960  
 tcttcattctt ttcgaagaaa ccaattctcc aaacgtcaaa atgaagttct ctaccatcct 1020  
 taccggctcc ctcttcgcca ctgccgtctt ggctgctcct ctactgaga agcgccgtgc 1080  
 tcgcaaggag gcccgcgccg ctggcaagcg ccacagcaac cctccctaca tccctggttc 1140  
 cgacaaggag atcctcaagc tgaacggcac ctccaacgag gattacagct ccaactgggc 1200  
 tgggtccgctc ctgatcggcg acggctacac caaggtcact ggcgagttca ctgtccccag 1260  
 tgtctctgct ggatctagca gctccagtgg ctacggcggt ggctacggct actacaagaa 1320

```

caagagacaa tccgaggagt actgcgccctc cgcttggggtt ggtatcgacg gtgacacctg 1380
cgagaccgct attctccaga ctggtgtcga cttctgctac gaggatggcc agacttccta 1440
cgatgcctgg tacgagtggg accccgacta cgcctacgac ttcaacgaca tcaccatctc 1500
cgaggggtgac accatcaagg tcaactgtcga ggccaccagc aagagcagcg gtagcgccac 1560
cgttgagaac ctgaccactg gccagtcctg caccacacac ttccagcggca acgtcgaggg 1620
tgacctttgc gagaccaacg ccgagtggat cgctcgaggac ttcgagtctg gtgactctct 1680
tgtggctttc gctgacttcg gctccgttac cttcaccaat gctgaggcta ccagcgacgg 1740
ttccactgtc ggccccctctg acgctaccgt tatggacatt gagcaggatg gcaccgtcct 1800
caccgagacc tccgtctctg gcgacagcgt cactgtcacc tacgtttaaa tgcattctcta 1860
tgcatgagat atcggctcgt tcaatgtctt cgagacgaag acaaaccctg gggatgaatg 1920
aaaaaatgag tgatgagcta tccggattga tctgatcttg ttgagttggt aattccgttt 1980
ctgttgatgt ttttgaatga ttatacctac ttttaagtag aagaaatgga tgagcgcggtg 2040
catgctgaaa atgactgtcc ctgcttatat tgtagaagat cttccagaaa gctgtgctgc 2100
cgatctgaag atctgaagat cactagttag atctcgcagc tcggctgtgt aagtgcattt 2160
gctctgtcga tcataacttt gtaaaagctt gtatgcatag cagacatctg tcgattattt 2220
agatgcttcg atttgatcat ctttactaga atccccattc gagtagagct tcagagcgctc 2280
gggtggaaat atcgggtcgt ggatggatc ggagaagtct cacaacatga acgaaagatc 2340
cgcggtata 2349

```

&lt;210&gt; 18

&lt;211&gt; 1495

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 18

```

tgattgtgca gacttcctca tcacgaagg agacaacaat gaaacccag ggagacacgg 60
aagcaggaaa acagactgcg gccggcgaga aagacacgat gtgacgaagg cttatctcgt 120
gacgccaaga caatgcgggg aaagctgccc ttccaagacc caactggcct gcctctttct 180
cattacaacc tcacgcctt gattgacttt ctggaccttg gtggcttgga ggccggctgc 240
atcgagcttg ctactcgcta cttgctttgt ttcgatgact ggctttcgtt gatcgcaaca 300
ttctttcttg gtatttttgt agggatagct agttgcttat catgggagat tacggccccg 360
gagtgtcgtc actcacggca cagctacctg gaaatccgcc tgtctctgaa acagatcagg 420

```



atgagatctc agtacttgta acgggctttg gggtaagctt ccagtgtcca taccattctc 480  
 ccaatatcgc aactcacatg ttctacagcc attcaagtct aatctagtga acgcctcata 540  
 tctgatagcc tcgtccctac caccctcttt cacattctca cctgcatctt cagacggctc 600  
 tgatgctgtt ccccgctcag tttcgataaa tgtccatcct tcacccatac ccgttgcata 660  
 ttcacgggtg cggacgaccc tccccgtcat tctcgatgac tatgccaaga cgcacggagg 720  
 ccgacgcccc gacatcgtca tacacattgg catagcagca atgaggaact actattccgt 780  
 ggagacgcag gctcaccgtg atgggtatct gatgtccgac atcaaaggca gatccgggta 840  
 cgaggatggc gagaagctgt ggagggagct cgacttgcca ctggtgctta gggctggccc 900  
 ttcagaggga cacgcctcgg agaagaaaca tctcagcccc cgtccaccgg acgaagattt 960  
 cctagcagca tggaagacat tttgccctcc agaaaccgat gcgcggatct ccaactgatgc 1020  
 cggacgttat ctctgcgagt tcactctgta caccagcttg gcactggcat accaggcggg 1080  
 tgaggatcgc aatgtcacct tcttccatgt tcccgcgtca tgcttgatg aggatataga 1140  
 gacgggcaag gaggttgccg tcgcgctaata caaggtctct gtgactagct ggagtgcgca 1200  
 gcagcacagc gttccctagt tctgaatgac tttttcaatc tctcggagt tgtgacattg 1260  
 catgtcccag cagtttttgt ttatcgggtg tcctatctga gtactatatt tttttggcaa 1320  
 tattttgcac tagtgaatac atatgggcgc ctgatgggtt atgatcgcat cacacctggc 1380  
 gccgcataga ttttgggcat aaggagtgtt ggtgtaagat caccatcaat ttattactgg 1440  
 tgttggaatt gtgtagggat agaaccaata tagattaaat tctcacgcca tacat 1495

<210> 19

<211> 2501

<212> DNA

<213> *Aspergillus niger*

<400> 19

gcgtcttcgg caagcggaag ggaccccgca aaagctacgc attgccattg ttcaggaacc 60  
 cactaaataa acacacggac atgtgggttt ggctgcccggt gcgccccgaa gccgcagccc 120  
 gaacggaggc attaaccttg atgcgtccgt tgattgttat ggtcttgtcc aacataacgg 180  
 ggaatttctg accgcacacg atgccaggca acccatttta tcacggctga gcatgttgat 240  
 aggtgttgaa ttcattttcc gtaggcagac gtctcctaga gcaatttctg ctgtatggca 300  
 gacattcgtg accgaaaccg tctcactcac ggtctaccat ggtagttatg cttcgtacat 360  
 aagacaagaa aggaatgcct tcaatcatgg caagaaggga atttggtaat ttgggtgcta 420

ctgccgtctt cctttgttgt gaaccttctc cattacacac agtgtccctt gaaggcccg	480
tatgccttca tactccgcca caatagccgc catcggggtt ttctgtctt cgcagccgt	540
catgggctca aggcaggga aggccccctt tggctgggtt actcagtcac ttgctcactt	600
tggtatcaac ccagaccttg ggttgcaaca ccagcagaac ctcaactccc tcatttcaca	660
ttcagcgatg gccactgctg tggagacgga atatgccacc gtatgaaaag caccagccct	720
ggctcttagt cctgatcact gattgtagac tcagatccct attgaccata acaacgcac	780
ggctggcact tatcaaaatc ggttctgggt cagcgatgaa ttctatcagc ctggcaaccc	840
gatatttgtg tacgataccg gggagtcgga tggcggatcg atagcccagt cctacctaac	900
ctccactctc tccttcttca gagaattcct gatcgaattc aacgccatgg gaatcgctg	960
ggagcacaga tactatggaa actcgacccc ggctcccgtt tcctatgaaa ctccaccga	1020
ggcatggcaa tacctacca ccaagcaggc gctcgcgga cttccgtact ttgctagtaa	1080
ctttagccgc gagaagtatc ctgacatgga cctgacgccg cagggcacgc cgtggatcat	1140
ggtggcgggc tcgtacgcag ggattcgtgc tgcattaact cgcaaggagt acccagagac	1200
gatattcgca gccttttctt catcgtctcc ggtggaagca eaggtaata tgagcgcgta	1260
ttacgaccaa gtctatcgtg gcatggttgc cagcggatgg accaactgct cggcagatat	1320
ccacgctgct ctggaatata ttgacgatca actttcggat gaagatacag ctacctcggt	1380
caaacaactt ttcttcggat ctggcgccga gaccaactcc aacggtgatt tcaactgcgc	1440
gctaactgcc atctacggct acttccaaag ttatggtatg gcgggaggta ttggaggtct	1500
aggcgcttc tgcgagtatc tcgaaattga tcccaagacg aacgggacta caggaccgga	1560
tggccttgcc cctacgtatg gcggccagta tgcgcccga cgatgggccg catggccaac	1620
ctttctcgag ctggtcaatc tgaatatggg gaccaactgc gggcctcagg acgctctca	1680
gccaattgac tgtgactttt ccaagccata cggcgatccc tcggccatca cttggacttg	1740
gcaatactgc agcgaatggg ggttcttcca ggcgaacaac gatgggccgc actcgtggc	1800
ctcgcgatat cagtcggtgg aataccagca agaagtatgt aaccggcagt tccccgatgc	1860
agtggacaag ggactgctgc ctccgtcgcc gcggcggtat gatgtcaacc aagagtttgg	1920
gggatggacg atccgcccgt ccaatgttta cttcagcggg ggagaattcg atccgtggcg	1980
atcattgtcc attctgtcga cagaagattt cgcacctcaa ggggtggagt ttacgagcgc	2040
gatcccagcc tgtgggtgac agaccaatga ggacaccgtc ttggatagc tcatgcagaa	2100
ctcggaaacat tgctttgact ttcaagcgac gccgaccgtg gggaagttat cagcggcat	2160

cttcacatcc gccttggtgc aatggctcga atgttttgga cagaactcaa gccaatccag 2220  
 gtgatctggg gggccagggg gtgtgtgggt gtgtaggtgt ggggtgtgtt gggtgtgctg 2280  
 gagcctggag ccaggataaa gaagatagga caaggatgac tgagtggatc ctgggatgct 2340  
 cctacttact tagaaaggta cagggcgctg cacggcgaag gtagactcgt accccagatt 2400  
 agatgatcaa cgagaagcct cggaggtttt ggatcaacgt tgggttttag cgtcacgtcc 2460  
 aaagtctctg atgcaggtgc cgcttttccc ttttgggaga t 2501

<210> 20

<211> 2660

<212> DNA

<213> *Aspergillus niger*

<400> 20

agagtccgcc ttgacaatgt ctaagaaagc atgctgagcc ccctccccca gtgtttatag 60  
 gtgagtagga atggagtata gtgcttgagt gctttcacgc tggtaaacgg acccgctggg 120  
 cggctagact gccttgtttt cgggtctagga accattcaag attcaacggc tacaagtcaa 180  
 gtcagaccat ctatcaatag tgcgagatag cagagagtcg gaccggagtc tcacaggcat 240  
 ccttggcggg cgaggagtga tgagtgtgc gaccagcgcg tgttccttat ttaagccgcg 300  
 cgcgcacctc tgacgcaacg gtctcaaagg ggggtctcac ctcttgcatg ttcggctgca 360  
 ttcaattcga cctctccgtg tctgtctagc atcaccccaa atcctatcgg aatagtcctc 420  
 cggttaagtc aacattgcaa atcagtcctt tcatttttgc ccagctcagc gctcggcctt 480  
 ctgtgaccct tggagcctga tcaattgccg aaaggtgttc gggcggttca gccttgga 540  
 gctcatttgc agtgagagg ttcacagca tcagctgtac tacttgactt cctatcatca 600  
 ttattgatta ttatattata tcctatcttc tccgccaatc ttccatcgcc ggtagttttt 660  
 cgtagacaac atgaagctct caatagctct tgcaactcgg gcaacggctt cgacgggggt 720  
 gttggctgct gttgtaccgc agcaagaacc gctgataacc cccaagatc cccaactca 780  
 tcatcatcag gagaagttct tgatcgagtt ggctccttat cagacgagat gggttaccga 840  
 ggaagaaaag tgggacttaa aactggtata gcaacattcc ccattttatt actgtcacia 900  
 tagcacatct cactgatcgc tctgcgaatg ttccattagg atggcgtgaa cttcatcgat 960  
 attactgaag aacgaaacac tgggttctac ccaacgttgc atgctggtag ctatgttcac 1020  
 tatccgccga cgatgaagca tgcggagaag gtggttcccc ttctgcgggg tctctccaag 1080  
 gacaacatgg agcaaacct caacaaattt acctcatttc aactcgccta ctataggtcg 1140

```

tccactggta ttgagtcgc aaagtggcta tacagtaggg ttccggatgt cattgagcag 1200
tcgggtgcag cagagtacgg cgccactgtg gagcagttcg ctactcatg gggccaattc 1260
agtatcattg ctccgatccc aggccagact aacaaaactg ttgtcctggg cgcacatcag 1320
gacagcatca atcttttcct cccctccatc ctagctgcac ctggtgccga tgatgacgga 1380
agtggaaccg tgactatact cgaagctttg cgtggtctgc tgcagtcaga cgccattgtc 1440
cggggcaacg cttccaacac aatcgaattc cactgggtact cggcagagga aggtgggtatg 1500
cttggttcgc aagccatatt ctctcaatat aagagagata agcgagacat caaggcgatg 1560
cttcaacagg atatgactgg ttataccag ggagctctgg acgccggtcg tcaagaagcc 1620
attgggatta tggttgacta cgttgatgag ggactgacac aattcctcaa agatgtcact 1680
actgaggtaa ggtcactccc gctttccttc tttgtgagac atataactaa cgattgcggt 1740
caaagtattg tggattggc tacatcgaaa ccagatgtgg ctacgcctgt tcggaccaca 1800
cgccgcaag caaatatggc tatccgcag ctatggcgac ggaatccgaa atggaaaaca 1860
gcaacaagag gatccacacg actgatgaca gcacccggtt tctaagcttc gatcatatgc 1920
tggagcatgc gaggttgaca cttggcttcg cttacgagct ggcctttgct caattctagt 1980
gtccttcatg attttacgtt gtaaccgggt ctagcagata attctggcta actagtgagg 2040
cttatatgtg ttcaggtttc ctatgtcggg ttattgtggc attagacaag attacagagt 2100
aaccaatact ccattttgta atggaataga tgtctgaggc ccaagtgttg gcaaggaacc 2160
ttgcctatat accacagatt aatactattg gctttgggtg ttcaagaata ggcctatggc 2220
tggactttat atatgttgac attctatttt gtaccggcaa cagactctaa cactagcacc 2280
taacaaataa aacacgtgtg actcttatgg gtggcatgat gatagtctgc agaatggccc 2340
gataagataa acgaaggaga tcctactata ccgattgag tcacactagc ctgaaacaga 2400
aagacgggtc ctccgccggg gcgatcactt ccactggctt caatcttcga gtcattcctg 2460
cggctctgtt tctccttggt accactccct ttgcccttca gatcagatcc tgaacggaga 2520
aagctcacc ctcatactac ataattttc acataacttg cttggactga attggcgata 2580
ttccgtcggg cgtcctatc tatcgctac gtcaccagcg gtgccctcc aaggaagacc 2640
ccaccatcag accttgatc

```

<210> 21  
<211> 2047  
<212> DNA

<213> *Aspergillus niger*

&lt;400&gt; 21

```

ccgagctata caaatgcgca tacaaaaatg gacagagtta catttcaacg ataaacatga      60
atgataagct tccagcaatg ggggccaagc gatatgcaaa ccgatttttag tacgcattcg      120
gtttatctgt tatctctctc ggagtaaact gtatgctctt cgccgaaacc acaaaagtaa      180
gcggggaaac gtatactacc aatcaaacac cccgagatgg tgactccgaa cgcagcagac      240
ctatttagat atatttaggc atgacaagta tcaatggatg acagaaacac cgagacctgg      300
tacaatctaa gttgaggaga gatttgaatc agaaagcagc tcgcacattt catcatgaga      360
actactacgt cttttgctag gcttgcatcg gcagtggcct cagttgggtat tgtctttgct      420
agtccaacaa aaaataacga tgggaaactg gtatatggct caccagaatc cgtcggcatg      480
atatccgccc ctttgacca aatgggtccaa aatgttagcg catatacaca tgctgccaac      540
tatagcaagt tctcgtagc caaagtccat cccatcgagc cagggctctgt taccctggtg      600
gctctcgacg gtgtcatcgt cagcgaattt gccttgggca agagaaatct ctacgccgat      660
gtcaacggca ccaatttacc tcgatacctg caggaagaca ccacctgga tacagtctac      720
gatatggcaa gcctcacgaa gctgttcacc acggtagctg ctttacggga acttgacgct      780
ggtcgaattg cgcttaatgt aactgttgca acttatatac cggactttgc gacgaatggg      840
aaggagaata ttactatctt ggagctgttc acgcatacaa gcggtttcgc ttctgatcca      900
tcgccaccac ttttctctgc ttattatacg acgtatgatg aacgcattaa agcaattttg      960
acgcaaaaaa ttatcaatac ccccggcagc acatacctct acttagatct caactttatg     1020
tcgctggggc tcgttatcga gaccgtaacg ggacgtgcc tggatgatct tatttatgac     1080
ttcaccagac cgcttgaaat gacatctacc ttcttcaacc gcgggaatat cgaaggctct     1140
acacccagc cacccaacta cgaccgcaca gccgtacaag aatttcagat cgcagccctc     1200
ggacctcag aaccacagcg tccacaacca gtgcgcgga cagttcacga cgagaacgca     1260
tggtccttag acggcgatc aggtcatgca ggtctattct ccaactgtgcg cgatacagcg     1320
acattctgcc agatgatcct caacaacggc acatatgcag gccaacggat cctttctcga     1380
acagcggtag acatgatctt cacaacttc aatgccaggt ttccggggga tgctcgtagt     1440
ttagggtttg agttggatca gtattctact gcgggaccga tggcgagttt gcaaactgcg     1500
agtcacactg gatttactgg gactacgttg gtgatggata ggacgtataa cgccttttgg     1560
ttgcatttta gtaaccgggt gcatccgtct agggcatggg ctagcaatac tattgtgaga     1620

```

gaggcatttg ggtattgggt tgggaagagc ttgggggttg atgttgcggt tgctctgttg 1680  
 taatgggtga gcgaggagc taccagatgg gatcctggat tcattccttc gatacacttg 1740  
 tatgtacacg aggaatgtat tcgaatgcaa atacctcata tattacagaa tccgcagtat 1800  
 gaatccggat aattttgtta aggcaaatcc agaaatttct aaagggttcac taccataaac 1860  
 acaaattatc accattcaat atggcatggt atcatccatt ctcatataag accctcgatc 1920  
 cggaagaccg atcctgtcag ggaattagtc aaccctctcc aataaatgca gcatgaaaga 1980  
 aatctaccat gaatcaacc cgagccctaa ataatccgaa aagatccagt ctggtgacag 2040  
 tgcaggg 2047

<210> 22  
 <211> 2730  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 22  
 tggccacgcc atcctcttat gctctctcta tccactctct cctcagctt ctctcaacca 60  
 cttccttacc catctttcac cctctcttcc ccttccccc ttccaaatct cttgaccttc 120  
 aagtctggcg cgcgtctgga cagcggctct tgtgctagag gtcttaactc ctaccccgcc 180  
 ttctctggc cttgaccttc tctgttctg aaccagggtc cctcccggtc ctctccgccg 240  
 acgttatccc cgacattgtg ctgctcatta cctccgcccc caaggtaacg ggtaagcgaa 300  
 aagtgaagg cccagttggc taaatttcga tgactccttg agcgcgactc caagtccgct 360  
 tgggaccgtt tcctccgctc cgtcttcggc aatatctact actactacta ttactattac 420  
 taccctggtc agccgcccgc gccgtattac aagtacccat cgcctactga tgggtctcctt 480  
 atcattccgc ggggagacca cttccattcc ctccatggcg tcctgggtgc tctcgacgct 540  
 cctttttctg agcccgctct tgggtgcagc caaatcgccc gcagactatt atgttcaactc 600  
 cttgcccggg gccccgagg gcccttgct gaagatgcat gccgggtaag cttcgctgtc 660  
 ccggaacggg ccgcttagca cctatatact gacttattgc ctccacgctc agccatattg 720  
 aggtggatcc acagaacaat ggaaatcttt tcttctggca ctaccagaat cgccatattg 780  
 ccaaccgcca gcgactgtg atctgggtga acggtgggtc cggtatgtagt tccatggacg 840  
 gcgcgttgat ggaggtcggg ccgtatcgcc tgaaggacaa tgaaaccttg acctataatg 900  
 agggttcctg ggacgaattc gccaatgtgt tgttcgtcga tcagccagtc ggaaccgggt 960  
 tcagttatgt caacacggac agctatcttc atgagctcga tgagatgtcg gctcagttca 1020

ttgtctttct ggaagagtgg ttcagattat ttccggagta tgaacgcgat gatgtatgct	1080
gcaatcacct atgctgccct agtcctgcac cttcacggat tctgttctaa catctgcgac	1140
agatctacat tgccggcgag tcttacgccg gtcagcatat tccatacatc gccaaagcca	1200
tccaggaacg gaacaagaac gttcaagggg agaccatcgc ttcgtggaat ctaaaaggcc	1260
tattgattgg caatggttgg atttctccta atgaacagta catgtcctac ttgccctacg	1320
catatgaaga aggccttata aaggaaggca gccggaccgc gaaggaaactc gaagttttac	1380
agtcagtctg taagtccagg ctggaaactg gcaagaacaa ggtccacctc aacgactgcg	1440
agaaggtcat gaatgctctg ttggataaga cggtcgaaga caacaaatgt ctcaacatgt	1500
atgacatccg ccttcgtgac accaccgatg catgcggtat gaactggccc accgacctgg	1560
aggacgtgaa gccctatctg cagcgggaag atgtgggttaa agcgcttaac atcaatccgg	1620
agaagaagtc tggctgggtg gagtgttcag gtgcagtga cagcgctttc aatccgcaaa	1680
agtccccgcc ctcggttcaa ctacttcccg gcttgctgga atcgggactt caaatcctcc	1740
ttttcagcgg agacaaggac ctgatttgca accatgttgg aacggaacag ctcatcaata	1800
acatgaagtg gaacggaggc acgggtttcg agacctcacc tggcgtctgg gctcctcgac	1860
acgactggag ttctgaaggc gagccggcgg gtatctatca atatgccaga aacctgactt	1920
acgtgctcat ctacaacgca agccatatgg ttccctacga ccttcctcgt cagagccggg	1980
acatgctaga tcgcttcatg aatgtcgata tcgcgagcat cggaggcagc cccgccgact	2040
cgcgcattga cggcgagaag ctgccccaga cgtcgggtggg cggccatccc aacagcaccg	2100
cggcggaggga gcaggagaag gagaggatca aggagacgga atggaaagcc tacgccaagt	2160
caggcgaagc cgttctcctc gtcgtcatta tcgggtgtaft agtttggggc ttcttcatct	2220
ggcgcagccg ccggcgtcac cagggatacc ggggcgtctg gcataaggac atgagcggaa	2280
gctctgttct cgagcggttc cacaacaagc gcacgggagg cgcagacgtc gaagcggggg	2340
atttcgacga ggcggagctc gatgaccttc attctccaga cctcgaaga gaacactacg	2400
ccgtgggcga ggacagcgac gaggatgata tttcacgaca gcattctcaa caggcctccc	2460
gagccggggg cagtcataat ctatcctagt tcatctttgg ttgggtaaac ttgtgatggt	2520
gtagggtgat ggcttgcttg gggctcttgc cttttgtttt tgttttcttg gccacgaaag	2580
gacgtgcctc cttatatgtg catttatcat tttatctagc tggctgcctg gcacatttta	2640
acatttagac atgaacaaag tttatgaccg cttcctgata catagccagg cggaaattcc	2700
tcccgtctat aagccaacag tctcatccac	2730

<210> 23  
 <211> 2660  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 23  
 actttattgc caagcgaatg acttcgactt tcttatttct gcaacgcgtt tggccagtta 60  
 ataatttgct agactcaact gattgctcgg tgccatctta ccagggatcg gcaagccgaa 120  
 aagtagccta ttgcacccaa tctgtaaaga agactttctc aaactccaaa gtagaacaga 180  
 cccatcttta gctttaataa ctccaatcat gacgattgga actatcggaa aatataatct 240  
 aagttcaatg gatctggtcc gtcgctagaa tatcggagta atgagccca acccctggcc 300  
 atcagggttcg acggaggaat tcttctggtt gggtagaaga ttgacacgat ccccttggcc 360  
 gctgaacgtc actcttccgc tgtcaaagct tgttggtga cttcgatccc ggatgatgtt 420  
 tctgatttca cctgcagtga cagttgcggc tgcaattctg ctgatcaacg gcgcaggagc 480  
 aactcaatct gaacgaagtc gggctgccgc tcatttttcc aaacgtcatc cgacgtaccg 540  
 tgctgcgacc agagcccagt cgagcaacac ttccgactac egattcttca ataataggac 600  
 caagcgtatg tattacaccg gccatgaact ctattcgtcg ctgacatgtg gtcacccctg 660  
 gatagcccac ttgggtgaaa gcttaccga tgtgcaattc gatgttgggg agatgtactc 720  
 ggggtcgcgc cctatcgatg acagcaacaa tggatctcga tccctgtttt atatcttcca 780  
 acctaagata ggcgaacctt cagacgacct taccatttac ctcaatggag ggccaggctg 840  
 ttctccgaa cagggtattct ttcaggaaaa ttgcagggtc acatggcagc ctggtaccta 900  
 tgcacccgtc atcaacgaat attcttgggt caatttgacg aacatgctat ggtacgcttc 960  
 ttcttgagga ttaaattgga ggtatgcact ctgtacattt tatgagacta atgtgaataa 1020  
 attcagggtt gaccaaccag tcggaaccgg attttccgtt ggaaatgtta cagccaccaa 1080  
 cgaagaagag attgccgccg attttctcga cttctttgaa aagtttgaag atctatacgg 1140  
 gataaagaac tttcgcattt tcatgaccgg tgagagctac gccggtcgct atgttcccta 1200  
 tatctcgtcg gcaatgctag acaagaacga caccacgcgt ttcaatctga gcggtacgag 1260  
 ccctgtctac tcataactac taccctata agcttagttg actgaaactg actttttaac 1320  
 gtccctctag gagcccttct ttatgacgcc tgcacggcc aatgggacta catccaggcc 1380  
 gaactccctg cctaccctt cgtcaagcag cacgcttcac tattcaactt caatcagtc 1440  
 tacatgaacg agcttgaac cacctacgaa gaatgcggct acaaggccta cttcgatgag 1500



tactttgcct ttccaccaag cggcatccaa cccccaaaat acatgaacta ctccgagtgc	1560
gacatctata acatgatcta ctacgaagcc tataacccga acccatgctt caatccctac	1620
cgcgtcattg atgagtgtcc acttctcttg gacgtcctgg gctggccgac agacttggca	1680
tacgagcctg cgcccaccac atacttcaac cgtatcgatg tcaagaaggc cctgcacgcc	1740
cccatggatg tggaatggga gctctgcagc tacgacctcg tcttcgctgg aggcgacgct	1800
gacccggttc cggagcagca aggggatgac tcaccaacc ccaccgaggg tgtcctcccg	1860
cgtgttattg aggcgaccaa ccgcgtgctc attgccaacg gtgactggga ctacctgatt	1920
atcaccaacg gcacctcct cgccatccag aatatgacct ggaacggcca gctgggcttc	1980
cagtccgcac ctgccacacc gatcgatatt cagatgcccg atctccagtg ggttgagatt	2040
tttgaggccc aggaggata tggagggtg gatggccctc aggggggttat ggggtgtacaa	2100
cattatgagc gcggtttgat gtggcgagg acatatcagt cggggcataa gcaggctcag	2160
gatcagggcc gtgtctcgta tcgccatctg cagtggctgt tggggcaagt tgagattctt	2220
tagtctcccg ccttagatat aattgatatc aactgtaat gtccctcca aaaagcttca	2280
tttattgata gtttcagtga attttgttac ttccagtaac aactctatta tggcattccc	2340
tggtttttaa tgctgcctcc ttttaccgta gctacggcta tgactacata taacggactg	2400
atttttctat ctcaacttaa ctttgtattg cccctggat cctgactaca gaaataaat	2460
aattcaaatt gatatttatt ggctttttat tggcagcata atatctttct catataagca	2520
cgcgagaaac ttgttcctca tcatactata tttatcccca cagctgatgc cgtgattcgg	2580
taatgaagat ggagattatg cggattgcgc acttcataat caaacatcgt ataagtgtgt	2640
cagtaatata tatctataat	2660

&lt;210&gt; 24

&lt;211&gt; 2800

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 24

aatgccgaag cttgacctga tacgacttca aggtatcgtc accgacaatc gttatcatca	60
cgctacaggc ccgcagtttc cgcttgaatt cccgcattag gaaatgagca tcgcattcct	120
cttcccacga ggtctctttc cgagggcagc cgctgcaaca tcattgggat catgcttggt	180
tctcctctcc catagctgtc cgcgagcttc tcattgggtac ctcttcgcta cctcgttgca	240
tcctattcgc gcatggcccc gccagagatg tttctgcaag gtcccatcac cttgccgcgt	300

tgctattccc cgccctcgag ttcccgacaa gttactttgt gtcagtggct gagaagcctg	360
gttctgagag tgtactcaga caatcatatg gttccctcca tgtgctacgt cgtcctagcg	420
tcgctgcact acatcatcgt taggcagcat ggaactggca cccgcacata aagcccccg	480
cacccccatc gataggctcg gtgttcgtgc acgcctgtcc actggcccct cccccaaagg	540
cccttcatca gtatgctgtt tcgcagtctg ttgtcgacgg ctgtcctagc cgtctcgctg	600
tgcacggata atgcttcagc tgctaaacat ggtcgatttg gccaaaaagc tcgcgacgcc	660
atgaacatcg cgaagcgttc cgctaacgcc gtgaaacact cgttgaagat ccctgtcgag	720
gactatcagt tcttgaacaa caagactaag cgtatgtatc tcagttcgat attgaacgat	780
ggctgatttg cttccgtcgg acagettacc gcgtggaaag cctgcctgat gttcacttcg	840
atctggggcg gatgtattcc ggcttgggtcc ctattgagaa gggcaacgtg tcacgggtccc	900
ttttctttgt cttccagccc actattggcg agcctgtgga tgagatcacc atctggctga	960
atggtggccc tggttgcagt tcccttgagg cctttctcca ggagaatggt agattcgtgt	1020
ggcagcctgg aacctaccag cctgttgaga acccatactc gtgggtgaat ctcaccaatg	1080
ttctgtggta agtgtgatat tactggatcg ctagttagt ttacatgggc ggtatcgacc	1140
taacctatct tttgtagggt tgaccaacct gtgggaacgg gattctctct ggggtgtcca	1200
accgctacgt ccgaggagga gattgctgaa gactttgtga agttcttcaa gaactggcag	1260
cagatctttg ggatcaaaaa cttcaagatc tatgttactg gagaaagtta tgcgggccgt	1320
tatgttcctt acatatccgc tgctttccta gatcagaatg atacagaaca cttcaaccta	1380
aaaggtagt tatacttcac caaagtaatc ttaactagg gcttgtagt attgtactat	1440
ctagggtcac tggcatatga tccctgtatt ggtcagtttg actacgtgca ggaggaagca	1500
cctgttggtc cctttgtcca gaagaacaat gccctcttca atttcaatgc aagctttttg	1560
gcggaactag agagcatcca tgagcaatgt ggatacaagg atttcatcga ccagtatcta	1620
gtcttcccag catccggtgt ccagccgcca aaggctatga actggagcga tcccacctgt	1680
gatgtttatg acatcgtaa taacgccgtc ctggatccca acccgtgctt caaccctac	1740
gaaatcaacg agatgtgccc cattctctgg gacgttcttg gattccccac cgaagtcgac	1800
tatctccctg cgggcgccag catctacttt gaccgcgctg atgttaagcg tgccatgcac	1860
gctcctaaca tcacctggc cgagtgtcgt gtggagagcg tctttgtcgg gggcgacggc	1920
ggteccgagc aggagggcga ctacteggcc aaccccatcg agcatgtctt gcccagggtc	1980

atcgaaggca ccaaccgagt tctgatcggg aacgggtgatt atgacatggg catccttacc 2040  
 aacggcaccc ttctctcgat ccagaacatg acatggaatg gaaagcttgg attcgacacg 2100  
 gccccagca ccccatcaa catcgacatc cctgacctga tgtacaatga agtggttcatt 2160  
 gagaacggct atgaccacaca aggtgggtcag ggtgtcatgg gcacccagca ctatgagcgt 2220  
 ggtcttatgt gggctgagac cttccagagc ggacacatgc agccccaatt ccaaccaga 2280  
 gtgtcatacc gtcaccttga gtggctgctt ggccggcggg ataccctgta aggcgggtag 2340  
 gctaccacgg gggacgatgt cacgatgata gtcataagtt atgatctgta gatacgttgt 2400  
 atgcgaatgt acatgaattg cttttactgg cagtctctaa agcaaaattc atagtagagt 2460  
 actggcctac ttaccctcac ttcccctatc ttttcaacct gaagaccgga agaattgtaa 2520  
 ctaacaagca taacgtagct gatttgaagc agagcataac acactctacc cctcggcact 2580  
 tctacttatg acgctatgtg actgctaact cgggtttaat cctgaagctg cagtccaatc 2640  
 gtacattaaa ctcaatgtgc cttgcccagg aaacgatatt tgacttatat gatctgaaaa 2700  
 tgaacaattg tccccgagag agagagagag agcgagcggg aaatacttag caagtcagtc 2760  
 acgcagtatc ctccactaat gccgtaacac aggaaatgga 2800

<210> 25

<211> 2165

<212> DNA

<213> *Aspergillus niger*

<400> 25

gaatcaggat ggaggccccga cggccatcaa ccgccgaaca tccggctgct cgaccgaatt 60  
 cggagacatg gtcggagcta ggcgggaata gccgtccaaa gtcacgatag gtcgcttgta 120  
 ctgtgtagaa gtcagaccct ttggatccag cgttcgttgt gaatggctcc acgcagcctt 180  
 tgctttgacc aatttggggc tgagtcactt ggtcgatgat gactggctat accagtgcaa 240  
 agtgtgagca ccattgcttac actattgcct tagcctggcc gttgaagctg acatgagagg 300  
 aacaggcaga agagaaatgc tgccttgccct cttgggggcc aatttaacct cccagactg 360  
 cggcacatcc gtcttggaact tgtgcttctt tgcaacttac gttataacga gtctgtgaac 420  
 aggaaaacag acgcccgggc agtcaagatg aaagggtcgg cgctaattcc tcttgccggc 480  
 ggcattcctt ttgcccatgg cctgtctctc cataaacgcg acgggcctgc cgtcgttcgt 540  
 atgcccattg agcgcaggag cggccagtc ttcagaaaac gagattctac ggtcgggtgtg 600  
 actttgcaga actgggtatg ttaagctata cggccgtgaa gtatagatca tgctgacaat 660

```

cgctaggatg cgacctatta cgcagtcaac ctgacgttag gaacacctgc gcaaaaggta 720
tcattagctt tggacactgg cagcagcgac ctctgggtga acaccggcaa ctcaacttac 780
tgctcaatcg acaatctatg cacccttat ggcttgtaca atgccagcga atcgtctact 840
gtaaagaccg tgggcacaca cctcaacgat acatatgcgg acggcacaaa cctttacggc 900
ccttatgtga ccgataagct cagcatcggc aacacaacaa tcgataatat gcagtttggg 960
atcgccgagt caacgactag taaacgtggg tgaaccgttt gtccatgaat gatcgtcgct 1020
gactaggctt actataggcg ggatcgccgg cgctcggttac aagatttcga cctaccaagc 1080
cgagcatgac gacaaagtct acgccaacct ccctcaggcc ctcgtcgaca gcggtgccat 1140
taagtctgct gcgtacagca tatggctaga tagtttggag gcgtcgactg gctccctcct 1200
tttcggaggt gtcaatacag ccaagtacaa gggcgatctg cagactcttc cgatcattcc 1260
tgtgtatggc aaatactact ccctcgccat cgcccttacg gagctcagcg ttgcgaccga 1320
ctccaactcc agtagcttca ccgacagtct cccctctct gtgtcactcg atactggcac 1380
caccatgacg gcactgcccc gcgacctggc caacaaggtc tacgatgcgc tcaacgcaac 1440
ctacgacaag acatacgaca tggcctacat cgactgcgac actagagagg cggattacaa 1500
tgtaacatac agtttctccg gggcaacgat caccgtgagc atgagtgagc tgattatccc 1560
cgcaacggag ccgggggtggc ccgacaacac gtgtgtcttg ggcctcgtgc ctagccagcc 1620
gggctgtaac ctgctcggtg atacattcct gcgcagtgcg tacgtcgtgt atgatctcga 1680
gaacaacgaa atctctctcg ccaataccaa tttcaatcca ggcgacgatg atatcctcga 1740
aatcggaacg ggaacgtctg ctgtgccagg agccacaccg gttccctctg ctgtctcttc 1800
tgcaactgga aatggactga tctcgtctgg caccgcagtg cccacgctgt cgggtgtcac 1860
aataactgct acagccacag caaccggctc aaccggcact ggctctagcg gtggttcgtc 1920
ggctgaagcc acgagtactt cctcggaggg cgctgcggcg caagctacga gcaaccgat 1980
gaacctgctc ccaggacttg cgggtatcgg cctacttctc gctctgtaac gcgattgtac 2040
ctactcaa at agatatcacg acgagactct aatgtaataa tgtggtatac aataacccca 2100
atatctacat ttccttaacc gtaaactgca tactctacac caaatccacc accaaaatac 2160
atacc 2165

```

```

<210> 26
<211> 2800
<212> DNA
<213> Aspergillus niger

```

<400> 26  
 gccagccaa tcataagaaa cccggctctg gcaaggtctt ggcggggatg gtgcaagcca 60  
 gccaaacaac cggtttggtg gacgccctgc ggtacactga aatcttgggc tgttcgacaa 120  
 aaacaaagca ggtaacacaa agatataata cggcggaatg ataggatatc cctgtcgatc 180  
 agccggacag gatggcgcta gtgtcacctc cagcttcggc taccctcgca gcggacccaa 240  
 tcagcgtccc tcccagcccc cgatacagta atggtatgca catcgcagtc ttaatcgctt 300  
 gcagcggcag taatgatagt cctgccggtg aataataccc cataacaaac aaataaataa 360  
 tactacttat ctctcctcgt ccctttcact ttccctttgc cgtcttcaat cccctcatct 420  
 tggctctctt gccagccctt caccatgctg tcgtctctcc ttagccaggg agcagccgta 480  
 tccctcgagg tgtgtgcgt gtcctctcg cctgtagccg cggagatctt cgaaaagcta 540  
 tccggcgctc ccaatggtga gttatagacc ccaattcttc attttgagcc acatactgac 600  
 gtgattcctt cgaatactac caggctggag atacgccaac aatcctcaag gcaacgaggt 660  
 cattcgcttg caaatcgccc ttcagcagca tgatgtcgct ggtttcgaac aagccgtgat 720  
 ggatatgtcc acccccggac acgccgacta tggaaagcat ttccgcaccc acgatgagat 780  
 gaagcgcagtg ttgctcccca gcgagactgc cgtcgactca gtccgcgact ggctggaatc 840  
 cgccggtgtc cacaatatcc aggtcgacgc cgactgggtc aagttccata ccaccgtaaa 900  
 caaggccaat gccctgctgg atgccgactt caagtggat gtcagcgacg ccaagcatat 960  
 tcgtcgtctg cgcacctgc aatactccat ccccgacgcc ctgggtctcg acatcaacat 1020  
 gatccagccc accaccgct ttggccagat ccagcccaac cgtgccacca tgcgcagcaa 1080  
 gcccaagcac gccgatgaga cattcctcac cgcagccacc ctggcccaga acacctccca 1140  
 ctgcgactcc atcatcacac cgcactgtct gaagcagctg tacaacatcg gtgactacca 1200  
 ggccgatccc aagtccggca gcaagatcgg ctttgccagc taccttgagg aatacgcccg 1260  
 gtatgccgat ctcgagaggt tcgagcagca cctggctccc aatgccatcg gccagaactt 1320  
 cagcgtcgtc caattcaacg gcggcctcaa cgatcagctt tcacgagtg acagcggcga 1380  
 agccaacctc gacctgcagt acatcctggg cgtcagcgct cccgtcccca tcaccgagta 1440  
 cagcaccggc ggacgcggcg aactagtccc cgacctgagc tcccccgacc ccaacgacaa 1500  
 cagcaacgag ccctacctg acttcttca gggaaacctc aagcttaaca actccgacct 1560  
 cccacaagtc atctctacct cctacggtga agacgaacag gtatgcacct cacctgacct 1620  
 attccatttt acatccctca cctctctcaa ccaaactaac aacaccaaca gactatcccc 1680

```

gtccccctacg cccgcaccgt ctgcaacctc tacgcccac tggcagccg cggcgctctct 1740
gtaatcttct ccagcggcga ctccggcgtc ggcgcgcct gcctcacaa cgacggcacc 1800
aaccgcacgc acttcccccc tcaattcccc gcctcctgcc cctgggtaac ctccgtcggc 1860
gcaacctcca agacctcccc cgagcaagcc gtctccttct cctccggcgg cttctccgac 1920
ctctggcccc gccctccta ccaacacgcc gccgtgcaa cctacctcac caagcacctg 1980
ggcaacaagt tctcgggggt tttcaacgcc tccggcgcg ccttccccga cgtctccgcg 2040
cagggcgta actacgctgt ttacgacaag ggcatgcttg gccagtcca cgggacgagt 2100
tgctccgcgc cgacgttcag tggcgatcgc gcgttggtga acgatgcgag actgagggcc 2160
gggttgcttg tgatgggggt cttgaatccg ttctgtatg gtgtcggaag tgagaagggg 2220
gcgttgaaat atattgtgaa cggcgggagt gtgggttggt atgggaggaa tcgggtcggg 2280
ggcacgccta atggtagtc tgtgtgccc tttgctagtt ggaatgccac gaccgggtgg 2340
gatcctgtgt cggggttggg aacgccgat tttgcgaagt tgaaaggggt ggcgttgggt 2400
gaggagggtg gtaattaagt gtgagatggg gggaaaggga tttcttttc gatgtgaata 2460
ttaggtgaat tgtgtggata atttcatac ataattaagt ctgcattggc agtgataacc 2520
tggaagaaat gtctaataag tgtgatttgt ttacttatgt atattgagta atggaatgta 2580
gatgacttgt ctttgtactg tataacgaaa tgattatttg agtggagggt attaaagaac 2640
tataaaatat atacaaagg taacccatgc agtcgtaacc cataatgcaa agctctactc 2700
tatctgtatc ggtagcagat aagtgtatgc aatctatctt tgttgatgat gcaatcaagc 2760
gggcacacca ccagtgcaca acagctccat cttgatgcgg 2800

```

<210> 27

<211> 2660

<212> DNA

<213> *Aspergillus niger*

<400> 27

```

ggagacagaa tacatggaat tgatgctcaa caacgacaag gagctcgcgt tccgtaatgc 60
caagttcatc gcttagattg ggaggatcgg ccaggctctgt atataggccg cgatagaaca 120
cgaaataaat gatttatgac tatttgccgg catgagccct cacgtagtgt gctatagacc 180
gtagacttgg taaacattgc tatcgatccc ccccttcgta tattagtcac aattcttcct 240
gatgtcaact ctcaaaacac agcattccac agcggtcata tgatgtcaat gtctcaatcc 300
ctaacgtttt gctgaaacag gtacctcttg gttatttttc atatagtagg aaggtcgccc 360

```

ttgcatgtgg tatgagacca ttggcggcat ctagcttgaa tggactcaa tatgaccagt	420
agtctccact tcagcagtgt gtttgtgata gccaagacat cggcagtagt tcctgcagag	480
cttctacacc tcttcatctt cacttcacca atccactctc tcactgctca cttctagttt	540
cgcaacacta gagaatcatg tggctctttc tcgtgtgcag tatcctgctg ccacttggag	600
tagtcaacgc acagtctcaa tacttcaaca aaaaaacaa aggtatacca catcgcgtca	660
gtttgaatcc cactaacagc gctagaatc gtcgtcaatg gctctgctat tccttttgtc	720
gatttcgaca ttggcgagtc ctatgcgggc tacctacca acacgccttc tggaatctcg	780
agtctatact tctggttctt tccatcttct gatcctgatg cgtctgatga ggtatgctta	840
tcgccgtctc atatgcttcg cacggctaataaacagatca ccgtctggct gaatggcggc	900
ccaggatgca gctctctggc aggcacatg ctcgagaacg gccctttct atggcaacct	960
ggtacctacc gacctgtcg caaccttat gcctggaaca acctacaaa tatggtgtac	1020
attgatcagc ctgctggaac gggattctcg cttggcccgct ctacgggtggt ctcagaattt	1080
gatgtagcca gacagtttat ggacttctgg aggcggttca tgaaaacatt cgatctgcag	1140
aatcgaaaga tatatctcac tggcgagagc tatgcgggccc agtacatccc atacatcgcg	1200
tcgcagatgc ttgaccagga tgatgatgag tatttcgggg ttgccggcat ccagatcaat	1260
gatccctaca tcaatgagct gccagttttg caagatggta tgcctctgac acaggttatt	1320
gcttactcct ctgacattga tgacttccag tgcctgcagt tgcgaccgtc aatcagcacc	1380
gtccctctt tccctttaat gacacctca tgagtcaaat caccaagctt tccgacgatt	1440
gtggctacac ttcgtttctt gacgatgccc ttacctttcc acccgttct caattcccat	1500
cagtgcccta taatgctagc tgcaacatct gggatatcat aaacaacgct tctctagctc	1560
tcaacccatg cttcaaccgc taccatatcc ccgacgctg cccaccccc tggaaccag	1620
tcggcgcccc catcgttgga cttggtccga ccaactactt caaccgcagt gacgtccaga	1680
aagccatcaa cgcgtaccca acggactatt tcgtctgcaa ggatggaatc ttcccgcagg	1740
ccaacggact ggacacatcc cctccaagct ccctgggacc gctgccgcgc gtcacgaac	1800
agaccaacaa taccatcatt gcgcacggcc tgatggattt cgagctgctg gcgcagggaa	1860
ccctgatcag tatccagaat atgacctgga atgggaagca ggggttcgag cgggagccgg	1920
tggagccgtt gttcgtgccg tatggtggat catcgggagg aggcgtgctg ggaacggcac	1980
atacagagcg tggattgaca ttttcgacag tatttagttc aggacatggt aggtccatat	2040

ctcagtatgc gatgcagcgg gttgctaaca ggaatagaaa tcccgggaata tgcaccgggg	2100
gcggcatatc gccagctgga gtttttgctg gggagggttg cgaatctgtc ggtgggttga	2160
ccggagacag caaagagaat gaagaaaaga aaaaaaaaaa aaaaaaacia tatgaataat	2220
tgcagacaat tattgagcag gtgcagataa cagagcagaa tggttgagct gtcagatcgg	2280
ttgacttttc ggcaatgaga tttggggaag ctagctctga gattggctct ccgccaaagc	2340
tatcgcaatc atgatccaat caacactgca tactaccttg atccccctgc tgtagacccg	2400
tattgccgga caaacaattg actagatatg aactcttgat tataaaccaa tcaagacccc	2460
cagtagcgca tattatcacc cccatacggt catgatcggc agcctaatac gaggtcggat	2520
cggaattcc ttcaaactct gaaaccgcgc tgggtccacc ccgcactctc acagtaaaaa	2580
tctaagattc cctcaatcc ctgctccatc tactttcttc cctctcatac cacttttgct	2640
ttttgtatag taaatatcca	2660

&lt;210&gt; 28

&lt;211&gt; 1540

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 28

taaacagaac taagcaaaag tccagatctt gtgtccctt cgactaccaa tcggaacaat	60
aggaattaac tattagcctg caactgtctg caccatcatg caaccctct cgttgtgatt	120
gtctctgttt tacattcccc gagacatgct catctagttg caagccatct ctaaccacc	180
tgcataaagg gtgcagaaac acgaacagtg gcgtggtagc acacactctc tgcagtactc	240
gatgccataa tttccaccag ctgaactaca atctccgcgt cagaattaat atataacat	300
caccaatacc ccttacatcc caactcagca actacagcaa tacttacacc taccctccac	360
aacccccaaa ctccacccca tcatgtccaa actctccgct gctatctcca aggtacttcc	420
ccatatccac aacacccccc acaccatccc tcaaatctaa caacaataac aataacctct	480
caccacccca gctctccctc tccaccatag ccaccaactct gctctctctt acccccccaa	540
ccaccgccta cttctacaaa tatcccgccc tcttcgtcta caaagacac aactgcaccg	600
atatctctct ctcacttgte taccctctcc tgggtaactg caacggcgga tactacgact	660
acgggggctc attccagatg ttcaatatcg atgctgcgta tacctgtaat ggcagtgact	720
cgacactgat gtttgagatg tataatagct ccggctcgga ttgtggagat gagagtgatt	780
tggtgttttag acagccggtg acggaggagt gtactgttgc ggatgtggag agtccggggc	840



cgttggagat gccggtttgg tttgagttgg ggtgatgta attgattcgt tgagtcggta 900  
 aggagggatg gacggggggt tataatagga gcttgggtgg taagcactat tggggaattg 960  
 tgggtgggatg gctgggtacta tgtgtgtcgg tgtggggatt cttgaggggt ggtagagac 1020  
 taaagtgagt tgtctgagga agtagtggat gacttctgct tctgtgatgc tggtagtga 1080  
 taaagttaat tacatatgca aatgtgcaat catagactga taggtggaaa cttgtctact 1140  
 cgttgagata tatagttata ctggaaatgt tattcatcaa ggctgaatac aagtgttaacc 1200  
 gtgcacagat tatctttgat actgtctatg ggctgtacga gcgtctctga ctctacaat 1260  
 gagttagcgg ctgcacatta ctatgaggac ctgtgaattc gacacaaaa ataaccagcc 1320  
 ctgcagccga ttacatctgc ctttccatct attttctgga gtcaagcagg tattccaaca 1380  
 tactcttact tgcttaatac accaactttc atatatctac ccagaattac tcaatcgtga 1440  
 tgtaggcact ggcaatcata gtaactatat ttcgtttcat tttatttgtt tgtacaattt 1500  
 tttttttccg gtagtttaat cattccaatc aaagaattgt 1540

<210> 29  
 <211> 2800  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 29  
 acactttctt cgatgctatg tcccagccat ataaggttca attctccgac tcaagtgaca 60  
 gaatcagcta tacacggttc actgcttctt atatagtaca tgaggattca ataaagccaa 120  
 gttcagcaga gtcttggttc cagagcttga atactcggta gcattccagg gattgtgggg 180  
 agacaatcca ggagcagcag ccattcattg gtgcctgagg cacacagcac tgcctcgtct 240  
 ccactcccaa tacttaccaa gtcacccacc attccttccc tctttcggcc tttctctttc 300  
 tctctctcac ttctgctctc gtgcaccact tttcttccca ctacgccat ccttctccat 360  
 ccatttcctg ccaaactttt gtctgtcatt ttaggttttt tgaaggagat gactcgggtga 420  
 ctactcttca atcccggcgt actcaacatc cataatgcgt cacctcttat cactgctgggt 480  
 gcttctgata gcacggccg cctggtctc cgccgtccc gccggctcca ttatcactcc 540  
 acaaccaccc gtcgagcccg ttacacttct ctcttccag cctctgata cccgaaggcc 600  
 atggatccgc ctccgtgact ggatcatcga gtccatatgg ggcacgaaa aaccgcac 660  
 tcgtcgattc cactcaacg attcccgcg caatcgctct cctccctccc ggattctggc 720  
 gcgctacggg agtgacgtcg tacttcgttt cagcctgcgc aatcacgatg aggccgaggc 780

attgccccag gctgcagaca ttctattcct ggacgtatgg gcgtctactc cagcattcgt	840
agatatccga ctggccgagg aagtcgtaag tggttcatcc ttccgtccat atctgcccgg	900
ttgactgatg cctgatccac tgtgaccctc gcaacagatt ccctcattat tgggcttgc	960
accaaattcc ctccagaccg catatactcc cctaatagac aacctggcag agagaatcta	1020
tacgacctat ccatctaaaa agccgatagg acttgaagga caatctggat ttgcgtcctc	1080
gagtcgacct gcgccaaagt tcggtgacct tttttccac gagtatcagc ctttgtccgt	1140
cattatcccc tggatgcggc tgctggcttc catgtttcca tcccatgtgc gcatgattag	1200
cgttgagta tcttacgagg gtcgcgaaat tcccgcctc cgactgagcg caggcagctc	1260
caccgcggcg tcaggccctc gtaaaacaat catcgttacg ggtggtagcc atgcccgcga	1320
atggattggc acctcaaccg tgaacatgt aatgtacacg ctcatcacca agtatggcaa	1380
atccaaggcc gttaccgcc ttctacagga cttegactgg atcatgatcc ccacgatcaa	1440
tcccgcggc tatgtttata cctgggagac ggaccgacta tggcgcaaga atcgacagcg	1500
gaccagccta cgcttctgtc ccggaatcga tcttgaccgc gcctggggct tcgaatggga	1560
cggcggtcgg acccgcgcta acccttgttc agaaaactat gctggagacg agcccttcga	1620
gggaatggaa gcacaacaat tagcacagtg ggcgtcaac gagacacaaa acaacaatgc	1680
cgacatcgtg agcttctctg accttcactc ttactctcaa acaattctct accccttctc	1740
ctactcctgc tctcgtatcc ctccaacgct cgagagcctg gaagagctag gccttggcct	1800
agccaaggcc attcgggtacg cgactcacga aatctacgat gtcacttctg cctgcgaagg	1860
catcgtcacg gccagtgcgg cagataacaa ccccgggcgg ttcttcccca ttggtggcaa	1920
ctccggtggc agtgcgttgg actggtttta ccaccaagtg cacgcgactt attcatacca	1980
gatcaagctt cgtgatcgcg gaagctacgg gtctctcctt ccgtctgaac acatcatccc	2040
caccggcaag gagatctaca atgttgttct gaaattggga tccttctca tcggaggcga	2100
ctcatttgac gtcgattggg aatcagaact cttcgatctg tcaaaggacg aatccgatct	2160
ggatagccgc tattcaaaat ccaatgaccg ctccccggcg tatctacaca acgccaacgg	2220
ccccctgcc aacattgacg aagacgaaga taaggaatgg gtaatggtgg aggaagaaga	2280
ctacacagac gatgacgacg acgatgatga tgatgatgaa gaagaggaag aggaagagga	2340
agatacatat tgggccaccg aacacacata cgaatttcgg cgacgacgct gatgatggac	2400
aaactaatca accctattta tatgacacc tcgccatat actctccttc tgatgacgat	2460
caataatgac taatgacggg ttgcgggag tgattgacgt gtttatcatg ctctgcttct	2520

cgattctttt tattatttta gatactgttc ccttcagggtg cctatagcct atagagctta 2580  
 ggggtattct ctacataatt aaatacagag taattcaatg aatcgtccta tcaaataatg 2640  
 gacccgagta actaactggg gtttcattcc ttccgtactg tacttaatct gtaaggaatt 2700  
 gaaagctaag cctcataagc tacttcaccc cactctttac ccagggtgcag tgtatcatga 2760  
 tcacgtcat acattcattc gttagggtatc ttccgatgc 2800

<210> 30  
 <211> 2380  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 30  
 cccgcctgta caaggctcat tgagcgacct ttatttctat gaaggcttct tgcagtgtag 60  
 agccgctggt tagaactcgg aaataggcgt gcatagtatg gacccaatca acagagttaa 120  
 tctatttact ctaacgccta gcaagcaatc agtgcccaga ggaagctaac ggatggctgg 180  
 ccaagctgcg ccagaaacga aatgagtcgg taataccatc cctgcatgct tatctgtatt 240  
 ctgtgcatgc atgatgcttt cctcatgggg cattaccag tagtccgaag acgcaatgtg 300  
 accatctgac tgagttttaa atatactgtc caagtgcctt ctgaccgggt ccccgcttga 360  
 tggcaatcaa caaaagggtga atgtgactga aaggcgcggt ccagacaaca ggacttagac 420  
 tttgttgtga gactataaaa ggatctaact attgcactac tgaaatcaag tattctagtc 480  
 taccattgac atttctcccc ttccgggtggc tactcgctca acatggcttt cctcaaacgc 540  
 atttctccgc tgctggccct catcttacct gcagttttca gtgccacaga acaggctcct 600  
 catccgacca tccagaccat cccggggaag tacattgtta ctttcaagtc cggcattgac 660  
 aatgcgaaga ttgagtctca tgccgcatgg gtaacggagc tccacaggcg cagcttagaa 720  
 ggccgcagta caaccgaaga tgaccttccc gccgggatcg aaagaacgta cagaattgcc 780  
 aattttgctg ggtacgcggg gtctttcgat gagaaaacta tgcaggagat ccgcaaacat 840  
 gaccatgttt gtgtccacgt atcctagacc gtatggtttc gactaattgc tgtacaggta 900  
 gcttatgtgg aacaagatca ggtctggtat ctcgatacgc tagttaccga aaggcgagct 960  
 ccttggggac tggggagcat ttctcaccgt ggtgggtcta gcaccgacta catctatgat 1020  
 gacagcgctg gggaggggtac atacgcttat gtagtggaca ccggcatctt ggctacgcat 1080  
 aatgagtttg gtggctgtgc tagcctggca tataatgctg caggggggtga gcacgttgat 1140  
 gatgttggac atggtacaca tgtagcaggg accatcgggg gcaaaacata cggggtttcg 1200

```

aaaaacgctc acctactgtc cgtgaagggtg tttgtaggtg aatccagctc gacatcggtc 1260
attctggatg gcttcaattg ggccgccaat gatattgtga gcaagaaccg gaccagtaag 1320
gcgggcgataa atatgagtct tggtagtggtc gccctctctg gggatctaata cccgctaacc 1380
gtgatgcagg tggagggtac tcctatgcgt ttaacaatgc agttgagaat gcttttgacg 1440
aggggtgtgct ctcttgtgtt gccgctggaa atgagaatgt aagctctgct gaactgtcca 1500
ccattgagct aaatttagac taatgttttg cagagagatg cagcacggac tagcccggtc 1560
tctgcacccg acgccattac tgttgccgct atcaacagaa gcaatgcccg tgcgtcattc 1620
tcaaactacg gctctgtggt tgacatTTTT gccccgggag agcaagtact ttctgcatgg 1680
accggctcga actcggccac caacacgacg tccggcagct ccatggctac acccatgtg 1740
acaggtttga tcctctattt gatgggcttg cgggaccttg ctacccacg gcctgcaacg 1800
accgagctca agaggttggc tacgcggaat gctgtcacca atgtggcggg tagccccaat 1860
cttctggcct acaatggaaa cagcggcgtg tcaaaagggg gtagcgatga tggagatgag 1920
gactaggtgc gtaacatgag tgaatatggc ttagaatagt ggggatcgga gagtagacta 1980
gtttatatgc gaaataaagt gtgtatcagc accctggcct gttcatgtaa gtcggcattt 2040
tcaacttttg cgacaccgca aatatgctgt gcttgaggct gttgcctccc cagccagcct 2100
tcccagagact gaaactcaca catccattgg atgtataaag ttctgcacat gcgaaatgcc 2160
gctgccgttt acctcccgac gtggtaccgg accgaaggca gacacagatc atggaccgct 2220
ataccgcaca gacaacttgt gctccttact gaaagtacca ttccacaggt cattgcagca 2280
tgatgagtga tgatgtactt ctccccatca agaaccactg gcggtggttg gaatgaatct 2340
agatcaaaga gatcaaccgc ttccccggac agatcaggcc 2380

```

<210> 31

<211> 2441

<212> DNA

<213> *Aspergillus niger*

<400> 31

```

aaacgacgtt ttaggtcaat actgaagtcg ttgaaaacgc ttgattcttc gctatctagg 60
cgcgctcgga ggagcagttg aagttacgga gttcgggtca cgtgacctcg actactagta 120
atctactgag attacgttcc aacataattt catcaggaag aatgcaaagg cccagagaa 180
ggagaatttc acgatcgggtg aaaacgacca agcagcatca catttgaatg aaactacatt 240
gctccgtgtt tattccgttt ctctctcttc tctctatcta ttgcttctct ttggctagac 300

```

ttcaccaact aattaatgct tacacgatga tagctgcac cattgaatca aactgacccc	360
gcaaagctga ctgaaccaac ccctccggtg ctgttgctac tgccagtttg aattcaatat	420
cctataaccc accctgctca atgatcacc ttttgctggc cctgttcggc agcgtagtat	480
atgccgctac gcagaccgtg ttagggccag agggggctga tccctttacg gtgtttcgca	540
gccacactc accggcattt tcaattcgca tccaggagca gaatgactcg atctgtgatg	600
ctcgttcacc ccaattcact ggttggtcg acattggccc gaagcatctt ttcttttggt	660
attttgaaag ccagaatgac cccttccatg atcccctaac gctatggatg actgggggcc	720
caggagactc gagtatgatt ggacttttcg aagaagttgg cccttgccgg attaatgagt	780
ttgggaatgg aacagatcac aaccctggg cctggacca gaattcatca cttcttttg	840
ttgaccagcc agtcgatgtc gggttttcct atatcgatga gggctatgag ctgcctcatg	900
actcacgtga agccgcggtg gacatgcac ggttcttgcg attattcata tccgagattt	960
ttctcacaa acagttcctt cccgttcacc tttccggtga atcttacgca gtaagataga	1020
agccgcccc agaaaaagct tgctcagtg tctaacaatt accttgatg acactgtgta	1080
gggcccgtac attccttacc tggcgacca aatcttgga caaatgaac tgtataaaga	1140
tagccccagg ataccgtga aatcggtcct ggtgggtaac ggattcatgt caccgaagga	1200
tgcaacgttc ggggtattggg aaacactgtg tactactaac tcaggagtcc catctcctat	1260
cttcaatgaa actaggtgag atattatggc ggcgaatatg ccgcactgta tggatctata	1320
tgacatatgc attcaacact cagacccgc gatatgtcat gcggcccagt ccgtctgtta	1380
cgatagtgtt gtaggtagt atgataacga ggcggcgct gatggcgta acagatttga	1440
tagtgagttg ttatcatcag aggctcatgg ccaaattatt gctaaggatg acgacagtca	1500
ctgcaccttg tgagatcgac gaaatgtgct atatcgaagc ggctctaatt gagagatatt	1560
tgaattcgcc atctgttttg gaggccctgt cgccaccgca acaggttacc gaatacaaat	1620
tcgtcgctac ttctgttatt gatgcatttg ctcaatcagc ggacggcatg gtgtcgagct	1680
cgaagcagat cgctttctta ctcgcaaata atgttgactt cttagcgtat caaggcaacc	1740
ttgatctcg ctgtaatacg gctggcaacc tacgttgggc gaactcgctt tcttggaag	1800
gccagacaga atttaccgca aagcccttac ttccgtgggt ctgatcaac tctgggagcc	1860
aggaacctgt ggggagtgag aaggaaattc aggtttcggt cgggtgaagg acggacgaaa	1920
cgtcacgctt tgcctttgtg actgtggaca acgctggaca cctggttaagt caaagtaaaa	1980

ttaggagaga ggggtttaat gatccagttg gctaacgagt agtggttgta ctatggtagt 2040  
 tgccccaaga tcggccggat gtagcgcttg acatgatgat tcgctggatt actggggcat 2100  
 cctttgttta acaaggaaca gttgcgggac tcaaagattt caaactgacc tactccttac 2160  
 cttttatgaa atgggcccgc tgcctagggtc aaacaagggt gtcggggcaa acaataccag 2220  
 ttttgacta ggggtccgtc tgctttcatc agcccttcgt agcttgact tttgtccatg 2280  
 tccctgtgc ctgggtccat cacacgcccg cccccccat ttcctttcct tcccttctct 2340  
 tttcgttcta ttatgcttga gtgcccgatc ttccctgcat gctatgccta tttcagtgta 2400  
 cgcagtttgg gtttttgtcc gaggaagaca atcatccatg c 2441

<210> 32  
 <211> 3500  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 32  
 gtttgtgtg gttgtgttt ggggtcccat ttgcaatccc tgaaccggac cctgtcaatc 60  
 cctcccaagt ccctcgttat cttccgcctt ttccaccccc tccacacttt atttttccat 120  
 ccatcatctt ccagtgcctc aatccaaatc actgtcgttg aatatagatt cgcattctgtt 180  
 ttccgtacgt gtattgttt actttcgga gggagattct cgccgttcat tccagatttc 240  
 cgcccgccg ccaaggcggc tgcgcctcca gccaaagcaa aacctccttg gatcgccagg 300  
 tggaaagaat ccctttcact ccccgctcga gtgagtctgt ctactgtc cctccggtcg 360  
 ttgcgcgcgc tctctcttct ctctccacac ctccagtata ctctctctgc ggggtgtgtga 420  
 gagactgcga cgatccggag aagaataaaa ccctccagtg cagcttaatc tccggagtga 480  
 tccgtcatatc atgacgggt cccgagccaa gatctcgact ggggtccatcc agtgaaaggg 540  
 aactcaatcg tttgacttt tcgtcgctgc ctgatgctgt ggaccgaagg gctctgttga 600  
 accctgactc tccggatctc tcggtgttgt tttgatgcca gcacgctcgt tccacactca 660  
 cctttaacct ctcccatcgg ctgtcttcac tcgctgacag caatgcggtt tctcacttat 720  
 tccctgccct tcattgcaag tgctatctcg ctctttgggg tcaatgtaca aggttagctc 780  
 ggcgacatcc ggcgcataga tttgttctaa ctggatcaaa tacagctcga tcacaagctc 840  
 caagtgccat ccgtcatgtg tcgacgcttg accagccac catcaagaca ccctcacagc 900  
 gggtcgatca ccttgaccac tttgacatca cttcaatat tcatgacaag caccagcgga 960  
 taaagctgga gctggagccc aacctagaca tcctggcgga agacgcatcc gtacagtatc 1020

tcgacgcgga	cgggaaactg	cgacggcacg	agccattgc	tccacatgag	cataaggtct	1080
tcaaggggag	gagtctactc	gggcgaggaa	aaggcatgtg	ggatccggtc	ggatgggcgc	1140
ggatctactt	gaagcaggat	ggctcagagc	cactatttga	gggagtcttc	agtatcgacg	1200
gcgacaacca	tcacgttcag	ctgaaatcgg	catacatgga	gaagaaacgc	cccgtggatg	1260
tcgaccttcc	cgactcagcg	actgactata	tgatcttcta	ccgggattcg	gatatgggtgc	1320
gtctacatac	ggaactcaag	cggtcgtcgc	tcggatcgac	ctcgtgtcaa	gccgatcagc	1380
tcggcttcaa	cactaacccc	aaccaccctg	tgctacaacc	gtatggccag	gcagagaccg	1440
atacgtgggg	agcaatttca	ttgaaactcct	tgtttggact	caacaagcgc	caatccgata	1500
tcggaagtgt	gtctggcaat	gcgggcggag	tcaatctggc	gtcgaccatt	ggtgatactt	1560
cgggctgtcc	gagtacgaag	caagtagctt	tgattggtgt	tgcaacggac	tgcgcttcta	1620
ccggctcatt	caacaacgag	actgccgcca	aggaatgggt	catcagtact	gtcaacagcg	1680
cgtccaatgt	ctacgaaaag	tccttcaaca	ttacgattgg	gctgcggaat	ctgactatca	1740
ccgacagctc	atgccccgac	aaccgcgccg	cggccacggc	atggaacatg	ccctgctcca	1800
gcggcaatct	cacctcccg	ctggatctgt	tttccaagtg	gcgcggtgag	caatcggatg	1860
acaatgctta	ttggaccctg	atgagcgatt	gcgcgacggg	caacgaggtc	ggactgtcat	1920
ggcttggcca	actctgcaat	agcgatgctt	cttcggatgg	ctcgagcacg	gtcagtggaa	1980
ctaacgtcgt	cgttcggtct	tccggctcgg	attggcagat	ctttgctcat	gaatctggcc	2040
acacctttgg	cgctgtccac	gactgtgact	cccagacctg	cgcggaggat	ctcgaagcct	2100
cgtcccagtg	ctgtccgttg	acctcgagca	cctgcaacgc	caacgggaaa	tacatcatga	2160
atcctacaac	tggaacagac	atcactgcgt	tctcgcaatg	cactatcgga	aatatatgcg	2220
cagccctggg	ccgcaacagc	gttaagtcca	gttgtctctc	cgccaaccgc	gacgtcacca	2280
cctacactgg	cagccagtgc	ggcaacggaa	ttgtcgagtc	cggcgaagac	tgcgattgtg	2340
gcggggaaga	tggttgcggc	gacaacaact	gctgcgacgc	gaagacatgc	aagttcaagt	2400
cgggagctgt	gtgtgatgac	tccaacgaca	gctgctgttc	aagctgcaa	ttctcctcag	2460
ctgggacggg	atgtcgtgcc	agtcgcggcg	actgcgacgt	ggcagagacc	tgacgcggca	2520
actccagtac	ttgtcctacc	gactcgttca	agaaggacgg	cacgagctgc	ggcagcagtg	2580
gctcgggact	tgctcgcgt	agtggccaat	gcaccagccg	cgactaccag	tgccgcagtg	2640
tgatgggcag	tctcctccac	agcaacgaca	cctacgcctg	ttcctccttc	agttcctcct	2700
gcgaactggg	ctgcacctcc	ccgaagatcg	gcacgtgcta	cagcgtcaac	caaaacttcc	2760

```

tcgacggcac tccctgcggt agtggcggt actgcagcaa cggcgactgc aagggccaaa 2820
acgtcgaatc ctggatcaag aaccacaaag gtatcgatcat tgggtgcgcc tgcgccgtag 2880
gcgcctgat ccttttggcc ctgatgacct gcacgtataa ccgctgtcgc cgggctcgcg 2940
cgccaaaacc cgtcccgcgt ccagtgcctt acggggccgtg gcccggcgt aggcctcccc 3000
cgccgcgcc catgaaccag tggccggcgc gaggtatca aggcttaggg aatgagccgc 3060
cgccccgta tccaggtgta cctggtcagc cagtaccgca acatatgcct cccagggggc 3120
ggtagccttg attgacgaga cttcttctgt gcttctttcc atgcgatata gtatgcatta 3180
cgattcttgc agcactagca ttacaaatgt gacgattact tcattgatcc tttattgacc 3240
ttacattctt gtcttgaggt ggaggcgtgt tctagagttt tggtttgatg ctgaattgtt 3300
cttttctata cgggggtctg ggcgtttcgt gaattgcagt acttacaatc caggggtgca 3360
atccccaggg ggttggttcg cgtcttcttt ccctttcttt gccatatta gacggggccg 3420
tgggatgtat ggtcggggtc tgatgtatgt attcctgccg tgtataatga acttttccgt 3480
cataatatat tgcttcttgt 3500

```

```

<210> 33
<211> 2520
<212> DNA
<213> Aspergillus niger

```

```

<400> 33
ttgatgcata atgctttcct tcagaggtaa tacttcgagg acggctatga agcgtatgcc 60
acatacgatt ggtatttgac gatatttgct atgctataca tgaaatttac atattgtata 120
tagtgtcatg ggtttgaata aagacatata gatgtatctt aatagcaggt caattgatga 180
cgctcttggt gctccgacga aaagcgactg catcgggccc atgcgggtcc agggtcgtcc 240
ttatcaacgc ccgctcagca ctaacagttg acatgtttct ccaggtcggc tagaaccgcc 300
ttttcgcgag aaacgcgtgc tatcgcgagt gcagggcaat tggtgcctag cagtagctaa 360
agcctgagtt ccgtgatctt cacttctact tcttcttctt ccctgctccc aaccattac 420
tctgcacccc acgccccaaat gcgtttccta agcagtgacg ccctattcgg cctggcgtat 480
gcctccaccc aggcggctct ccagccagag gaaccatccg acttccgtac attccacagc 540
ccatattccc cgcaccactc gatccgcata cgccagcaga atgaatcaat ctgcgctgcc 600
cattccgccc aatacacggg ctggctcgac atcggccgta aacatctctt cttctggtag 660
tttgagagcc agaatgaccc tgccaatgat cccctcactc tctggatgac aggagggcca 720

```



ggggggtcca gcatgatcgg tctgtttgaa gaagtcgggc catgtctgat caatgagtac	780
ggcaatggca cttactacaa tccgtggggc tggccccga actcctccct actatttgtc	840
gatcagccag tcgatgtggg attttcgtac gtcgatgaag gagaggacct gccgggcgat	900
tcgcatcaag ctgcaattga catgcacggc ttcttgagcgt tggttgcttc ggagggtttc	960
ccgcaattgc agactcttcc cgttcacctt tctggtgaat cgtatgctgt atgtatcttc	1020
tctaggtcac ctgagctaag actaaactcc acagggtcac tatgtccctt acctcggcag	1080
tcagatcgtc caacagaaca agctctatcc cactgagccc caggtccttc tgcactcatg	1140
tctcgtaggc aacggctact attctcctcg cgacactacc tacggctact gggaaaccct	1200
ctgcaccact aacctggag tccccgagcc cgtcttcaac cgaaccagat gcgacatcat	1260
ggcggccaat atgccgcgat gcatggaagt atccgacgta tgtgttcgga accccgatcc	1320
agctatctgc catgctgcgt cggaggatg ctacgagggc gtgatcggat ggtatgatga	1380
cgagtctggt gaagtggtgc ggaataggtt tgatagtga ctttgcccca tccagttgtc	1440
ccctgtcagc aaatctctgc aatttactga tatgaaacag taaccgctcc ctgcgccctt	1500
gacggcatat gctacatcga ggccgctcgc atcgagcagt acctgaacac acccgagtt	1560
tgggctgctc tatcaccacc caaagaaatc aaagaataca aggttacttc cgacaatgtg	1620
tcgcgcgat tcgatctcac ttcagacacg atgacgccag cgtctgagca agtcgcgttc	1680
ctgcttgcca atcaggtaca tttcctggcg tatcagggca atctcgatct ggcgtgtaat	1740
acggcgggta atctgcgctg ggcgcattct ctgccatgga gaggtcaggt cgagttcgcg	1800
tcgaaggcgc tgcggccatg gagttgggta gatgtggtat ctggaaaagg tggagtggct	1860
ggaacgacga aggaggtgag agtgaagggt agtgagagta cggataagga gtcgaggttt	1920
gcgctagtta cggttgatgg ggcgggacat tttgtgagta tccctttcgc cttgtgggat	1980
ccaagtatgc ggattactaa tggcttatta caacttttac agcttcctca agatagacct	2040
gatatcgcgt tggatatgat ggtgcgctgg atatccgggg catcgtttac tgagtgaagc	2100
atgaatgtcg cagacgatgg gataccggca tatttcacag gtttggtgta atatatgtct	2160
tgtagctgtc ttcagcagta tttacaatat gctgctgcct tctctgattt ggggtataatt	2220
atagtttaac acaatcaact gcatcggcag agatggatgg gcttgatttc gcacccgcag	2280
cagcgatgaa tttccgtcta accgagcgaa cggtagcgga cactaacact gattgtattt	2340
acaaccctgt ttctttcctc ttgatttgag acagaagtat gtaagctagg cgtagtagaa	2400

tacatttgtc atctacttct actgagttgc ataacgtaag cgactattgg ccgctacctt 2460  
 gccccagtta gttagttagt agtagtgggt gccgaagtca gcacacattt ttcagccctc 2520

<210> 34  
 <211> 1721  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 34  
 attgatacga ggcgttttga ggtggcggtc ctgaagagga tctgataccc actgggttttc 60  
 ccagtgggcc tatgttttctg tgatagtttc gccatttcta tccatctagg aaaattttga 120  
 tggcacctgc tagtcgatgt gcccttcctg atggagcgat ctcaaagtgt caaattttctc 180  
 ggcgaaacgc gtctacccct tctttgggat aattccctgg tatgcagcat tcctgacacg 240  
 agggattgtt tgggattccc cagattccac gttagcggtt gcaatgatgc ttatgatttt 300  
 ataattctca tcttgcctt tgtcctcggg gcagtagaga atcttctactg cccgatacca 360  
 atatgacatt gttactcaac ttccacgcgc tctttacagt cattcttgtt gccaatcttt 420  
 caaccagatg cagcgcactg ctctctggac gtgacttttg ctccacgcca gcgcccgggtg 480  
 agtcactccg agcggagcat aggaggctgt atgatgtaca ggcccaacgt gacagcaccg 540  
 ccgaggagag ccgggagggtg gtgccttgga ttgaaatcga gacatggttt catattgtaa 600  
 gcagcaatga agcagcaaac acagtatcag acgacatgat caccagccag gtccgtcacc 660  
 attcaacttt tgacctatgc ctgcgcaatg tcgtgttttg gactaacaag tcctagcttt 720  
 cctatcttca gaaggcatat gaaagtgcga ctatcaccta tcggttgag ggcataactc 780  
 gtcacataaa tgactcgtgg gcgcgaaatg atgatgaact ggggatgaag aatgccctac 840  
 gaaggggcaa ttatggcaca ttaaagtgtt atttccaaac agatctccag gcgtcatccg 900  
 acgagaattc tcgggactat ccaaagtacg gtaaccgacg aacagatgtg tcagatcaat 960  
 catcatcaac tgtcctaggc ttctgtacgt tgcctgacct gagtgtgaat tccagcagcc 1020  
 ctcgttccag ctacatcaag gatggttgta acgtgttagc ggatatcatg ccgggtggta 1080  
 gtttagcgca gtacaacaaa ggcggcacag cgttcatga ggttggccat tggaatgggc 1140  
 tgctgcatac gttcgaaggt gaatcgtgct cccctgataa tgaaggagat tacattgatg 1200  
 acaccccgga gcaatctgag cctacgagcg gatgtcccgc cgagaaagat tcatgccccg 1260  
 atcttctcgg ccttgatgct attcataatt ttatggacta ttcactctgat gactgttatg 1320  
 agagttttac tccagatcaa gcggagagaa tgaggagtat gtgggtccgct atgcgggaag 1380

ggaagtgacg gacggactcc aagggatat aatttgcaca tataccagct atagatagac 1440  
 aactatggta gcacgaatat tgatgtcaac atcttggctt ttcaattccg tgggaattga 1500  
 ctatcacaat tcatgaacct tttgtagaat ttgtgtattg gagagcgatt gatgcaaact 1560  
 agacactcgt tcgaaattca cagctagctg tcatgtggaa tgcgaaatca gatcatcgt 1620  
 tgcgcttttt tccacgatct tcatcgtcca ggccactttc cctgtctctt ttctttgcct 1680  
 ttgattcgag ttcgtcccag tcttcaccac tctcttcgtc g 1721

<210> 35

<211> 3550

<212> DNA

<213> *Aspergillus niger*

<400> 35

cctatcctct gctccgcccc gtggagagga tctattgacg ctatggttct tgagcaatgg 60  
 cgacaagacc caccagtggg gataagagga ccgaaactat ggcttgttca aggtctgctt 120  
 cgataaacc ctcacacgga taaaccaagt tgggcttact aacaaggcca atccttcaac 180  
 aatctcatcg cacaacgacc caaaatccag caaggcacga tccaacatac cctgtaatga 240  
 caggaaacaa attatcactc ctctgggtgc tgatgcagac caactcagta ttccgctggg 300  
 attgtccgac tccgaagaca agctttgggtg tctgggtgctg atcgtccgtc gtggagccac 360  
 cactagtggg ttgaattacc cacacacca ctacttatac tctttacgct gtctatcatc 420  
 ttcgtgctga tcaggggggt attttcttgc gctatttggg tcccactat gcttctgttt 480  
 tgcagggctg gtcataacaa tttggtagtt tgggttgggt ggcttgttat ggtcgatgtc 540  
 ggggaggggt tcaccgttga acaatatgct tgctgtagg taggttgaac tgatgcttgt 600  
 gttttgtttc caggcgccct ggacagcctt tggctatcag caatagctca atagctgggtg 660  
 ttttgctcgg acgcggtct tggtcgggtt gaccagtgat gatctacgct agacgctttc 720  
 ctgattggcg atggatgtca cgctctctat caggggttgg tgatcatatt tagcctacat 780  
 aggcagggtc ccttccgctg ggtatggaag tgcaaagccc agcgtatgga gagtgaagtg 840  
 atgctagtca atgggatcag cagcgttctt gtcaactagc atatattccg acgtttccca 900  
 ccgttctga tgatggcttg catgccacgc ttgctctgtc gctgcgatca acatgcatgt 960  
 ctacttttc ctactcagtg ttacggcagc gtttgccagc ccaacacccc ataactatgt 1020  
 tgttcatgag cggcgcgatg cattgcccag tgtctgggta gaagaaagcc ggctggacaa 1080  
 aggtgcccta ctgcctatgc ggatagggt tactcagtc aacctggatc gtggccatga 1140

tttattgatg gaggtgtatg tgttccgact cctcaccaga accaagctga ttgtccaggt	1200
ctcatccaca atcgtctcgc tacggaaagc atctctccag cgaggagggtg cagcacctat	1260
ttgccccgtc gaatgaggcc gtcgagaccg tccgaacctg gattgaatcc gccggaattg	1320
ctccaagccg catctcgcaa tcatacaaca agcagtgggt acagttcgat gcccattgcaa	1380
gcgagggttga gcagcttctg cagacggaat actacatcta caccatgcc gacacgggaa	1440
gttcccatgt gacatgccac gagtgagtcc attttctaca tgccatgaca ccgctaacca	1500
gttaggtacc atgtgcccga aaccatccaa tcgcacatcg actacataac accaggagta	1560
aagatgctgg aagtgcgcgg cagccctcc aaaaagagag atgcagagaa gcgtctcttt	1620
ggcagtctgc ccccaatctt agcaccacta ccaatcaata tcacgaagat ttctgacgac	1680
ccgctagcac actgcatctt ggcggttaacc ccagactgca ttcgaggtag gttcatccat	1740
cccaattcaa gatttcacgc taaccgtcta gccatgtaca acatcaccaa aggaacaaca	1800
gccacaaagg gcaacgagct cggcatcttc gaggacctag gagacatcta cagccaagat	1860
gacctcaacc ttttcttcgc caactttgcc aggttcgatt actctccacc ctcccttaga	1920
cacaactaac accaccaagc gacatccac agggaacca tccaaccctc gactccatcg	1980
acggcgccac cgcccaaca gacgtacca acgcccggcc cgaatccgac ctggacttcc	2040
aaatcgcta cccaatcatc tggccccaga acaccatct ctaccaaacc gacgaccca	2100
actacgaaga caactacaac ttcaaaggac tcctcaacaa ctctctctac gccatcgacg	2160
gtcctattg caacgaaacc tcctctctag accctcaata ccagatccc tcccaggcg	2220
gtactcttc cccaagcaa tgccggtct acacccccac aaacgtaatc tccatctct	2280
acggcagccc cgaagccgac ctcccatcg cctaccaacg ccgccaatgc cagagttca	2340
tgaaactcgg cttcagggc atcagcgtgg tcgtcgcac gggcgactcc ggcgtgcct	2400
ccagcacggg cacctgcttt ggcatgcag acaacgtctt cgtccagat tcccagcca	2460
catgtcccta tctaccgca gtaggaggca catacctccc ctaggcgca gacgcagcca	2520
aggaccagga aatagcagtc acccgcttc cctccggcg cggttcagc aatatctacg	2580
cccgaccatc ctaccagaac cactccgtgg agacctattt ctccactacc agcgacgacc	2640
tcacctacc ttactactcc ggagtaaact acacagactt ctccaacaca gatgggggtat	2700
acaaccgcat cggacgagga taccgatg tttcagctat cgcagacaat atcatcatct	2760
acaaccaggg cgaagcgaca ctgggtgggtg gtacgtctgc cgcggcgccg gcgttcgcg	2820
ccatgttgac gcgcattaac gaggagaggc tggcgaaggg gaagtccacg gtgggggttg	2880

tgaacccggt gctgtatgaa catcctgagg cgtttaggga tgtgactgtt gggtcgaatc 2940  
 ccgggtgtgg gactgatggg ttcccgggtg ctgggggggtg ggatccggtg acgggggttg 3000  
 ggacgccgcg gtttgaggat ttgatggata tatttggtgg tgatgattga tggctgagac 3060  
 aagatgtggg aaggtgtaat gaagatgata ctatttaatc cggtaatcta ccacacattc 3120  
 atattactag tttatagcct agtcagatat ataacattgt actactacta tagaggcgtg 3180  
 tgatgcaaat gctaaaatat tgatatacta ttaagcaact acattatgat ctaaacttta 3240  
 cagttcatag tacagaaagg ctttgatcag tcctagttca ataaaaggta tagactactc 3300  
 actacatatt aaacaccaca actcgggatg cttgggggtat agtgatctga gagtcgctgg 3360  
 aatgcccaaa tgctctgttc gatcatatct tggttgatgt catgttggtg gcattatata 3420  
 aaaagtcata tagcgctttt ctgaaagtcc tattatgaga attttgcttg tttatagcta 3480  
 gcgggtggat gattaatttt gtatgagtga ttctatagac gttgatcatt tccatgattt 3540  
 agaaactgag 3550

<210> 36  
 <211> 2280  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 36  
 ctgcctctca gcgaaaaccc caaaacaaaa catttctaga tcagacaatc aattgcggac 60  
 tgagttccct gaatggtgga agatgccata ctgttagcgg ggactatttt tagcatgtca 120  
 tgacttggtc ggcgtccgta catagaagggt tagcggatgt cttgatgata acacaaaaaa 180  
 gggataggat gaaactggat gtctcactgg ctatctcatt tgcccaacag catcagtcgt 240  
 tccggcccgcc tagttccacc acatgtcact tgtctcggat tattctcgaa ggtctgggtat 300  
 ttcaatgttc cacctgggtc ctctacataa atagaccttt acgctgtttt gttttcttct 360  
 tcgtttctac tcgtttatatt atccaaaatg gcttccaaga ccctcctact cattccggca 420  
 ctggccacag ccgctctggg aagtgtattg gacctagata tcaaggttca aaatggctat 480  
 gtatgtcaat gagaagctca gctccctgag aaatatctac taactcggcg aagaggacta 540  
 tcgaggtaga ccttgggaacc ccagggtggc cgtttgattt gatgtacgac accggatcat 600  
 caacactctg ggtgcttgat agcaattgta cagatgattg tccaaatgtt agcgggttag 660  
 ttgattcatc ccaccattcc ttaagcctac actaatcacg agcgccagggt actcccgaca 720  
 cggctacaac ctcacctcta ctggtgtcaa cttaggtgtc aacgacagca ttgcttacag 780

```

cggaggcact gtcagcggct tcactgccac ggatattctc acggttcccg acaccaacgt      840
ctcatatcgc cagagctttg ccgtcattac cgacagtacc tgggcggcct tagcagccga      900
tgggttcacg ggcctggcat cgtctaccat cgcattcaag aatactacga cagccgtcga      960
acagatgatg caggatggac ttttggatga acctcgattc gccatatatg caggttcagg    1020
ggaatcgacc gtgaccaacc ctaatccgga gaataatggc gtgttcacct ttggtggcag    1080
ccatgaggaa acctatgcgg acggggaact gcaatggatg aagatgctct ccccttttga    1140
aatatacaaa acaaactctc ttggaattca gggacacaac aactccgatg gccaggccct    1200
gtcaagcgac gtcctgaact ggtacggcca ggttattttc gataccggtg ggcattttct    1260
accacactgt tttcttttagc ttgctagact aatctattca acgtcgcagg tgcttcacgc    1320
ataagcattc ccaacgacca gattgaggcg atgtatgccc taacgccttt ctcatagct     1380
gacatctcat ctggataccg acctctgtgc tccgatttca atgatacatg gtcgatctct     1440
tttacaatgg gcttctatgg cgagggtgtc accttcaatt tgaccggtga tcagctggcc     1500
gtgcctggct atcaggacga cgaccactgc ttcctccctc tcaatccatg ggacagctac     1560
aacacgatta ttggtcagca ttggttgagc aatttctatg ctgtattcga cttcggatca     1620
ttcgacccgg agacatacga tatacgtgtt gggctggctc ctttgaagaa ggaatacctg     1680
ccgagcgctt gacctaagaa cttctattcg tgtctttgag catttagttc aaacctcttg     1740
ctcggacgtc aatgtttaag catgcgtaaa actatctact agaagttaat gttcatcgag     1800
agttcatcgt ttaaataagc agcttatctt cattctttac agccactata cgcgacatga     1860
caattgtttt atgggtcggg gcgataaagt ggccatctaa aggcaatagc aattaaaata     1920
agccaggaga tggaacatga aagaatctta ctctttgtca tggcctcatg caactttggt     1980
gcgggctgtc ggtgaccctg tggggcacat ctccggggag tggaggccgt taagcttcgg     2040
acaacattat ttcttcagct caaccatgaa aagggttcggg gacctgcatg catcccccaa     2100
gcccgaagt cgcgctcatc aacaaatatt gcgaagaaat ggtacgcttt agagccatgc     2160
gggctatatt ttcggttcta tagattgtta gatataatta ttgcttgtcg aaccagatg     2220
cagcattgat ctgttataat cctcatattc cgcgagtcac ttgattccgt gatcaagatt     2280

```

```

<210> 37
<211> 2287
<212> DNA
<213> Aspergillus niger

```

<400> 37  
tagttgaagg aggcttttgg ctttcttctt ctttatcttt cttctgttgt cagtgattct 60  
gatcgagaa gatgtgcaca agatgaagac cgccccgagt catctatgga tactgaagag 120  
atggaagaga tctgacaacc aaggagtgtt tattatccag ttccagtttc atgttttggc 180  
tccgtctgat agttccacca aagatactgc ctttttgtat ccgtagttag acggagacaa 240  
attgacaacg acagccttgg gggccaagtt cagacatact tccagccgca cgcattgatg 300  
tataccttgt tgetactgta gcgtacgcca gcttatcgac ctatttttagg acctgctccc 360  
acgtggagat tctgcagcaa acgcaggaaa caaggaccag aaattcgtca tcatcgtttc 420  
tccttagcaa tcggctagga tgtttccctg ctctcgtatt tggctctctgc tcgttgcagc 480  
cgccaccgct agtgctgtac ccaccagtct gcccaccacg cacctgcaat cggttgactt 540  
gcttctgact cgcagttctt acgggtttct tactgacata gcccttggaa ctccgggtca 600  
gagcctgccg tatctggttg actggacctg gaccggccac tatgtggtga ccacctgtg 660  
ctacaacgat cccaccgcca cctacgattg tctcaacgtc gatcagaaaa ttttcaacca 720  
gactttgtca tccactttta tcaaccaaac tgaccagtat ggctatcttt actgggatcc 780  
caaccacttc tactttacgg agcccgcagc agccgatgtg gcgacggaca tgctgcgcat 840  
cgggtcccacc gcggtgaaca ccaccatcca agcagccaat ttcgtcttca acgagactat 900  
tagcgcattc ctttctctgg gagtatatgg actctcacct gtttttcagg gtgacaatcg 960  
tgagttgttt cccaccgctc ataaaactaa ttcattgtta cacgaatcat aggatccgtg 1020  
caagcgtcct tctaccaagg atggaggagc ggcgcctggc actctccaat tgtctctttt 1080  
atctactgcc acgacaatgc caccaaagcg gtatgcagtg gttacgacgg ctttcagaca 1140  
ctaggcggat acaacacctc tcacgtccag ggagatatca cctggtacga catcattgtc 1200  
acggaggcga tcaacacgct ggactttgtc tatgcgccag ccgtgattaa ttattgggcg 1260  
ttgaacctca cgcgcttctc tatcggagac gaagagcaag agctcaacaa gaccactact 1320  
ctggatggaa agcaagccgc cgttgccgcg ttcgaccacg cttcgtatgg tcgcggtgcc 1380  
ccagtgtctg tgtacggtta ccagcgtcta gtcgagctgg tcggggcaaa agccgtcacg 1440  
ctttccgata ctccaaataa cggtgagcag ggattctatc agttcgattg ccggaactcg 1500  
agtttactgc caccgctgcg gtatgagttt gccgggtcag agcgggctg ggagattgtg 1560  
cccgagaact atgtggaggt gctggcgaac ggaaccaata agtgcacctt taatgtacgc 1620  
accctgggag atggagcgat ggtaatggga aattttggcg agacatttgc cattgataag 1680

tatgtcatgt ttgactttga gaagttgcag gtggggattg cagacttcgc gtggtaatgg 1740  
 tataaggatg tgtgtttgaa catgtgcatt atctcgagtt tgactgaata gacggagaat 1800  
 ccaagaccgt agatcatgat gctatctgct tgattatttt caatgtctct agtatgggga 1860  
 aagtaataca tgtgataata tctccaaagt agtaattaaa agagaaaact aatcaccact 1920  
 agtaattaat actgcaaata gcgctgttcc acattgagac aaccatataa taataagtta 1980  
 gtggatatac ggaatattag aggtcatctt aataccatac tagtggatac aaccatccgt 2040  
 acatacggaa taggaaggag gagcgagatg gtcattcattt gacactgagc atactgtgtt 2100  
 ggcccagtca agctgttgta tgggggagct cctagtgtgc ccaaggctcc agcatcttca 2160  
 ccttccgcaa cgactttact tagtttacat taggtgagcc tttctgttac atagttgatt 2220  
 gaaagcctct ccccaattgt cttagcatga tagaggttac tcggagaacg tactaatcag 2280  
 gaggccca 2287

<210> 38  
 <211> 1950  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 38  
 gatctttcta gagcattgtc ttgattgtgt cattctgtca ttgactccgg ctatgaaata 60  
 ttattctcaa tctgcctaaa accaaattct actctatcac tacacatttg tatcacctga 120  
 tctggctgag ataggagagt ccggcatctc atcgtctgca tcagacaatt gcgataaatt 180  
 cattgcttgc acctgttatt gattcttcca agttatgcat ctcccacagc gtctcggtac 240  
 agcagcgtgt ctttgcgcca gtgccacggc tttcatccca tacaccatca aactcgatac 300  
 gtcggacgac atctcagccc gtgattcatt agctcgtcgt ttcttgccag taccaaaacc 360  
 aagcgatgct ctagcagacg attccacctc atctgccagc gatgagtccc tgtcactgaa 420  
 catcaaaagg attcccgttc gtcgtgacaa tgatttcaag attgtggtag cggaactcc 480  
 ctcttgggtct aacaccgccc ctctcgatca agatggtagc gacatttcat acatctctgt 540  
 cgtcaacatt gggctctgat agaaatctat gtacatgttg ctcgacacag gcggctctga 600  
 tacctgggtt ttcggttcca actgcacgtc cacaccctgc acgatgcaca ataccttcgg 660  
 ttcggacgat tcttcgaccc ttgaaatgac atcggaagag tggagtgtgg gctatggaac 720  
 tgggtctgtc agcggcttgc taggaaaaga caagctcacg attgcaaagc tcaactgtacg 780  
 catgactttc ggacttgctt ccaacgcata ggataacttc gagtcgtacc caatggacgg 840



cattctcggg ctcgggtcgaa ccaacgatag ttcctacgac aaccaacat tcatggatgc 900  
 cgttcagaa agtaacgttt tcaagtcgaa tatcgttggc ttgcgccttt cacgtagccc 960  
 cgccaaggat ggcacggtca gctttggcac tactgacaag gacaagtaca ccggcgatat 1020  
 cacctacacc gataccgtcg gatcggacag ctattggcgc attcccgtgg acgatgtcta 1080  
 tgttggcggc acttcatgcg atttctccaa caaatcagcc atcatcgata ccggaacttc 1140  
 ttatgctatg ctgccttcaa ggcactcgaa gacgctgcac agtctcattc ccggcgccaa 1200  
 atcttcgggg agctaccaca ttattccgtg caacacaact actaagctac aagtggcatt 1260  
 ctctggtgtg aattacacca tctcgccgaa ggactacgtg ggagcaactt caggttcttg 1320  
 atgcgtttcg aacattatca gctacgactt atttgggtgat gacatctggc tcctgggtga 1380  
 cacgtttctc aaaaatgtgt atgctgtgtt tgactacgat gagttacggg tcggatttgc 1440  
 agagcgttcc tcgaacacca cctctgcgtc gaactctacg agctctggaa caagcagcac 1500  
 ctcgggatcc actacaacgg gcagctcaac gactacgacg agctctgcta gctctagtag 1560  
 ttcattctgat gctgaatcag gaagtagcat gaccattccc gtcctcagt atttcttctc 1620  
 tgctctggcg attgcttctt tcatgctttg gctctagtta accgcatctt actcgacgcc 1680  
 tgaacctcgg gaaacatatg cattatttac acatgctgct gatttgtatt tgcatatatt 1740  
 cttcgagcct ggacggcgtg cgggtcatat taccttacat tcgaagtcct tctctaata 1800  
 atcaacattt attcttactc caccagttct ggctcgcaat taacctgtc taagaaaaag 1860  
 ttggtataga acatggcatc cactacctgg aacattcaaa gaaccttgtc cgggatcagt 1920  
 gtgtatgact tcgggtacga ttctgacatg 1950

<210> 39  
 <211> 2660  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 39  
 accttctggg gtggattatc tgaagagatg aactgccccg cccaagtgca agaagatgat 60  
 gcctgacagt tgatgcctga gggatgcttg tatcaggtga tcccggtat ggtgggtctaa 120  
 ccagttggg ctgaattgac cacatttagt tagtgtcagc cttaaacaga tgaggctttt 180  
 cgcattgatc atttccaagg aaccaagga aatgggtcaaa cagcaaagga ataatgaccc 240  
 aacagttata cctagctatg cagcataaaa gagaaaaaaa acttgaactg atacgagcca 300  
 tcatgtaacc tccgtctctg gctcaattct ccatccaatc acaattcttc caagcaaact 360

tgggattcgc cgggttctcg gcaaccctaa cctctaccag taaagggtga tccttcccc	420
acccgatttc gcatggcttg gaccctgaa ataatgttcc tctacgtgcc tgaatatgga	480
gcacgttatt cgtctttcag ggtcttgggg ccttggcctt ggggctgcca agcggggcggc	540
ggagtgtgcc ccgtgggtgcc ctgttttgag cttggatgag attactatca tcaactaata	600
agagcaagac cctgcgtcga tattgacggt caatacactg acctcagaga accgtcgatg	660
tgcctgattt cgtccatca aaatgacgtc ttctaccttg cgccttgccg tcgcgttggc	720
tttgtcaact tgcagcagtg ccctatcgag ccagcgagat gattcacttg tggttccatt	780
tccttttggc aatcttgagg atgtccatat tgccaagcgg gatagctcca agacagtaga	840
agctcctcta gtgatatatg tcagtcagct ctcccactct ccatctatgt catcaactcg	900
acaaccctaa caatcaacag ggcgacagct actggatgaa cgcctcaatt ggaaccctg	960
cgcagtcact aagtttcccta ctagatctta cgcgctcaag ggtcgagccc gcatacacc	1020
tcgatgagaa ttacgaatgt tctgacgatg aactctgctc cgaattcggc ttctacaaac	1080
ccaccgattc atccacttat cagcatctca cctacacaca gagacacgat gcaggtgtcg	1140
actactccta ccttgatacc ataactcttg gagatcacgc aaccgacaat gtcccactgg	1200
acatgtatct ttgtcctac atttcctgtc agttccctct ctctccctta ccaccctatt	1260
tatccatcat ctgaccattg tctaaccacc acatagacag ctccctcggt ctctctctcg	1320
tcaacaccag ctccctctac atcctggctg atcgcggcct caccacctcc ccatccttca	1380
gcctaatacgg cgacaacgga aacaccacca cccccagcat catctttgga ggcataca	1440
cctccaaatt caacggggccc ctgcaagcct tctccttcgc agaccacagc atcaccaaca	1500
atccattcgt caccgtcgaa gctgactccc tccaactaac caccaacacc aacgataatt	1560
ccacctacc cttccctcc tccaccccca tgatgctcag aaccgaagaa ctaatcacct	1620
acctcccaa ctcgaccgtc caatccctct acaccgacct taacataacc atggacggcg	1680
tgatctccac ttcaagattc tacggggctc ttccctgcgc ccgccaggaa accgaatctc	1740
acacaatctc tctagccatc ggcaacatga cttctctgt gtccctgggat gagctcttcg	1800
tcccgctggac gcgtgacgga ctatgcaagt tcggcattca ggcccaggat tcagattaca	1860
aaactcgtgc ggagctgggt gttccctttc tgagacggat gtatgtcgct gtggattata	1920
ataatcagtt tgtgggcgtt gcgacgtga aggatgatga tgatcagaat ggaggtgaag	1980
atgagattgt ggagattggc actgggacgg cgttgccctag tgctgtcggg gattggccgg	2040
ctagtgttac ggcgtatacg cctgctgctt ctacagggac ggcggctgcg acgttgacat	2100

tcacgacggc gacgtctagc gggggaggtg tgggtccgac gggctctatca gagttgggta 2160  
 gggcggttttt ggtgccgggg gtgctgggga tggctgtttt gcaggctggt taggttagag 2220  
 attgtggtac gattattctg taggttaaag atgtatatg tctgttattg tacttgatag 2280  
 cttgatatgt ataatgaaag tagtatagtt tgaatttttg ttatacacca cgtgaaccca 2340  
 ctggaccgtt gtctactgct cgcagtgagt gatatagtg agaccggtat tactagtcac 2400  
 gtaggaccct accttgatac cataacactc ggagaccacg caaccgacaa cgtcccaactg 2460  
 gacatgtacc ttttgtccta catttcctgt cagccccttt ttgaatgtac ctacatccct 2520  
 ctaaactcta gtactatcac gaacagcaaa tgacattcaa tctattctat gcatattacc 2580  
 cttctaacia taccagatt ctatcaaata acgtgaacat acagccctcc caagtcacct 2640  
 gacaaagcgg acaacaatgc 2660

<210> 40  
 <211> 2501  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 40  
 tgattcccaa atcgaccag atgaagtga atcagtggta cagtttagcg ggtggctgtc 60  
 atgacagaca gacctcaaa ttgaagcaat ggcagataga tatggtctcc agtccaccga 120  
 ttgaatgcag ttggagaagt caatccccc ttggaaagcc cccaacgttg cgctttctga 180  
 ccacctgaaa tctgacaatc agcaatcctt cagctcttct cagcgtctct tggggccgat 240  
 ccccatcgga tgaacacgcc tcacccctca ttaggcattg ctgagctgca tgtcagcgga 300  
 gtcccaacac ccaaaccaat ccttttagcg gcaccgggccc tgcgaagcca tcaccatcgc 360  
 ccgccttgca gcaatgtgct ccccggtcgc attcctttcg tttcataatc tcacctccgg 420  
 ccagcccata tccttcattc cgcagctttt ccctactcct tcttttcttt tgctttcttc 480  
 ccccatcgca ggctgtttga atgcctgctg aagtatccat ggtatgatgc gaccgatact 540  
 tctcccccta ctgggggtat ttctgcagac ctctctggca tccaatccct atgtaatgag 600  
 ctggtcttcc caagcctacg gtccagatgg cccgtggcag gccgtatcca tcgacgtggg 660  
 cagcaaccag cagacggctg atctttaccc cggagccaac tatgctagca cgatcctgat 720  
 gagcactctc tgcacgaaca aaacctgtc atccacctgc tacgctgccg aagcaggcac 780  
 gttcaaccaa aacacctcca cactgccta caccaccgcc agctcgtggg aaacaactta 840  
 ctggggccgtc gaggggtggaa gccaaagggc tgtgctcggc gatgaggtca ccttagggtc 900

```

gtttgtcgtc cccaatgtga gcttcgaagc catctaccag acctaccaga cctatcccaa 960
tggcatcgcc tatcctgtct cggtcggcag tctggccctg ggggggccgt acttgtcggg 1020
taccgtctcc aattcgacgg tcctgaacat gatcgagga tggctttact cgtccaacga 1080
cattccgtcc tactcgtacg gcatgcatat cgggtcggta gacccccaaa tcccaggctc 1140
cctgatcttg gggggctacg ataagagccg agtgatcgga gacgtgagtg cgcagggagt 1200
agtgtcttcg agtgggtcttt tggaaacttg attaaaggat attgggctgg gtgttgcggc 1260
gggttcctct cccttcagct tcaacaacga aagtggcttg tttctccaaa gcagtgggtc 1320
ggttcaggcc aagaccgtcc agattgatcc aaccaagccc tacatgtacc ttccccaggc 1380
gacatgcatg gccatcacct ccaccatgcc gatctccttc aattccagct tggggctata 1440
cttctgggac accacgagcg atgattatct gaatatcacg tcttcgcgcg catacctctc 1500
ctttgtgttc aacatgaatg gggtaacaa caagaacatt accatcaaga ttcccttttc 1560
ccagctcaat cttacgtctg aagaaccgct ggtcgatcaa aacgtcacct acttcccgtg 1620
cttctcact acctccacc cgggtgctcg tcgagccttt ctccagtcg cattcgttgg 1680
gggtgaactgg ttcaacggga acaactcggg cacatggttt ctggcacagg cccccggccc 1740
gggttacgcc agtgaagaca tcaccggat cgcagtgagt gacacgtcg tttctgcctc 1800
taacggtacc tgggaagaga cctgggctac gtactggggc atcaaaacat ccgacaactc 1860
gagcagctcc aagagtggcc tgtcttcggt tgccaaaatt ggaattggcg tcgggggtggg 1920
tgtcgggtga gcagtgttga tcgcagcagg tatagccatt gcattctgtc ttcgccgtcg 1980
ccgcggggcg agtcaagagg cggctggaga gcaacggagg tcgatgttta ggggctttgc 2040
ggagctaccg ggaggtgctc acagtgaacc ggcgaaggag ttggatacga agatgcataa 2100
gccgccgcag gaaatgatgg cttcgcagga ggtagagcga tacgagctgg ggtgatggct 2160
aattctaaat ttaatatgc gaagggatcc ctacaggata ctacaggata ccatatacgt 2220
gcgaatataa tagctagttg ttccaatatt atgtatcaag cttatactgt ggattaacca 2280
acgacttgtc tccgatacat agggtagtac gtagtcatgg atccggggtg tattgtcatt 2340
cagcatgacg cattgtctca gccaaaagta agctgggcca gtgtatcacc catgaaagca 2400
acctctctc acctctgtac tgatgacttg gtggaaattt ggatcctcgg aaattgtgat 2460
taacacgtgg atctagacc gaccaggcgg gagcttgga t 2501

```

&lt;210&gt; 41

<211> 3570  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 41  
 gaaaaggatt gtccccatgc ataataggcg ttccaccacc tgcatatcca tacatgcagc 60  
 ccgagttatg cgatgtgacg gggcctggaa taacatgacg tccgatctaa cgggggcccc 120  
 aaaggggcag ccaagatctg ctaggcccac ccaggctagc ggcgggccaat ctgaggcggt 180  
 gatccatttt gggcgaggaa aaggcaaaaa gtggatcggc gaaaggcaag ttggagtgtc 240  
 gggagtttgg tctcccgccc cagggccgcg tattagtcta gctctctttc tattcactcg 300  
 ggccaactcg tcaactctct ccctcgcttt cattcagatt tcattatttc tcttacggtc 360  
 ttgccattct tgcactttc ggtccttatt attgcttttg atccccagtt cctttttccc 420  
 aactgggtgg cgctcctaca gaccgacaca tacctggcgg actttccttg cttctggctg 480  
 tacaccggga cccgcctcat acccagtagc tgttggtcca tggcaagcct cctacttggc 540  
 ctgattacat cgtcctgaga gagagagttc accaaaactc tcccccaaac gatgcgtctt 600  
 acaggtggtg tcgctgcggc tctgggcctc tgcgctgctg cctccgcttc tctccatccc 660  
 catcgttcct acgagaccca tgattacttc gctctacacc ttgatgaatc cacctcgccg 720  
 gccgacgtcg cccaacgact aggtgctcgc cacgaaggcc ccgtcggaga attaccctca 780  
 catcatacct tctcgatacc ccgtgaaaac agtgacgatg tccatgcgct gctggatcaa 840  
 ttgctcgatc gtcggagggt acgccgccc tccggagatg acgccgctgt ccttccctcc 900  
 ttggtcgggc gagacgaagg tctaggtggc attcttttgt ccgagaagct ggctccccag 960  
 agaaagctcc ataaaagagt gccgccgaca ggatatgctg ccagatcgcc cgtcaacact 1020  
 cagaatgacc cccaagcgct tgcggcgag aaacgcattg cctcggaatt gggcatcgcg 1080  
 gaccccatct tcggcgaaca atggcatttg tataatactg ttcagttggg ccatgatctt 1140  
 aacgtgacgg gtatctggct ggagggcggt acagggcagg gtgtcacgac ggctattgtc 1200  
 gatgacgggt tggacatgta cagcaacgat ctaggccga actattttgc ggcgggttct 1260  
 tatgactata acgacaaagt accagagccg aggccgctg tgagcgatga ccgccacggt 1320  
 actagatgcg cgggtgaaat cgggtcgggc aagaacgacg tgtgcggggg tgggtgttgcg 1380  
 tatgatagtc gcatcgctgg tattcggtat ctctccgac ccattgatga cactgatgag 1440  
 gctgcggcta ttaactacgc ctatcaggag aacgatatct actcgtgttc ctgggggtccc 1500  
 tatgacgatg gcgccacaat ggaagccccg ggcacctga tcaagcgggc catggtcaat 1560

ggatccaaa atggctcgtgg tggaaaaggc tcgggtttttg tgtttgccgc tggtaacggt 1620  
 gccattcatg acgataactg taacttttgac ggttacacca acagtatcta cagcatcacg 1680  
 gtgggtgcca ttgatcggga gggtaaccat cctccgtatt cggaatcctg ctccggcgcaa 1740  
 ctgggtggttg cctacagcag cggcgccagt gatgcaattc ataccacgga cgtcgggcaca 1800  
 gacaagtgct cgactaccca tgggtggaact tcggcgggccg gcccgcctgc tgcgggaacc 1860  
 gtggcgctgg ccctcagtgt gcggccggaa ctcacctggc gtgacgttca gtatttgatg 1920  
 attgaggcgg cagtgcctgt tcatgaagat gatggaagct ggcaggacac taagaacggg 1980  
 aagaagttca gccatgactg gggatatggt aaggctcgaca catatacgct ggtgaaacgg 2040  
 gcagagacct gggatctggt gaagcctcaa gcctggctcc attccccctg gcagcggggt 2100  
 gagcatgaga tcccacaggg cgagcagggc ttggctagtt cgtacgaggt gacggaggat 2160  
 atgttgaagg gagccaacct ggaacggctg gagcatgtca cggtcaccat gaatgttaac 2220  
 cacaccgcc gaggcgatct cagcgtggag ttacggagcc ctgacggtcg ggtcagtcac 2280  
 ctcagtacgc cccggcgggc agataatcaa gaggtgggct atgttgactg gaccttcagt 2340  
 agcgttgctc actggttaagt aaactttttc tcggttgtcg gttcttctgc taatacatat 2400  
 ctaggggcca gtccgggatt ggcaaattga ctgtgattgt caaggacacc aatgtcaacg 2460  
 agcatactgg gcaattcatc gattggcgac tcaacttgtg gggcgaggcg attgacggag 2520  
 ccgagcagcc tctccacccc atgcctactg aacacgatga cgaccacagc tatgaggaag 2580  
 gaaacgtggc taccacgagc atcagcgccg tcccacgaa aaccgagctg cctgacaagc 2640  
 ccactggtgg cgttgatcgc ccggtgaacg ttaagcctac aacatccgcg atgccgaccg 2700  
 gtagtcttac agagcccatc gatgatgaag aactccagaa gaccctagt acagaggcaa 2760  
 gctcaacacc aagtccttct ccgaccaccg cgtcagatag taccctgcct tccttcttcc 2820  
 ccacgttcgg tgcgtcgaag cggacgcaag tttggatcta cgctgcgac ggctccatca 2880  
 ttgtgttctg cattggcctg ggcgtctact tccatgtgca gcgccgcaa cgtattcgcg 2940  
 acgacagccg ggatgactac gatttcgaga tgatcgagga cgaggatgag ctacaggcaa 3000  
 tgaacggacg gtcgaaccgt tcacgtcgcc ggggtggcga gctgtacaat gcttttgccg 3060  
 gcgagagcga tgaggaaccg ttattcagtg atgaggatga tgaaccgtat cgggatcggg 3120  
 ggatcagcgg cgaacaagaa cgggagggcg cagatggaga gcattctcgg agatgaagtg 3180  
 cagtagatga ggggtgattt tatttcggac agtggttctt acttggttga tgacctgcgt 3240  
 tgaacaatat tcctgctgtg tatgctgcat agagaaagcg tgtatatacc atgtatgtgt 3300

gcatcatctt tgatecgggtt attattcttc atctgccatg gtttgtgate tccggaatag 3360  
 taccaaagga aactaaatt aagggtcttg gcgatgacgc ttcccgctgc tgcttttgac 3420  
 ttctccgca tctcgtctct cctgctgttg accgcccgc aaccaacctc catctctca 3480  
 ctctcccac cttaatcttg ctgtcctgct tctagagccc ccagtttaa tttaaaaacc 3540  
 ggcttttcct agtccacgt attgtacctc 3570

<210> 42  
 <211> 1236  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 42  
 aggtcccga cagatgacaa ggctctaaga ctgtatgtct cattcagggt ctagccgtgc 60  
 ccgctcttat tggcccggac gcttcacgcc gcgattactg cgcgccgca tgtctctctc 120  
 tccgctcgt atcgatgcgg tgtttgcccg ccattgatgg gaggaatgtc tcaacttcggg 180  
 cttgtgcttc gcagatccat acccctcaat gacctagtat agcaaacagg cgtgatgtca 240  
 atgatttgtt ttctattcag agcatcaggc ctcccatgtc tatacctcag ttatggagcc 300  
 ttggccgcct tgggtaggca aggcctcccg ggtattctca ttgccatttc accgctactg 360  
 cagcttcaag tgaagagaaa gaggggaaa aaagaatata agtagcttga caatctctg 420  
 cacgtcctcc tcttcagctc acatcaaaca tctattcttc actcctcaag agtaaaccac 480  
 tactacaaa cacaatctca tctatagctc acgagtacca gcatcactca tctaccacaa 540  
 tgaagacctt ctctaccgtc acctctctcc tcgctctctt ctctcgggt ctggccgcac 600  
 ccgttgacag cgctgaagcc gccggcacca ccgtctctgt ctcatagac actgcctacg 660  
 atgtctctgg agcttccttg accaccgtct cctgctcgga cggtgccaac ggctgatca 720  
 ataagggtca ctccaacttc ggctcccttc cgggtctccc caagattgga ggccccccta 780  
 ccattgcagg ctggaactct cccaactgcg gcaagtgcga cgccctgacg tacaacggcc 840  
 agacagtcaa cattctggcc attgattccg cacctggtgg cttcaacatc gctctggagg 900  
 ccatgaacac cctcaccaac aaccaggccc agcagctggg tcgtatcgaa gctacctata 960  
 ctgagggtgga tgtcagtctt tgcgcataaa cgccaaacat tcagcaaatg cttgggggat 1020  
 gaattcggcc atggcaggga atggttatag ttggatatga ttctgggatt tacgattgat 1080  
 acgcttattt gggatacttt cctttatctt acctattgtt aatagcataa tacggagcat 1140  
 cacatacgta catacacata catcaatata gtgatatatg aacttgaata cagagctttt 1200

tgaaaatgaa atgagagatt ctaaggctgt atctac 1236

<210> 43

<211> 1750

<212> DNA

<213> *Aspergillus niger*

<400> 43

gtgaaagata tcggatagcc gtagaccctg aaagattatt tgagcctaag ggctcttgca	60
gtgacgctag caacagcgaa cccactggga tccaaaacac tagatgaagc tattgtaagc	120
cggaaccctt ccggcgcccc acccagctcc tgcaggggag aaaacatgac tctctaactt	180
aggagaaatc acagccaagg cccaagttca ctgagagacc gaaatggcgt gaatttaa	240
gttgcccttc gcgcacttta ctattccctt gttccatca gcagtcactg cttggcctcc	300
tttctagtga gcagttccat tcactttagg ccccacggct tcgttacaag agcagtatgg	360
ctcaaatatt ctggctttca ctcttcctgc ttgtctcttg ggtcagagcc gagtccaacc	420
gcaccgaggt ggacctgatt ttcccaagaa atgatacctt tgcgccaatg cctttgatgc	480
cggttgtatt cgccgttcaa gccccttcgg tcgcccataa agttaatata tacatcgagt	540
acggctatta cccagtaggc cgtccaatg aaacagttat tggccagacc gaccatgtgt	600
ccgactcaac aaacgaaacc acttatttca gtgtctcttg tatcggcaga acgttcaata	660
ccactggcag ctgggagctg ttttggaggc tgagatggac caattgttca atctcagaag	720
actcgagata ctacaaccaa tcctaccctt ggatatactc cccatacacc gacggtagcc	780
tcaacatcga caaggtctat gagggcttcc actacacagc atacaatgtc attgtcgaca	840
gggttacctt cagcactcgc gaagatgcta gccaaaccaa cctcacgacc ctcaccaata	900
gcgagaactg cgataaagtc tcgtctcttg ctctattgtc gattgtggac tccctaagga	960
ttccacccca gttaccccaa gaagatattg ataccgtgtc aatgtgccca caactcgccg	1020
atgccaggct aaattcaact tcaacttcaa gccctgcag cgtttagcatt agtcccagg	1080
ttgagtctaa tctctggcc aagatcgag acaatgaatg caataacgca cttcaccgcc	1140
ctgtgagttg caccactgaa gaaaccaagg aaggcagcgc gagcagccat gaccacggcc	1200
atgtgtgatg gcttgtcatt acgctagctt ttgccttctt tttctaaagg atccaatgct	1260
agatgtgtc gactcaggtt ttgagacagg tagacaggaa aacaggcttt attgtcacgt	1320
cgccagtagg ggaccatcaa ccacacatat gtccctacga gaccatagct atcaggaaca	1380
atgtacgggc tggaactcca ctactctta ggttgtaa	1440



ttgtgagcaa accacgcttt tcttgaatca ttgcatcctc tttagcttca attccttacc 1500  
 cacaacacag agaggagcgg acccgccatt ccacatagtg tcttggcagg gtcgcctctc 1560  
 caactacaat gcccaacttc agaggccag actatctctg ccaagtgccagggtggact 1620  
 caaattacgg aactctcgga tgcttgtgcc atggcttatt gcttgaagggt tttggaggtt 1680  
 tcggtggtta gcgcccggat aggcagtaga acacctcaa atgaggaatg cggccgaagg 1740  
 taggtggggc 1750

<210> 44  
 <211> 2030  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 44  
 tggatgccga gcaaattaat taactgcgct tacatggctg tctaacaaa tcccttggca 60  
 ctcttagcag tggtagcctgg atgggacgaa gccctgggca tagcttgctc atcggtaggc 120  
 cgaaactctc ttttacgtac cgtacggcca atatcagtgt gaaccgcaa tttagatact 180  
 attaacttac aagtaccctc acgttatgta gccgaatgtt taaaagcgat ggaccgggtt 240  
 aaagtctccg ttgtgcgatg gctgttatta acttggatta acttgcaatt tgcacaaagt 300  
 aagacgtgct tctttttgga tctttttaca cacattactt acggcggatg ctctcgacac 360  
 tccggatttc accagggtagg tgtagtcca ccatcggact ccgatgcac ttaacatggg 420  
 tggtagagat gtcgccattc tcagcaggca ctttgcgtg acatcctcac aaagtgttaa 480  
 tggcgttgct tctgggatgg tatgaggaag aatgatgcc tccgtgaaga gtgtcgactt 540  
 gatagatact caacaaaaag tcacactata agtattgggt tggatctgct gttcttatca 600  
 tttcgtctcc atcccactgc aatcttcttc aagacttcaa agtccatagt tccaacacac 660  
 agtcacctct tcaccagct tcactaccaa ccaattcttc aagaagaagt tcaactgctgc 720  
 aattgctact gccattttcg caagcgttgc cgtcgcagct cccagcgtg gcctcgaggc 780  
 ccgctcaag gcccgcgga gcagcaagg atcccgacc ctccaggcag ttgctagacc 840  
 tgcacaaacc aagaaccaga ccaacgttga gtacagctcc aactgggtccg gtgccgtgct 900  
 ggtggagcct ccctctgctg cagcgaccta cactgcgggt accggcacct tcaactgtccc 960  
 tgagcccacc ggcaactctg gaggcagtca ggctgcactt gcctgggttg gtatcgacgg 1020  
 tgatacctat ggaaacgcca ttcttcagac cgggtgtgac ttcaccgtga ccgacggaga 1080  
 ggcctcgctc gatgcctggt atgagtggta cccggattac gcctacgact tcagcggcat 1140

cgacatctcg gcaggcgatg agattgttgc cattgtggag tcctacacct cgactaccgg 1200  
 tattgccatt attgagaaca agagcaccgg ccagaagggtg tccaaggagc tgctgtccag 1260  
 ctccagcctc ggtggacaga acgctgagtg gattgtggaa ggtaatatga aacatacatt 1320  
 cctcattcaa cattaccaa cgctaacgag atcttagact tcgaggaaaa tggttcgctc 1380  
 gtcaacctgg tggactttgg caccgtcacc ttcactgggtg ctgttgccaa ggccggcggt 1440  
 ggtgagagtg ttggacttac cgatgcgacc atcatcgaga ttgaggagaa tggccagggtt 1500  
 gtcactgacg ttaccatcga cagcgactct gaggtgacca tcacctacga gtaaatttgc 1560  
 acacgaggcc tgtcactgtg actgacggtg ttgagtgtct caatacaaag cgggttgatt 1620  
 ggtatgcagg gatgtgatga tgtgatcagg tcagcgcttg atttcaatcg acgaggcagt 1680  
 ggagaacgaa gatgtagata gttttgattt ctagtactac tttgcggggc ccctgttgaa 1740  
 tttgagtcac tcttttgatt gatcctccgg aatcatatat caagtaatgg tgcagcgtag 1800  
 ggagtactcc ataaggcaga tgaagtacag gtcttaaaac ggtatgatcc agtaagacaa 1860  
 agcggatctt gtattccaaa caatcacgtc ggtaacatgg actactactt tcatctataa 1920  
 tgtttgtatg ccagttgtgc tgcagattat taatttgtat aggcatgtga cagggtgcgt 1980  
 acattgttca gcaagtaaac gtgattttga agtccccaag aacacaaagc 2030

<210> 45  
 <211> 3080  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 45  
 ctccggctgc gtcattgattc atgcgtcaaa tcagtggact cttagtaggt ggatgtacag 60  
 cacttatttg atacttcgag tgtccgcca catccggcg tctatattct ataccaatcc 120  
 acattatgcc caacgaaact gtatgctgtg atttaagcag aagtgcgcaa agcactgtgt 180  
 cagctgatct aatatactat atgctccgat taaacccaag cagtctgcta ccaggagac 240  
 taccaggcag aaagtatctg gctgcatttg tcccagtctg cacaggactc gctatgttat 300  
 ggagcagaag tattgtgcat ggattccatc tgtccacta gcatgactat ctcaatatcc 360  
 accgggtaca tgatttagcc ggtatcactc ccccgccct gtagcaaagg cccgcgcaag 420  
 aggtgtttcc agaaagggt ccacgcttag caccgttcag caaattctgc atcagccgcg 480  
 gggaaactgc ggtttgttgc caggctcagg tgcctaaata ccaccgtctt ctgcgtcgtc 540  
 agtgcctctg tcaggcgtcg ctcatgcaag ttcagttcaa gactcaggat atccgggcag 600

tectccgcaa ctatgcgctg ctccctcctc tcccttctag gcctggcggc catcccggcc	660
cttgagggt gtcccttcgc acacactgcg aacatgggca ttgataacat ggtgaaagca	720
caegtcaca tgtcccgacc gttgattgcc tccaagagca gccctcaac tgttcctacc	780
tcctctagca ccccttctgt cgggcagaaa ggcgtgttca tgatgaaccg cattgtcctt	840
ggcacatccg agctctacat tgccaacaca gatggcagta atgaacgcc actcctctcc	900
aaccccgctct acgagtacca tgccctcctc tccccggatg tagaatggat caccttcacc	960
agcgagcgca atggtgacgg taactctgac atctaccgcg tacggaccaa cggctccgat	1020
ctccaggaat tgggtgccac gcctgcagtg gaagactccg ttgttatctc tcccaacggc	1080
cgcctggcag cctacgtctc caccgccaac aacatgaagg caaacatctg gatccttgat	1140
cttcagaccg gcgcgcagtg gaacctcaca aatacaccca ccaactgccg caactcctcc	1200
ctcatggaga gctatctccg tcctgcctgg tctcctgatg gcgaatggat cgccttctct	1260
tggaccgca acaccaatg ggacggacac ggcgtaccga ccttcctcgg ccgcacgggc	1320
tgggagacga cgcaagaact ctctctctac gccatccgtc ccaatggctc tgacttccgt	1380
cagatcatct ccaagccata ctactctctt ggatctccga aatggtcagc agacggtaaa	1440
cgcctcgtct actacgaaat gaccgggaa gacacctaca acgcccctcg tccagaaacc	1500
attaccacag ccaactcgac gatcatgtcc gtagacttcg agacaggcac cgatgtgcgc	1560
gtggaagtcg cgggctccgg tgtcaagcaa ttcctcagc acctggacaa gaacggcacc	1620
atcgctaca ccctcaaagg cggcaccagc gagggcttct acacgaccgc gggactctac	1680
gtcaacacga cctcggcgac cctcaggtec ccggcggtgt ctcccgacgg caagcaagta	1740
gtctacgaaa agagcaçctg gagcatccgc tcggggtaca agcagctcta cagctgggac	1800
agtgactggg actaccgctt cacggacgtc ttccctcagg tctcgacca ggagcgcgtc	1860
gccatcacac agaagcagct gggcaattcg tccatcgtga cgttgaacac aaccggaggc	1920
gacttgcaac tcgtctacga ccccagcacg gcggactttg tcagcgatga cgaaaccaca	1980
ggactgagcg cttaccagcc cagctgggtc ccctgcggcg agtggctcgt cttcggcgtc	2040
ggattctggg tcgagacgag agaagcctca ggcggatgga tcgtgcgggc caccgccaac	2100
gggagctact cggaggttct cgtgaacagc agctactcca tcaccgagga tggagccctg	2160
aacagcgggt tcccagttt ctcgccggat ggcaagaaag tgggtgatcg ggtttgggga	2220
gccgacactg caacctacgg caacgccagc gagatcgggc tgcggggtgct ggacctcgag	2280

```

acgcgaaaga caaccgtcct aaccacagaa tgggacaatc tgccccagtt ctctcccgat 2340
ggagagctca tectattcac acgcaaaacc agcacgtaca attacgatgt gtgcacgatc 2400
cggccgggatg ggacagatct cgcggtgttg acgagcagcg gtgctaata tgcgcatgcg 2460
gtctgggtcgc aggatggacg gattatgtgg tctaccggca tgtatgggtt ccggttttag 2520
tgtgcgctgt atggtgatac gttccagccg tatgggcagg ttatgattat ggatgcggat 2580
gggggaaata agaagttgat gaccaactcg atgtgggaag attcgatgcc gttgttcttg 2640
ccgaggggagg tacttttagtt ggtggcggga ggatgctctg attttttagag gatatgtgac 2700
gtttgatgta tgataagaat tacacaagta gttttgatca taacgcggtg aagaggatga 2760
aaaaaaaccc cgttggttcg acttgatctt ggcgatccgg ttaggggttg ttggacgagc 2820
aggatgtact gcttaattca agcaagtttg ctactccgat tcagtatgga ggggcaatta 2880
atgatgacga tattctgcac tttctactct acctactact tatctgtata tgaatgagaa 2940
aaaaatagta tgcaacgaat atagatcgta ttgacagaac ctgtcagaga gaatgacctc 3000
gatagtcgac tccatagcat ttgatctttt actaacagcg aaagattccg gactaactat 3060
ccatatatag tactcctaca 3080

```

```

<210> 46
<211> 3290
<212> DNA
<213> Aspergillus niger

```

```

<400> 46
ttccaacttc ccatgaagtg atgtagtagt ctgctaataa tacctcaaga tagaatatag 60
tatttactac ttatcgtcag ctttgtcgaa aattcaaagg tttgtggaag gccacctcat 120
ccgcacctgt tgcctacagg gatagcatcc tgcgagggtg ttatccgctt atcagcaaag 180
gtggcagggg gggtaaggct atcccgggtt aggaaggccc gcggcacgat gcgaccttc 240
cagactagga agctacctaa tagggacagt aagggaacaa tctcaggact aaaccgtgca 300
gcctactgaa tctcaccact cggacctgat atttgccttc ggcttgcagg ggtatatcat 360
ctcaatatcc tctagtggac ggaaactagc aactagtact ttgagctgac tcggccacta 420
taaatatgcg gtcttatgct cctcaacgac aggcaactgc tctgactacc aaaatctgag 480
taggactagc accgttgcca gctcctcttc acgataccga atcttttata agcaagtgg 540
ccaatatcca ggtctaactg atccatacaa tgctccgga tgcaaaatcg cctggctacc 600
agcctgggat ggcagtatta ccatctaggc cacatcctgc caagggaaaa gccattcgat 660

```

tcctcctttc ccttgcatgtg gtcgctgttg ctattgttca attatgtggg aatttccaca	720
aaaataggag cgttgaacaa cagcttcaga gtcaaacact tgatgatgag tcctttaaat	780
gggaagatgt gtgtaaactc atcacgttgg gatgtaacgt tctaacgcac tctattaggt	840
tactcctacc aagcaactcg tataccatcc atgctttggg gatcacgaat gcgctcgctt	900
gtcgcttcca atgaattgga accgaactga tggggaaggg tcaaaaattg ccttggcggt	960
tatcaaactt cctgccaaagg tacctgtcac agatgcgcga tatgggtggg ccattcttct	1020
gaatccaggt atgtagagcc atattgctac tcttcagcgg ctgtgctgag tttcaaatag	1080
gtggtcctgg tggatccgga gtgagcatgg tctttagata cgggaaagct atccagacca	1140
tcgtcgactc ccagaatca ccaagtgcag attcagcgag cggaaagtat ttcgatgttg	1200
ttagctttga tccaagaggg gtcaacaaca caacacctaa ttttctctgc ttcctgacc	1260
ccgcgacgag gaaagcgtgg ttactgcagt cagaggcaga gggctactt gggagttctg	1320
aaggagtctt cgatactcga tgggcaaggt acgaagcttt tggatatgagc tgcaatcaac	1380
aaggagtcac agcgtcaaag gatggagaat ggataggaaa attcatgaat acggcccccg	1440
tgggtggcga tatggttgaa ctctagagc gccatggaga gtggcgtgaa cgggaaacag	1500
agcggctact ttcgacagct ccgaacactt tcccagttgg aacaaacgtt gacgccgaga	1560
ggataaggct gcacaaccgt tggaaaaaag gggaggagaa gctgctatac tggggctttt	1620
cctatgggac aatcctgggt tccacgtttg cggctatgca gcctcatcgc ataaaccgtg	1680
ctgtcataga cggagtctgc aacgctgatg attattacgc cggcaactgg cttaccaatt	1740
tacaagattc ggatgcagca ttcaataaat ttttcgagta ctgctacaca gctggcccat	1800
cagcgtgtcc gtttgcgctc ggcggagatc ccgaagatct caagtctcgt tatgagcaga	1860
ttttgaccaa tcttacatcg agccctattg ctgtgtctcc ttctggaaat aggggcccag	1920
agataataac ctatagtgat gtgaagtcac tggctcgtgca agctctctat gtgcctttga	1980
aattattcga tttgggtggc aggcctattg ctgagctcga gcaaggtaac ggctcttcat	2040
tcgctgactt gaagtatgaa gccaaacaat ggccagtacc gcctccatgc gattcctcgt	2100
ccacacaata caaagtacct ggcgagagtg atcaggaggc cgggaggaat atcctatgta	2160
cagatgggcc aggcctcgac ggaactgcc aaggagattt cgggagctac tggaatatgc	2220
tccggggaca aagtaaggcg gttggagatt tctgggccga ggttcgcatg tcgtgtgtca	2280
aactggagac gcgacctgag tggcgctatg atggtaggtc cgaccaacac catattatac	2340
acacaatata agctgacagg tatgcgtatc caagggccct tcgcaggcaa tacatcgac	2400

ccattgctgt ttatcgggaa tacttatgat ccagtaacgc cgctacggaa gtaagctttg 2460  
 ttcacctgat cgtagcagac tttgaagtac agactgacgc ataggcagtg ctcatcacgat 2520  
 ggcgcggtgga tttcctgagt caatcgttct agagcagaac tctgtcggag tgagtacctt 2580  
 atctgttccc caacccatat gcaagatgac taactgttca atgtcgcagc attgcacact 2640  
 gagtggccca tccttgtgta cagcgaaagc gatacgccag tatttccaga' ccggagagtt 2700  
 acctgacccc ggaactgttt gccaggtaga ggagcttccc tttcgtcttg ccggatatga 2760  
 gagaagtcag gtcattgtgc caggtgacac agaattgatg tccgccttgc attcgctgag 2820  
 cgagttccgc catctgctag gcgcgtgaaa aaggttaaat aagtgtcgcc agcgagcgct 2880  
 gcagttatta atcctttaca tcataggagc tggctagaat gttaacgatg cagtttgccc 2940  
 ctgtatctcg accaagagca tgaataacac attatatcag caaatgttat tgagcaaadc 3000  
 aattattcac ctgcactcaa ttcaatttaa gatctgttgc ctagactacc agaattatta 3060  
 aggcgacctt atcgaagcat ttgcagacca acccctgtcc atcgtcaggg gcaagacaga 3120  
 cttttcttct agaaccggga tgatgtataa tcgcgggtggg gaagatcatc ctaaaccatt 3180  
 gccccagact cgcctacctt aggtaatcca taaaaatgcc ggggaaatca ctgaggtgtt 3240  
 gttcatcacg gcgttgaatc ggcttctgcg gtattaccac cataactgta 3290

<210> 47

<211> 3080

<212> DNA

<213> *Aspergillus niger*

<400> 47

gaaaatcccg accgttaggc tacctaactct gctgtcttta cccccgtag ccacttacc 60  
 cagctttagt ctctcgaagg aaaagaaaac aaagtaatcg ggagcctata atattcggcc 120  
 agaagtgggg caatcacttc aaccgttcat ctgttattga gttatcaagt ctgtcaagtt 180  
 cgtcggagct ggataaggta gtcgccatcc ccatttccgc tgtgcaatgc cgcagcgccg 240  
 aagtgtctgc agctagctct attttgttca gctacgtatc tgtctcttaa ccaaatggat 300  
 gtcgccatcc gccactaac aacgccatcc cccacggccg acggactccg gcgcaagggc 360  
 ctgataagcg ttagctccga ctccgagtta gtcattgggc ttattacgcg cccttctccc 420  
 ctacagatgt tgatgctttt tctggtatct ctggcataac tggcaaagat caggctgtgg 480  
 tcataagagt atcattgcct tcagcttctt cgccatgttg agtagtctgc tgcttggggg 540  
 tcttctgggt ctacgacccg ctcaatttcc tcccgagccg gaaggcatca ctgtgctcaa 600

gtccaagttg catgagaatg tgactatttc tttcaaagag gtgtgtgcag agtatctaga	660
aatagctttt atgctcgatg ccgtgctgat tgtcagcctg gaatttgca aactacgccg	720
ggtgtccgat cttattcggg ctatgtacac cttcccccg gtttcctttc cgacgggaca	780
ggagaagtgc aggattatcc tatcaacacg taagccaatc tcgaaacatt ggaggatgag	840
caattactga gcctcaacca gcttcttttg gtttttcgaa gcccgcaaag atcccagcaa	900
tgcgcctctg gccatctggc tcaatggcgg tccgggtggc tcgtcgctca tggggctcct	960
tgaagaatta ggtccttggt ccattgcac agactccaag accacagtcc tcaatccttg	1020
gagttggaac aatgaagtca atcttctatt ccttgaccag ccaactcaag tcggcttctc	1080
atacgatgtc ccaacaaatg gcactttggt tcggactgcg gacggcgaag aagagatagt	1140
ttccggtgat ttctccattg atgttcccca gtccaacttc acccatcatg ttggtacctt	1200
tgcaagccag aagcttgca acagacgtaa tgggactgca ttccgggtc acgctctatg	1260
gcatttcgcg caaacctggt ttttcgagtt ccacactac aagccaaacg atgatcgtgt	1320
cagtctctgg gctgaaagt acggaggcca ttatggtcca ggcattcttc ggttcttcca	1380
acagcagaat gacaaaatcg cagaggggac tgcagaagac ggtgcacagt atttgcattc	1440
cgacacgctt ggcattgtga acggcttgat ggatatggtg atccaagaag aggcttacat	1500
tacttggtcca tacaataacg taaggctcgc cccttcttca ttcaactcgc gtaatgccta	1560
attcagttca gacctacggc ctcgaaatct tcgataaacc cctctacgaa gaactgatgt	1620
ataactggac gcatccagga ggctttcgcg atcaggccct cgcttgcgaa gcggctttga	1680
aagaacgcga ttccggcttg cctcactcag ggaagaatat ctctgaaatt tgcggaggcc	1740
ttgcactaga atggggagat ggccccatca cctactacca caccttcaat cgcggttggt	1800
acgacatcgc ccattcctaag aacgacccat tccctgccaa gcacatgctc ggatatttga	1860
cgcaggagtc cgtccttgcc gctcttgggg taccagtcaa ttccacatcg tcttcgagtg	1920
ccgtggctac acagttcata aaaacctttg atatcgtcca cggcggcttc ctggatgcaa	1980
ttggctacct cctcgacagt ggtgtaaaag tacacatgat gtacggagat cgtgattacg	2040
cctgcaattg ggtcgggggc gaaaaagcca gccttgacgt tccgtattcc cgtatcacgc	2100
aatttgccga cacgggatac tccccactcc ttacgcccga cgggatcagc ggcattgacc	2160
gccagctggg caactacagc ttactcgcg tcttccaagc cgggcatgag gtcccctcct	2220
accagcctgt cgcggcgat gagatcttca tgcgggcgac attcaacaaa gatatcccta	2280

ctggcctctt ggctgttgat gacgaattcc agtcggttgg acctaaggat acgtggcata 2340  
 tcaagaatat cctcctatt atgccaagc cgcagtgcta tgttctaagt cccggcacgt 2400  
 gtaccccgga ggtttgggag accgttttga acggatccgc gacggtaaag gattggtatg 2460  
 tcgtggatga tagcgcggtt gttgaggacc acgaggggtt cagcattctt ggaggggatg 2520  
 agttgtagta gcttagaagt ctaccgaaa gccttgctag ctcttaaaat acgacacaaa 2580  
 tagttgagcg acatagtcta ctctctcact tacgaacacg tgatgaatct ctccagcaat 2640  
 aaagtggacc aatcaattgg aggaaaatat atccacgatg gtcggacggg ccaacgaaaa 2700  
 gggccaacta gcgcccctct gaggatgatg gtctagtctg caggatatga gattgttcac 2760  
 atcttatggg tcttcaactg cacaatttag gcggaggctc cctcaccgaa agagacgtaa 2820  
 gctgcttttt ggtggattca ttattagccg ttatgccatt tactaaaaca ccgcagttcc 2880  
 agatcgcgta gatggcctca aagtgttcgc cagatttgat tgagggctac ttcgccaag 2940  
 cctatggcct gtagatgcca atttcttcaa tacaaagata ggcgaaacat gttgaaaatc 3000  
 catcatatc aattaaattt caaaacatag cgagacatta agtattacat atatttcaat 3060  
 gaatagagac ttcttgaca 3080

<210> 48  
 <211> 2520  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 48  
 tctcgctgc ctgcaccttc ctgctatggc aattctttcc ccaagctgag cggttccatc 60  
 cgcttcccga ccgccaact tatcaaccgc agcgatagcg agaggggaaa ggctatcacg 120  
 gcaatgattg cgcaactctg cgataagata accccatgtt ttgacgtagc ctcggccctg 180  
 tcttctcctc attattatcc tccgattccc ccagggttcc tgtcttctgc agaaagtgct 240  
 ctcggaatcg aagatgacca ggtttcaatt gcttcccctt gtcgcagggc tgcttgcccc 300  
 ttcaattgca gcccttagca tcccttcccc gcagcagatc ctcgattctc tcaatttcgg 360  
 agagcacacc gacggctttt gtccgctggc acccaagggt gaggttcctg acgatggttt 420  
 ctttccagct ctcaagttcg tagaagatgc ctcggttcaag tcgcgccaag tcaatcgtct 480  
 ctccagggcg gttcaagttc cgaccgcaat cgacgactac atgaaggatc cctacgacga 540  
 aaagttcgcc ccattcctcg acttccagaa gctcctgcag accctctttc cctcacgta 600  
 cgtccccagt ccccgctctc atggctccat ctaacgcaat ccagccactc ctacgcccgc 660



gtagatcaca tcaaccgatt tgggtctcgtc ttcacccctca atggcacaga tgactcgctc	720
aagcccctgc tattcaccgc gcaccaggac gtcgtgccca tcaacgaccc tgccgactgg	780
acctatcccc ccttcgatgg ccactacgac ggcgaatggc tctggggccg cggtgcccagc	840
gactgcaaga acgtcctgat cggtctcatg tccgttggtg aagacctact ctcccaaaag	900
tgggagccaa cccgcacagt cgtcctggcc ttcggattcg acgaagaatc ccacggcttc	960
ctcggcgccg gatccatcgc caaatcctt gagaagaaat acggaccgga cagcttcgaa	1020
tttatcctcg acgaaggcgg catgggcctc gaagtcttag acgacaacaa caacggcgctc	1080
gtctacgctc tccccggcgt tggcgaaaag ggcagcatcg acgttggtgct cactctggcc	1140
gtaccaggcg gccacagctc cgtgccccct ccacacacgg gaatcggcat catcgccgag	1200
atcatctatg agctagaacg ccaggacctc ttcgtccccg tcctagacac tcaccacccg	1260
acccgcaaga tgctcgaatg ccaagtccgc cactccccct cgcaagtcga accgtggctc	1320
gcctccgccc tccaatcaag cgactacatc tccctagcag agaaactggc ctctcgcgc	1380
ggcgacaagt tccgcttcac cctccaaacc tcccaagcag cggacatcat caacggcggc	1440
gtcaaatcca acgctctccc cgagaaaatc aacgcctcgc tcaactaccg catcgctctg	1500
caccaaacc cagacgatat caagaaccgc gctgtggaga tcatctctcc catcgtaag	1560
aatataacc tctccctcac ggcttcccc gaaagcgaca ccgttgacct ctccctcaac	1620
aaccacctca cccttactac cctcagcggc gccctcagtc ccgccccggt cagcccaacg	1680
gacatcgaca ccgacgcgt ctgggcccgt ttctogggcg tcaactcgctc ggtcttcgaa	1740
tctgtcccta gtctcgaggg cagaaaggct gtcgtgagcg gcgacatcat gaccgggaat	1800
acggatacga gattctactg ggctttgtcg aggaatatct acaggtggag tccgtcgagg	1860
gcgggtaaag cgctgaatat tcatactgtt gatgagagga tcgatattga tattcatctt	1920
gaggcgatga tgctgtatta cggatgcat ctctcctttt atggatactc ctatcagact	1980
aacttgatc tctagatctt attcgctctt tcgatggacg gaccgattca tctgtcatctt	2040
ctgctcgctc ggcagctgct gatgatgaac ttgctcacga cgtgctgtga gtctgtagga	2100
actctctac tctttagggg ggctcaggat gaatgatggt tatgaatcat gtggtctact	2160
gcgcaaaaag ttcattgtctt tcctggagtt caacgagaa cagatctata tttccacgaa	2220
tagctccagt atatagccaa atgcaaccac gtatttgctc atcgatctga cagtctaatt	2280
ctttacctta tactaggggt aagaaagggt aagaaaataa aataatatct gcagcggcct	2340
atgaagataa ttatgtactc gacgttgccc aatgcactgt agccccctc cctgtaacag	2400

gagtagccat aaaagcaaaa cgaaagtggg aagaagacgg gggcaatata cctgcttttag 2460

caatatacaa caatagtaac aatcgagagc tcaatatgaa tgtataacga gtgacctgca 2520

<210> 49

<211> 2730

<212> DNA

<213> *Aspergillus niger*

<400> 49

tttagttgtg atctcaatcg caaatggaca ggagatgata ttcatgtcat aatcagagtg 60

ccatgtcagc gaccatgtct tgccaagagt catcatttcc ggtaaaaccg acggagggtaa 120

aaccccggtc attcactagt tcgagggagg gaatagtctc gcagggtctct tcttctttct 180

tcctcggggt ggcggatgga tcacttcttc atttgatggg tgccctgcaa cgaccactt 240

gactaggttt cccccttgat gggattcggt ggttttacca gacagagcct cttcacagcc 300

cagcgcgtgt tccgcaaaag caacagccca agggctctgaa ggctgacatt ggagcgggtc 360

tgacgcagga tggcttgctg ttaaaaaaac tcaggaacag gccaaagacga agcgaccgcg 420

caaggctgag cagttctccg atttccccgt gccctcctg cgccctccat gggcgacttt 480

tgatcccaga tccatcgttt ctgcaccgac catataagaa gctccgcacc cccaaactcc 540

cctggcaagt tcctgcccc aaattacgtg agacagggaa ccatcacagc aacaccatga 600

agagcaccac tcttctttcc ttggcctggg ctgccagtc cgcctattcc ctctctatcc 660

acgagcgcga tgaaccgct actcttcagt tcaactttga acgtcgtcag atcgccgacc 720

ggtcccgtcg gaagcgatcg acggcctcgg ccgacctcgt taacctggta tgttcccatc 780

ccgagtctca aatcagggga attatgacgg tcgctaatagc aggtttctag gctacgaatc 840

ttggctacac gatgaacctc aactcggca ctcccgcca ggaagtcagt gtgacgttgg 900

acaccggcag cagcgatctc tgggtcaatg gggccaactc gtccgtctgc ccctgtaccg 960

attacggctc ttacaactca agcgttctt ccacctacac ctctgtgaac gatgagtttt 1020

atatccagta tgtcgacggc agtgaagcca caggcgacta tgtcaacgat actctaaagt 1080

tctccaatgt gactttgacg aactttcaat ttgccgtcgc atatgacggc gactccgagg 1140

gtaagtcttc gctattccct cactttcatt ttacactttg ctaacggttt taccatgcag 1200

agggggtcct cggatcggga tacgccagca atgaagccag ccaggccacc gtcgggtggg 1260

gtgaatacac caacttcccc gaagccctcg tcgatcaagg cgcgatcaac tggccggcct 1320

acagtctatg gctcgatgac ctcgacgaag gaaaaggcac cattctgttc ggcggagtca 1380

```

acaccgccaa gtactacggc agcctgcaga ccctgcctat cgtctccatc gaagacatgt 1440
acgtcgagtt cgcgggtcaac ctgacggccg tgcaccttga gaagaacggc aactccgtct 1500
cgggtcaaaa cagcgccacg caattcccca tccccgccgt gctggacagc ggcacggccc 1560
tgacctacat cccgacctcc gccgcagcca gcatctacga ggccgtcggg gcccaatacc 1620
tgagcgagta cgggtacgga gtgatcgagt gcgacgtcaa ggacgaagac ttcaccttcc 1680
tgttcgactt tggatccttc aacatgagcg ttgacatcag cgagatgatc ctcgaggcca 1740
gttccgacat gaccgacatg aacgtttgta cgtttggcct cgcagtgatc gaaaatgagg 1800
ccctgctggg cgataccttc ctgcgcagcg catacgtcgt ctacgatctc ggaaacaacg 1860
agatctccct ggccaaggcc aacttcaacc ccggcgagga ccacgtcttg gagatcggca 1920
ccggatcggg tgccgtgccc aaggcgacgg gggcgacggc gaccggcgcg gcagccacat 1980
ccacggcctc gagcgacaag tcggacaagg agagttcggc tacagtgccg cgcagccaga 2040
ttgtctcgct ggtggcgagg gtcttggctg gtgttttctt ggttctgtaa atatagagat 2100
ttcacgttgc atgttgatga tacataccat agatttgctt ctaattgccc cttacatctc 2160
gaaatgtttt ctgttttttag cttgatatac catcgcttca ggtttcagat atggaaatga 2220
aatgaaaatc ggaatgcaag atctgatcga atagttgttt cactgccgcg tggctggtcc 2280
gatcggcacg aagccagtaa tcgacaacca atcatacatt gtgatttcct gtcaacctcc 2340
ttgcgactac tactaatttt atcatatcat gccgttgatg cctatcctac tcggtgtccc 2400
cacaccgatg atagccaccc gcgaccggat aatcggtaac ctgccaagag tcgaacggct 2460
ttcctgtgga aaggggtggc gcaacctgtt tgtttcagtt tttgtgttgc agaattgact 2520
atccttctga cctgtgaatg atactgggat ggtgacgtat tgaaaatgtt ggtggagcga 2580
ttaaggtttg tgcctgtcag cctcgtcaag tccatcatca tgtcttttcc ggactatcac 2640
ttcctctact ctgaagtacc gggactcccc gccagtattc gtttcgcaa tcagagcatt 2700
cgatgtgaac cggattgaag agtgcccggg 2730

```

```

<210> 50
<211> 3231
<212> DNA
<213> Aspergillus niger

```

```

<400> 50
ccgacgcgac ggcattagtt cctcgatagc gtgggaagac catggagaga ccggccgata 60
agctgcagag gagctttctg tgggctgacc agtgcctatc agcaaatgga cagcggtga 120

```

cacccccgca atcgcaagac cgcctcgaca ccgtccatcc aggcaccatc gcaacggcaa	180
accagcctct cctccaatca aaccatcgat gtgatattgc tagcggcggt gagaacagca	240
ggtcgaatgt cgcaattaat tctcgcateg tccctcactg caagggggccc actaccagag	300
ctctgcgcg ttgttattta aatccgttgt tgggacctt cggtcatcag ccactgtgtc	360
tggtcactat cgcgctggtt caacctcaac atgttggtcc gtcagcttgc cctggctctg	420
gccattgcgg ccttgtccga tgccattccg acatccatca agcatgtcct gcacgagaaa	480
cgtcacaagc ccgcatccga ctgggtgaag ggtgcgcgcg ttgagagcga tgcggctctg	540
cctatgcgca ttggccttgc ccagaacaac ttggacaagg gctatgactt cctgatggaa	600
gtgtgagtca aaatctacct tttttatgct atatgcctag ttttaggac gcaatggatg	660
acctcgaaac atgctgacat gagattggcg cagatcggac cccaagtctt ccaaatacgg	720
ccagtactgg tcggcagacg aggtgcacga catcttttcg ccatccgagg aggctgttga	780
ggcagtgaga gaatggcttg tcgcctctgg tatccatccg tcgcggttg tgcactccga	840
caacaagggc tggctcgcgt tcgacgccta cgcccatgaa gccgagaggc tgttcatgac	900
ggaattccac gagcacgaga gcgaccgaag tgctaagatc agggttggat gcgaccagta	960
agaagattct tctatcacct tccatgagta gctattaatc ggaatctaga taccacgtcc	1020
ccgaacacat ccagaagcac atcgactaca ttacccttg agtgaagtc acccaggtcg	1080
tgaagaggac caacaaagtc aagcgtgctt cccaactagc tcaactctcc aaggccaagt	1140
ctgctgcca aggtccgcag ccactccca acaaggcca gttcctgcct gaagacctcc	1200
gcggctgcgg ttacaacatc acccctcgt gtatcaaggc cttgtatcag atcccagacg	1260
ctaagacggc gacccgaac aacagcctgg gtctgtacga gcagggtgac tactttgcca	1320
agtccgacct cgacctcttc tataaggagt atgcgccgtg ggttcccag ggtacctatc	1380
ccatcccagc cctgattgat ggcgccaatt actcggttcc ttctacagc tccctgaaca	1440
cgggtgaatc cgacattgac attgacatgg cgtgagtcac ttctgcacct tgtcatcaga	1500
cccctactga cgttttgaag ctactccctg ctctaccctc agcagggtgac cctctaccag	1560
gttgacgacc agctctacga accagtcgag gtcgacacaa ccaatctgtt caacaccttc	1620
ctcgacgctc tcgatggcgt gactacagac ctcggttctca gtcttaccga gctaacaccc	1680
ctagtcctac tgcacctaca gcgcctacgg cgagaccggc gatgaccggt cgatcgaccc	1740
cgtatacccc gacaccgcgc ccggcggtca caaagggtacc tacctacacc acctcttccc	1800

catacaatcc aacctaacac accaacagga aagctccagt gcggcgtcta taagcccact 1860  
 aacgtaatca gcgcctccta cggccaatcc gaagccgacc tccccgtcag ctacaccaag 1920  
 cgccaatgca atgagttcat gaagctcggg ctacagggac actccatcct cttcgctgtct 1980  
 ggcgactacg gcgtcgcgtc tttcgccggc gacggtgacg agaacggctg tctcggccca 2040  
 gagggcaaga ttttcaaccc ccagtacccc tccaactgcc cctacgtcac ctccgttgga 2100  
 ggtaccatgc tgtacggcta ccagaccgtc aacgacagcg agagcgtcat gcacgttaac 2160  
 cttggcgga cgcgaagtaa cttcagcact tctggtgggt tctcgaatta cttccccaa 2220  
 ccggcatatc agtttgctgc tgtggagcaa tacttccagt ctgcgaacct gtcgtatccg 2280  
 tattactcgg agtttgaggt cgatgttaac acgaccaagg gtctctacaa taggcttggg 2340  
 cgtgcttata cggatgtctc ggcgaatgga gcgcatttcc gcgcttatat ggatggatac 2400  
 gattatcatt ggtatggatc gagtttggcg tcgcctttgt tcgcgtcggg tcttactttg 2460  
 gtgagctttg tcacccccca ttactaatta ttgacacatg gctgaccgac ttagctcaac 2520  
 gaggaacgct tcgctatcgg caaggggccc gtgggattcg tgaatcccg gctttatgct 2580  
 tatccgcaag tgctgaacga taccactaat ggtactaatg ctgggtgtgg aacttatggg 2640  
 tttagtgtca ttgaggggta agtgctcagt acttggttct gtcaggaggg gtgtgtcaat 2700  
 tgatgactat agatgggatc ccgctagtgg tttgggtacg cctaactacc cattgatgaa 2760  
 ggagctgttc ctctctttgc cttaggattg aacggtgctg tgcagaggg tgataggtgg 2820  
 tcaagctgtg tatatatgtc tgatggggaa atatttacga tcataggata atgtgtcgac 2880  
 gagcatgaat ggccaattat ctgcctgtc accgtgaata aggtcaaag tagatcgggt 2940  
 taatagttca actacagaga attcttggat attgtcaaat gttgactatt cgctgtctct 3000  
 ttatcgtcta atgtataata tcatcaaata acctaaccga agggatatca aaaacataag 3060  
 aaaataataa accggtacta tgtgtcgaaa aaaggaatgt ttgtgaattt tttaaaaccg 3120  
 ttcatacctc ccgtccatgt ccaccaaag cacagcgtg gtcgaatccc tctccgaccg 3180  
 tgtcgtatag tcaacggaga tattcactga cttggaaatc ttgctgttgg t 3231

<210> 51

<211> 2660

<212> DNA

<213> *Aspergillus niger*

<400> 51

tcctgagcaa gcagctaccg gtaatctgag acctaactct ggtaagtggg tcgagttcat 60

ttacctcatc atctaacctc gcttcatgat tgcaggcgc tttccgcgac tagtcgatgc	120
cagtatccat ttgcctgcag atccgatgct tccaccgacc accgttactt ctctccagac	180
ccccatccgg ctttccgacg gcctcctctg catccctca caaagcaagc ggagacctgc	240
ctgaataggg agagttttt caatgagccc acacgcagtt acctcgcttc cgcgatgagat	300
gggtccattc ttgacaatgc tgcctaatgc gcagaagggc cgtcatgcgc ctggagaact	360
acataaatag ggaccacgca tgccccgacg atgtatgaat tgttcaaact tctccgcca	420
agtgagttct cttttcattc cattccgaag ggagaatcac cagtatgcgg gttaccacgg	480
caattgcttc attactactg gtcggctcgg ccaccagtct ccaaaatcct catcgtcggg	540
ctgttccgcc cctctctctg catcgacgcg tagcgtctcg ctccgtgcc gttgagcgcc	600
gaaccaccga ctttgagtat ttgactaaca agactgcaag tgcgtgattc cgttttttaa	660
ctaccgcatt tatcgttcta agatcaattg caggattcct ggtcaatggc acaagcatcc	720
ccgaagtcga tttcgacgtc ggcgagtcct acgccggcct tctccccaat acgcccactg	780
gcaattctag cctattcttc tggttcttcc cctcgcaaaa tccagaggcc agcgatgagg	840
ttagtggtcg ctctgttttt tccggtcatg cgtcagccag ctaacaatta acaaagatca	900
ccatctggct caacggcggc cccggatgta gctccctaga cggcctgctt caagagaacg	960
gcccattcct ctggcagcct ggcacttaca agcccgcttc taatccatac tcatggacca	1020
acctcaccaa tgtgggtttac atcgaccaac ccgccggcac aggccttctcc ccggggccct	1080
cgaccgtaaa taacgaggaa gacgtggctg ccagttcaa cagctgggtc aagcacttcg	1140
tcgacacctt cgacctgcac ggccgcaagg tctacatcac cggtgaaagc tacgcgggca	1200
tgtacgtccc ctacattgcc gatgccatgc tgaacgagga ggatacaacc tacttcaact	1260
tgaagggtat ccagatcaac gaccctcca tcaacagcga ctcggtcatg atgtactgta	1320
tgtttccctt catatacctc cacctccacc accaccacca ctaacaacat caccaccag	1380
cccccgccgt ccgccatctg aaccactaca acaacatctt ccagctaaac tccactttcc	1440
tctcctacat caacgccaaa gccgacaagt gcggctacaa cgccttcttc gacaaagcca	1500
tcacctaccc accccccagt cccttcccca ccgcccctga aatcaccgaa gactgccaaag	1560
tctggggacga agtcgtcatg gccgcctacg acatcaaccc ctgcttcaat tactaccacc	1620
tgatcgactt ctgcccctac ctctgggacg tgctcggtt cccctccctc gcctccggcc	1680
caaacaacta cttcaaccgc tccgacgtcc agaagatcct gcacgtccct ccaacggact	1740
actccgtgtg ctcgagacc gtcattctcg cgaacggcga cggcagcgac cccagctcct	1800

```

gggggtcccct acccagcgtc atcgaacgca ctaacaacac tatcatcggc cacggctggc 1860
tcgattacct cctcttcttg aacggctcgc tcgccacaat ccagaacatg acctggaacg 1920
gtaagcaagg gttccagcgt cctcccgtag aaccgctctt cgtcccttac cattatggtc 1980
tggctgagct gtactggggc gatgagcctg acccgataaa ccttgatgct ggcgctggat 2040
acctgggtac agcgcatacc gagcgcgggg tgaacttcag ctcggtgtat ttgtctggtc 2100
atggtaagtt tattatatcc ccttggaagc ggtatgatga acgtagaga gtgctgactg 2160
ttgcttcttc ctctgatag aaatcccgca gtatgttctt ggtgcggctt accgccagtt 2220
ggagttcctg ctcggtagga ttagtagtct ttcggcgaag gggaactata cctcttgatt 2280
tcagcggatg acgacaaaaa gatgatgagg aagatgattg gatgctttca gatgggaatg 2340
cgtgcatagg agatgagatg agatgatgta tcattgaggt gtgatgactt gtacatatgt 2400
agatcggtag taaaagggat actataggat atggtatctg atgtatcatt tatgtacacc 2460
acgtggattc aattgagggg agcttcaatt cctggttatt acttatcata tttccaacat 2520
gtccgcgtat aaccggtaac aactaacggc ttcattgttg tcaagtgact gtcttggtac 2580
aatactactg tttctatatt ctactgttgg taacttaatc tggacatatt ctatatccac 2640
gtacagattc tcgctagatt 2660

```

```

<210> 52
<211> 3150
<212> DNA
<213> Aspergillus niger

```

```

<400> 52
ccaatcaacc acggatgatt ggggtcaggc cctggaggga cggagtcgga ccaagacact 60
aaggtagcgc actagcgaga caatgtgtta tcgctattat tggcaaaatg gccgcgggat 120
ctcttatgca ggggttcggc ccatcctccc ccctcttctt atccagtcaa tccgcctcgg 180
ttattgaagg agatcctgag ctgtttaact gacgcctcac cgatcaggcc ggaaatggtg 240
gcgggataca acatcgtttc cacacaatag tgcttgcttc ctgcgatctg catggcatgc 300
taatctccgc cagcatgtat cttctatcca ctggatatga attttctctc cctcacacca 360
tgtgggcctg ggggttttcc ctcaaaactt gtcgctcatg taacgatgta tataaagccc 420
tgaggatggc atccccacc catcggctctt ttgctgaccg ttctccttga agaaattctc 480
gagtggcttg tggatcatgt atagatttaa tcttcgaggg ttattaacta ggtatagctg 540
tgactaagtc tgtccttgca ttgaacaaca caccatgcgt ggctctcggg tgggtgctctt 600

```

gttgcccctg gctgcactta gttgtgctat gcccgagaat gaatgggtcat ctacgataag	660
aaggcagtta ccaaaagcgt ccactggcgt caaatcgata aaaaccccaa acaatgtcac	720
tatcagggtat aaagaaccag gaaccgaagg aattttgtgag acaacacctg ggggtcaaate	780
atactccgga tatgtcgatc ttctgccaga gtgcataact ttcttttgggt ttttcgagtc	840
acgccgtgac cccgaaaatg atccagtgc tctgtggctg aatgggtggcc ctggaagcga	900
ttccttgatt gggctttttg aaggttggcc aaatatcctg acggaaaaga taaaattcag	960
cttgcatgtt ctgacgcctt cacaacagag ttgggtccgt gtcacatcac accagagtac	1020
gaatcaatca tcaatcagta ctcttggaaac gaggtcacca atcttctttt cttgtctcag	1080
cccctcgggtg tgggtatgga atattgctgc cttcatacat cctgagtaca ttgcttacgg	1140
tcttatctgc gaagggttct cttacagtga aaccgaggcc gggctcctga atccatttac	1200
tggagccgtc gagaacgcct cctttgctgg agttcagggt cgatacccag ttattgatgc	1260
cactatcacc ggtaagttgt ccggtttgac tctcacctag cattctcctc aatgtcctac	1320
tttacagaca cgaccgatat cgctgcacgc gcaacctggg aggtgcttca gggcttctc	1380
agtggcctgt cgcagctaga ttccgaagtc aagtccaagg agttcaacct gtggacagag	1440
agttacggag ggtgagtga actttcatac cagaccgacg taagctgact tgatcaagac	1500
actatggacc agcggtaggt tgtcttttct ggttgcacac atattgatct aatgaccgaa	1560
gttcttcaat catttctacg agcaaaattc gaagatcgct agcggggaag tcaatggcgt	1620
ccaactgaat ttttaactccc tcgggattat caacggcatc attgatgccg cgattcagggt	1680
acttagaaat cgagctcgcg cagaggctgc ggcctagaag gacatcgcta aagtaattaa	1740
taggcagact actacgcaga ctttgccgtt aataatacat atggaatcaa agctgtaagt	1800
ttaaatacac gtacatcgct gatttaagat caaccgtgct catgcttgct aggtcaatga	1860
cacagtgtac aactatatga agttcgccaa cagcatgcca aatggatgcc aggatcagggt	1920
tgcttcgtgt aaattgacca ataggacctc gctttctgat tatgctatat gtacagaagc	1980
agccaatatg tgcagggaca atgtcggta gtggttctac tgtttctctg caggggtgca	2040
atgatgaagg actttgctaa gctgtcatgt acagaagggc cttactacca gtttggcggc	2100
cgtggcgtgt atgatattcg gcaccttac aatgtaagtg gcaaggataa ggattgtact	2160
ttccgaacag ggacactgct catatgtcaa cgtaggacct gacccgcgcg tcctactttg	2220
ttgactacct caagaaagac tcagtcatgg atgctatcgg cgtggacatt aactacaccg	2280



agtccagcgg cgaagtatat tatgcattcc agcagaccgg cgactttgta tggccgaatt 2340  
 tcattgagga cctcgaagag atcctccaac tccccgtacg cgtgtcgttg atctacggcg 2400  
 atgccgacta tatctgtaac tggttcggcg gtcaggccat ctactcgcga gttaactacc 2460  
 cccatgcagc tcagttccgt gcagcgggat acacacccat gacagtagat ggggtcgaat 2520  
 acggtgagac tcgcgagtat ggcaactttt cgttcacccg cgtatatcag gctgggcacg 2580  
 aggttcata ctatcaaccg atcgagcgt tgcagctgtt caaccgtact ttatttggat 2640  
 gggatattgc agcgggtaca actcagattt gggccgaata tagcaccaac gggacatcgc 2700  
 aggctacaca cacggagtcg ttcgtgccac tgtccacggc gtcgagtacc accgtcaatt 2760  
 aggattgggg gaaatttttc cctcttttgt atggctaatt ctgtgttatt cattccgata 2820  
 cttgtccata acctaaaaga gtggcacgga agctttccta gacatgcttg ctctagtcaa 2880  
 cttttatcct accactgtgt ggtcctacca taatgtcatc ctaaacttat cagggtgtctt 2940  
 acatcatttt gcagtgacca taaaagtcac gtcataataa gtccattacg gtagttcgta 3000  
 acttgctgat ggcttacgta attgtgcctc agcaggatgt cgtgatacgc tccaaaaccc 3060  
 aatctgatca tggatatcca gcggaataac aaaaagaaa aaataaacat aaccaaccac 3120  
 caaatgaca gaggctaatt cctggacaac 3150

<210> 53  
 <211> 3221  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 53  
 ccatcagctc ttgttgttat gttttatgtc atagtgtaat gctagcctta gcgtgcgtgg 60  
 tgtttgaatt tcagattggg catggatacc tgggcgtctc gggatggata ctgggacgtg 120  
 gtaagatgct tggagcgtt gattttgagt ttgacaatat atccctatgt ttctcttctc 180  
 cacacccttt taccgtaatt cgacagcatt gtgtagagtg cattgcctta attagaacct 240  
 acgaatcctt gatttgtata tgacacccga tcaccatcga gccacctaca tcatggcgcg 300  
 ctctcagatc ctccgaacca aaacagtaat gtcgatcgtc gcgcctgaac caaggctgat 360  
 tttccctgct gaagcgtgtc ataaagtga acatactttg tagataaaact cggcaattaa 420  
 ctgccactta ccccatatc cgctaccgga gaggggagcg agtgcacggc catcaagtga 480  
 aactgataac cggcgatccg ccggcttatt ggcgatggcg ttatcagagg gaccttagta 540  
 ggttgcacag ttcactagta ttattacta agtacttctt tcgccttgct tattgcccac 600

gattcgteect tctctttttc tttgggttaat tgaactactc tccatgagag ttctgtacag	660
gttgagatag accaaccacc accaccatgc cttttccctt ttcgtccgct cttctcggct	720
atatcttaac tacgagcact actctcacct ccctagtcgc aggacagtat taccctccga	780
cgcctgagga tctcaccgtt attcattcgg agatattccc tgggtcggagg atctcctata	840
agcaagtgag aaatacacca cccttctcct caatcccaat ctaacacccc atactaatac	900
tatgtgacca gcccctcggc atctgcacca ccacccctc cacccccagc tactccggct	960
acatccacct cccccacac acccttacca atctctccat tccaggaatc agcatctcgc	1020
aaccataccc tatcaatacc tttttctggg actttccttc ccgccatcac cacaacaatg	1080
atacatcccc actcaccatc tggatgaacg gcggggcccg cggatcctcc atgattgggc	1140
tatttcaaga gaacggggcca tgtactgtga atacggactc gaattccacg gcctataatc	1200
cctggtcgtg gaatgagtac gtcgatatgt tgtatatga gcagccggtg cagacgggat	1260
ttagttatga tgtgttgagg aatgggacgt tagatttggg tagtggggag atagatgtta	1320
gtattagtga tgggtgagagg gatggagtag gacagaatga gacgtttttg gtggggacgt	1380
tgccgagtca ggatgtgcat gggacgggtga atgggacggg taatggggga agggcgcttt	1440
gggttgcgtt gcaggtttg tgggtgaat tctctgaata tgtttcttct gttgacggga	1500
atggtggtgg tgatgacagg gtgagtatat ggacggagtc atatggggga cggtatggac	1560
cggcatacac ggcgctcttt caggagatga atgagaggat tgagagtggg gaggtaagca	1620
ccgggaagaa gatccatttg gatacgctgg gcattatcaa tgggtgtgtg gatttactcg	1680
tgagggtccc ttcgttccct gagcaggcgt ataacaatac gtatgggacg gagggaatca	1740
atcgcacgct ctacgaccgg gctatggata gttggagcaa gcctggcggg tgcagggata	1800
tgatcatcga gtgtcgcgat gctggcgagc tcggagatcc cctcatgtat ggcgacaatg	1860
agacggtaaa tagcatctgc gaggaggcgt cggactactg ttcgcgggag atcaagagcc	1920
tgtatacgaa tacctccggg cgaggatact acgacatagc gcatttcacg ccggatgcag	1980
ctctcgtgcc ttacttcgtc gggttcttga atcgcccatg ggtgcaaaag gcacttgggg	2040
tcccggtgaa ctataccatg tcgtcagagg cagtggggaa cagtttcgcc tcgacgggcg	2100
attatccgcg aaatgatccc cgcggaatga tcggggatat tggatacttg cttgactccg	2160
gtgtcaaggt ggctatggta tatggggacc gggactatgc ttgtccgtgg cgcggcgggg	2220
aagatgtcag cctgctgggt gagtacgagg atcgcgagaa gttccgtgct gctgggtatg	2280
ccgaagtgca gacgaagtca tcctacgttg ggggtctagt aaggcagtat gggaacttct	2340

cgttcacgcg tgtctttcag gcgggccatg aggtgccatt ttatcagccc gaaacggcgt 2400  
 atgagatddd taatcgcgct cagtttaatt gggatattgc gacgggagge atttctctgg 2460  
 agcagaatca gagctatggg acggagggac cgtcgtcaac gtggcatatc aaaaacgaag 2520  
 tgccggagag ccctgagccg acgtgctatt tgttggcgat ggattcgact tgtacggatg 2580  
 agcagagggg acgggtgctg agtggggatg cgggtgtgag ggattgggtt gttgttgatg 2640  
 atattgagge tgaaagctcg ttcagcgggtg ttgggtgatca gctggcacag gtccctttgg 2700  
 gacattgacg ttggttgcca tatgttgaca gtgttgggtg atgaaagtga tatagatgga 2760  
 taaagttagt gcataagtgc atagctgact aagaatgagc atcattcata tatggataag 2820  
 tctggctagc tcatccggc aagtggccgg ctgactgcct aaagtgaag actggaagcc 2880  
 ttcagatttc catcagcca tctcaatata tccatctggc ttgtcaaact cctatatcca 2940  
 ccggccggac ccttctatta ttaacagcgc cgctatcacc cggacaatcc gtatggcatc 3000  
 acgggttgac ccctccattg cggccatcga accttctcga accttctatt ggtcgaccgc 3060  
 tgccgtcaac gtcacacgtc accgcaggct cacctgaaag ccgccggcgt tgcactatac 3120  
 atcagccctc gtctcacac ctggctttct ccgctaacc tccaagtaca cccttactg 3180  
 tgcttgatg tcttgaatca acatctataa aaactgcatt a 3221

<210> 54

<211> 2590

<212> DNA

<213> *Aspergillus niger*

<400> 54

gagtgagtaa attgatctaa cggcgtcgcg ctgacaaaaca tcatagctat caatcagaaa 60  
 aagcgaagca tatttcacat acgatcggat agcctaccaa ggaactgagg atatacgtac 120  
 agctttcgct tggctgacac gtaaagtcatt ttgggtgattt tggagcgact ttggatctcc 180  
 ttccatgtaa gttataacct accgcaattc caaagtatag ctagtagctg tcagtcactc 240  
 aagaacttgc agcaaggcga tggcaagaca aaacaatcga tggtagcgag tagatagaag 300  
 aactaaagc actttcacat gacactgttg acatagtgtt tatgtctttt aactcaaca 360  
 tgagtcactt tgataagggtg atttcgccag atggtggcat tattgactcc tgattggatc 420  
 caccgataag gaaccacttt ttggctggca atgtactatg ttattgacag gcacgaact 480  
 tcccaaatac tcaggctggg ccgccagcaa atggcgcggt tccggactcc ggcgggggct 540  
 gacagggcca accgttggtt gcttgtccct tgccgccgga gagcttattt aactcttgtc 600

tctcctcttc cccacaaaag ctcaactcagc actcaaggcc tcaccgcgcc atagtcccg	660
tcttgatcat ccttagcaaa acggctgtaa atcatgagaa catctactct tttgctctc	720
tggagcactg caggagcagc tttggcttct ccgtaaccgc ttcccgactc gcaagtagtc	780
ttcgccgcgg atcacgaggt cccgaataca cagggcaaac acgtcgtgga cgaggccata	840
ctctcggcgc tgaacgtca ttctgacca gtcgctgcaa tgggtgtctct acgtcccga	900
actgcagctt ttctagctga acctcgtctc ttgcacattc ggggcgaaga gaaggcggaa	960
tggatgaccg aaggcgacaa gctgcgcctc cgccaacgcg gaaagaagtt catggacatt	1020
accgagcatc aggacttcta cgcagagcag gcgatggctt cgtttgctgg ggatcctagt	1080
taatctccct tttgtcgagg taattaatac tgtgttaacg ccctttagat cttcccaagc	1140
tgtcccataa aggtctcgtc aagccgctgt tctctcaaat cgagacggaa cgaatgcacg	1200
atatcctgca gcacatgacc tcctactaca atcgatacta cggtgattat cacggcgaga	1260
tgagctccga atggctgcac gactacattg ctgcggtatc tccacccctc acagccacaa	1320
tttttgaaca tgaacttact caaccaagat catctccaaa tcgcctttcc gcaccacat	1380
ctctctcgaa tacttcaccc atcctttccg ccaatcttca attattgcac gcttcgagcc	1440
taaagttcgc agcttctccc aacctttgac catcattggg gcgcaccaag attcggccaa	1500
ttatcttttt cccctgctgc cggccctgg cgctgacgat gactgttccg gcaactgtcag	1560
tatcctcgag gccttccgcg ttctggcgga gaatggctac acgccaagg acgggcctgt	1620
tgaattccat tggatgcgg ctgaagaggc cgggctactg ggcagccaag ccatcgcgcg	1680
gtacaagaag gagcagggcg ctaaaattga tgccatgat gagttttag gttcccatca	1740
tccaacggac ttggaatcac ttttgacttt cggttattaa catctgcata ggatatgacg	1800
gcttttattg ccgtaacgc caccgagacc atcgggtttg ttgcaacca agccgatgca	1860
gcgctcacia actgggccct caacctcagt cgagaatata tctccattcc ggcggaagtc	1920
tatgaacttg gccgtaaga cccagaata tcccagagg catgtcaagt gctgaatgat	1980
ttcttagcaa cgctggatcc gactacatgt catacactaa gctcaactac cccgctgcct	2040
ttgcatccga aggcaaccgc ctgcgtgggg gctctttccc gggtgaaatg gaccctacg	2100
tacacggcat caaggatagg atggacgttg acgatgaaac gggcgtcttc tctatcgaag	2160
taagttgacc gcactcaacc tgtccatctt cttgctaacg atttgccagc acatggctcg	2220
gttctccgag ttggctatcg catttgttgt cgagcaggct ggggaggata atacatggcg	2280

gtagagtata tacagggatg tttccagctt catagcatat agagctggta tatagtcatt 2340  
 gtgcttaciaa tatataccat tctattgagt tcttgacaga gttattatgt cagaatggta 2400  
 atcagtctaa atcaatgcgc ccttaaatca agaagtacac tagtgcccat gacaaaaaca 2460  
 atttccactt acacatacca cctatctgcc tcaactacgaa acccttacca tacaatgttt 2520  
 acgttgtgct cctttcaata ctccatttcc atagttcatg ctatcgtggg ataaacatgc 2580  
 acatatcctc 2590

<210> 55  
 <211> 3290  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 55  
 gagaggcaga aggagtcatt tatcacttgt attccaatgt attttccatt tatagatact 60  
 gcattcaa at gcaccgttta gcatagcatc ccacattcta tttcattcca atctcatgcc 120  
 attgccatcc ccggtattaa tttactttctc cgccttatct tgcaatcttg caatctcttt 180  
 ctctcgtta tcacgcgttc ctgcaggcgc acctccgatg gcaactgcgc cggagtcacc 240  
 gcggcgccgg cactactaaa gactaaagtg tctagtctag cctccaatgt gctcacctcc 300  
 atcagcatct catccattta tcttctgacg atgtcatctg caggctccac cccctccggc 360  
 cgccccgacg ctctccgacg gtgcacaaca atcaattctg cagtcacgct caagattcgt 420  
 ccctgcggga ctctcatgc cgtgcctggt ttaattctatg caatggagta aggtagtatc 480  
 gcctagcagg agcggagttc ctgctgcgct cagccatgg tgccggcgca gacataaatc 540  
 gctcgtttcc tccggcgctg gccgtttctc cgagccagtt tgtctgttgt ggtttagga 600  
 tcctctgttc cctcgcacg ctcaaatgc gtctcttctc cgttgctcgt gccgcgtcac 660  
 tggcgctctc ttgggcgtct ctggcccagg ctgctcgccc ccgtcttggt cccaagccta 720  
 tctctcggcc agcttcgagt aagtcggctg cgactacggg tgaggcttat tttgagcagc 780  
 tgctggacca tcacaaccgc gagaagggaa cgttttccca gcggtactgg tggagtactg 840  
 aatactgggg tggacctggg tcaccggtgc gtctctgaca tttggtctta tgaccggcca 900  
 tattgaaact tagccggtgg caaggtccgc aatcatgagg aacattgctg attaaactag 960  
 gtggtcctct ttaaccctgg agaggctctc gccgatggct atgaggggta tctcaccaac 1020  
 gatactctca ctggtgtcta tgcgcaggag atccagggtg ccgtcattct cattgaacgt 1080  
 gagtgtcact gctaccatgg aaaaaagaca ttcgctgacg gacccaatc tagaccgcta 1140

ctggggcgac tcttcgcctt atgagggtgct caatgccgaa acacttcagt atctcacact	1200
ggatcagtc attctggaca tgacctactt cgccgagacg gtaaagctgc agttcgataa	1260
tagcagccgc agcaatgcgc agaatgctgt atgttacctt caccgctcta tgtttctgat	1320
aggtactgac aacgtagccc tgggtcatgg tcggtggctc atacagcggg gccttgacgg	1380
cttggaaccga gtctatcgcg cctggaacgt tctgggctta ccatgccacc agtgcgctg	1440
tggaggctat ctatgacttt gtaggtgtag cctgctcttg ttatctatac ttgcagctaa	1500
ccaagccagt ggcaatactt ctacccatt cagcaaggta tggcacagaa ctgcagcaag	1560
gatgtgtctc tggtagccga gtatgtcgac aaaattggga agaattggaac tgccaaggaa	1620
cagcaggagc tcaaagaatt gtttggctctg ggagctgttg agcattacga tgactttgcc	1680
gcgtgagtac ttcaaagtct atagacgagc tttcttgaca ggaacagtgt cctgccaac	1740
ggaccgtacc tctggcaaga caacgacttt gtcacaggat actcttcctt cttccagttc	1800
tgtgatgctg tcgaggtgag ttaccaccag attcctcttg attgaagcaa tatactaacg	1860
gacacagggg gtcgaagccg gcgcggcagt gacccccggc cccgagggcg tcggacttga	1920
aaaggccctg gccaaactacg caaactgggt caattcaacc atactcccta actgtatttc	1980
accatctctt gtctcgttcc tctcccttat cctcccagac taacctagt acagactgcg	2040
caagctacgg ctactggacc gacgaatgga gcgtgcctg ttctgacagc tataatgcct	2100
cgagcccat cttcacccgac acctccgtgg gtaacctgt cgaccgcaa tgggaatggt	2160
tcctctgcaa cgagcctttc ttctgggtggc aggagtgcgt accccttacc tcattcatga	2220
taacacacga acaattccac taacaaagat ccagcgggtg ccccgaggga acctccacta	2280
ttgtgccccg gctcgtcagc gcctcctact ggcaacgcca atgcccgtc tacttccccg	2340
aagttaacgg ctacacgtac ggcagcgca agggtaaaaa ctccgctacg gtgaacagct	2400
ggacgggtgg atgggatatg acccgcaaca cgacgcggtt gatctggacg aacgggtagg	2460
tctcccccta atttccgttg aatgtgatgt gaagataaac tcaatgctaa taaattgaga	2520
aggcaatatg acccctggcg cgactccggt gtgtcgagca ctttccggcc cgggtggccg	2580
ctgggttagca cggcgaacga acccgtgcag attattccgg gcgggttcca ttgctcggac	2640
ttgtatatgg aggtacta tgcaatgag ggtgtgagga aggtgggtga taatgaggtg	2700
aagcagatta aggagtgggt ggaggagtat tatgcttgat gaagatactg gtggacatat	2760
ggagtgtaca taagatgaat ggtcataaaa tgatgatggt agatacggct atggctgttg	2820
attagatggt cctttcgcat ttcctaatta ctgagcacgt gctccatggt atgggaagtg	2880

gagacgttgc tatatatatt gactgtcggg ctattgttca cggcgtagaa gctagacgct 2940  
 ttgtctatgt ggccttctact aaagaccgtg actctgcccc gtcttcccc cttcgaggac 3000  
 ctggtattag ccaaaccac ccacaaacct aacaaagatc atcgtgacat tgaagtcact 3060  
 ctaggtactg ctggcgctga ttacagtggc tcaattcgaa catttcaaca gcacataagg 3120  
 gaagggtcgc ttcacttgct accttgatac gaaagcagcc acgccaaca cttatagggg 3180  
 tgacaaccat cggcatgctg gggtatctac tatactctct gattctgtgg atcctggaga 3240  
 tcgatctggg acactaatct actacaatgc atgtgaagta gggataggca 3290

<210> 56  
 <211> 2044  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 56  
 ggctttgttg ggctgagcgc tacttcttct tctctcttgg tctgttcggt gctccgccag 60  
 ttggttctact cagcctcgta acatcagtat accaggetaa gtcaggactt tggcccccat 120  
 actgcttccc ctttttttat aaaactcaat ccttctggaa aggattctat ttctcaattc 180  
 tcagactact taatacgttc tttgttttca aattgttttg tttctgaaac ttgccgggccc 240  
 ctatcccttc ttttttatag tccgcctgtc gacatcatat ccagagttag ccaccatgca 300  
 gctcctccag tccctcattg ttgccgtttg cttcagctac ggcgtcctct ccttacccca 360  
 tggcccgta aaccagcaca aagcacgttc cttcaagggt gaacgggtcc gtcgtggaac 420  
 cgggtgctctg catggggccc ctgctctccg caaagcatac cggaagtacg gaatagctcc 480  
 cagcagtttc aacatcgatc tggcagactt taaaccatt acgacaaccc atgctgctgc 540  
 tgggagcgag attgcagagc ctgatcagac tggcgctgtc agtgctactt ccgtcgagaa 600  
 cgatgccgag ttcgtttcgc ctgttcttat tggcggccag aagatcgta tgacatttga 660  
 cactggttct tctgacttgt aagtcttga tgcagctgtt tactcttttg tacagtgatt 720  
 aacgtcgatc tacagttggg tgttcgatac gaatctcaat gaaacctga cgggacacac 780  
 ggagtacaac ccttcgaact cctcgacctt caagaagatg gacggataca ccttcgatgt 840  
 ctcgatggg gacgactcgt acgcctctgg ccccgctgga acggataccg tcaacattgg 900  
 cggcgccatt gtcaaggagc aagccttcgg tgtccccgac caggatatcc agtcgttcat 960  
 cgaggacacg aactccaacg gcctggctgg gttgggcttt tcctccatca acaccatcaa 1020  
 accggaggcg caagacacgt tcttcgcca tgtcgacca agtctggacg agcccgtcat 1080

gaccgcctcg ctcaaggctg acggagtggg cgagtacgag ttcggcacga tcgacaaaga 1140  
 caagtaccag ggcaacattg ccaacatcag cgtggactca tcgaacggat actggcagtt 1200  
 ctccactccc aagtactccg tggcagacgg agagtgaag gacattggaa gcttgaacac 1260  
 ctcgatcgcg gacaccggta cctcccttat gctgctggat gaagacgtgg ttactgccta 1320  
 ctatgcgcaa gttcccaact cgggtctacgt gagcagtgcc ggtggttaca tctaccctg 1380  
 caacaccact cttccagct tctcgcttgt cctcggcgag tcgagcctgg ccacgatccc 1440  
 cggtaacctg atcaatttct ccaaggttgg caccaacacc accaccggac aggcctgtaa 1500  
 gttgctcccc ttcttttgca tgattgaaca tgattgactg attgtgctgg ttagtgtgct 1560  
 ttggcggcat tcaatccaac ggaaacacct cgctgcagat tctgggcat attttcctga 1620  
 aggccttttt cgttgtcttc gacatgcgcg gccctcgct tgggtgtgccc tctcccaaga 1680  
 actagtttcc ttttctgta cttttcccc gcgtgtaata atatcgctg attttttgga 1740  
 ctgtctccta cgtgggcaag atggatggat agtttgctca cgtgcattgc tttacctgg 1800  
 gtctgtgagt caaggcagga gtgcgtggct gtatctacaa ttcaagttac agtgccgacc 1860  
 gttattgcct tccacatcga aaaacataga cactctttct aaccctaac catgatacaa 1920  
 gtatatactt cgagtccata ttatgggtgg gtatcaaggc gccatgttta tatctaata 1980  
 aaccaacgta ggtctcatct tcatacgttg tttaaaaggt gccgaagaat atacgaagat 2040  
 agat 2044

<210> 57  
 <211> 3916  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 57  
 ttcgcagata ttcgagtcaa taccttgtat attaacggaa aagggtttgg gaagcgttgc 60  
 cttcaaggat gaaattcaaa acgtagagta tcttgacctc aatgacctca tgatccccctt 120  
 gaccgtacag ctagtgatct cacggtggta attgctcgat tcgattccaa actacagcaa 180  
 gaagcatgcc cgacaggaaa gtcaagttac aagagatcta gaacggggct gctacggctc 240  
 tgaccaacct ttgtctgttc tagatgagggc tgcagtgcg taactccggc ccaagaaaat 300  
 ggggtgtaac cgaccgttgg aaatcccatg gaactggcgg ggttcaaatt cccgataact 360  
 gtaccgaatc cttgtatccg gatataggcg accgatagta gtagctatag tcagacgtag 420  
 cacagcatta ctgtgtcccc ctggtcataa gagtatttgt tacaataaga agggaccgtc 480



tagttgtgta tcacaacaac tgacacttgc ggaacaggta tcagatcctt gcgctggcat	540
cgactccagc aatggcttgc tctgtttcgg acgaatatca tcgggctaga ctgtgacctg	600
aaggatcgat ccaggagttt gacggcttgg gtttctaate cgatctggaa gattattggt	660
tagtcaagac cggaacagc aagaaccgga agattatctg tttaactact ttgcaaaac	720
agttattcaa tgtcatgctg agtgcgatgg ggaccaagc tcacgagtga tgctgatcaa	780
agggctcgtt cgggttggga aaggaagggc gccctgtgct tgccgttggga atccacggaa	840
cgattccgat tgactgcacg ggatttgcaa actgactccc agtgggacga agaaagaaac	900
ccatcttact ttgcgaggc aggatggcac tttgtgtcgg aaggggtgtg actcctggtg	960
ttgccgagaa gatggaatgg tggagaattg ccttgaaaat gaggtgtag gggcactaac	1020
ccagtcgggc cgagcgtgac gcctttcccg atgaggcagg tcaggtgggt gtcacgggtc	1080
tatcttatcg cttatcatct gaccggttcc tggcagaagc tccccctccc agctcctcgt	1140
atctattcct cccaggttg ttgtttgctc ttctccctgt ctgccttct ctccagcctc	1200
cattcaacgg gctccatccc cttctctccg gatccctcta tcccttattc ttccttagat	1260
atcattattc atatagtgcc ttgtttcgtc caccatgcgc attgactccg cggcgctaca	1320
tctgggtcca gtcctcctgg gccaggtcgg tgctttacaa ttacccttgg tccaagactc	1380
caattcacag tggcagaaac caaatgcagg tgataaacc ctaattagct ctccgttgc	1440
tcaagagcag gtcaaggcgg agaactctgtt ggacagggcc cggcagcttt acaagattgc	1500
ggagctggga gaagacgagt ataaccaccc cactcgcgtc attggcagta aaggtagcat	1560
atattttttc atcatgtccc tggaaatcga taattagctg acaacctttg ctccccaggt	1620
caccttgga cgtcgaacta catatactcc acccttaccg acctcgggtga ttattatact	1680
gtcgtcaatc agtccttccc tgccgtgagc ggtaatgtct tcgagtctcg ccttgtcctt	1740
ggtcacgatg ttcccaagtc agctacacca atgggtctca ctcccccaac gaggaataag	1800
gagccggtat atggctccct ggttgctgta tccaacctcg ggtgtgaggc ctccgactac	1860
tcgtccaact tgaaaggcgc cgttgcatth atcagtcggg gaagctgtcc gttcgggacc	1920
aagtctcaat tagctggtaa agcgggagct gttgtgtccg tcatctacaa caacgagcgg	1980
ggtgacctaa gcggaactct aggaaaccca acccccgatc atgttgctac ctttggtatc	2040
tcagacgagg atgtgcccc agtcctggag aagttgaata aaggcgagaa ggtggacgct	2100
atcgcctacg ttgatgcgat agtagagacc atccacacca ccaatatcat cgcgcagacc	2160

acggatgggtg acccgaacaa ttgtgtaatg ctgggtggcc acagtgacag cgtggccgag 2220  
 ggcccgggta tcaatgacga cgggtccggt actctgacct ttttgagct tgccacattg 2280  
 ctacccagct tccgtgtcaa caactgcgtg cgatttgctt ggtgggcccgc cgaggaggaa 2340  
 ggccttctcg gatctgacta ttacgtgtcc gttctcacac cggaagagaa ccgcaagatc 2400  
 cgcttggtca tggactacga catgctcggc tcgccgaact ttgcgtacca agtttacaat 2460  
 gccactaatg ctgtgaaccc cgagggatct gaggagcttc gtgatctgta caccgacttt 2520  
 tacgaagatc atgggttcaa ctacacgtac attccgtttg acggacgcag cgactatgat 2580  
 gccttcattc ggcatgggat cccgggtggg gccattgccg cgggagcaga gggatcaag 2640  
 actgtcgagg aagcggacat gtttgggtggg gttgctggcc aatggatga cccgtgttac 2700  
 catcagatct gcgatacggg ggccaatgtg aacttgactg cgtgggagtg gaacaccaag 2760  
 gtaggaccgc atccagcatt agttactgtt atgccgatca ttcttttgct aactgggatg 2820  
 atttacctta gtcgttgcc cactccattg cgacttacgc caagtccttt gacggattcc 2880  
 cggaacggtc cgatgaaccc atcagccctg ctgcttttga ggaaccgaag taccatggcc 2940  
 acgcgttgca attgtaagat ccgtgtgccc caaagcttgg tagtggggca aatatctgta 3000  
 gcagagacca agtcctttct cgaacctgag tcccacttgg tctttccatc ttttgagtgt 3060  
 aacaagtaga ccgttactcg tcatgtagac gaagacctgg cagaaccgtt gtactatgta 3120  
 gacatttacc ggggattgtc tggtatgaat tcatgtgctt gtgggatag gttaggtatt 3180  
 tctcgcaaat gaccacggct tctctatca tttcccgct cgcacctca taccgatttc 3240  
 cgtaactta atatcatctg tagacttcgc ggtaatacta cagggacca gagcgtcctg 3300  
 tggggagccc aaatccagaa tggaacagct gcatcgggtg ttaatctatt gtccatacga 3360  
 cgcagaggca ctttcagtct aagctaaaag caagcattat tcagagatac agtgagtgtc 3420  
 aatatgccgt tgggtcatgc gcgattcgtg caaaaacagc ccaccgccct atataacaga 3480  
 gtatattgct ctctgcctct cgggtagag atcgacattt cgggaccgc catgaaacgt 3540  
 tgggtggcct cggagcgtcg aggattgaca ctagggccgc gctagaatcc ccagggtct 3600  
 gcaaaatacc ctatggggtg acctcgaaca gggcgtgaaa cggcaattcc tccgaaagcg 3660  
 ttgcgaaagt gtctacaaag tggatgacca gaccatcacg cggttccgga acaattgccc 3720  
 ttcttatttg gcactttacg gcgtggagtg gagtcacccc cctttgttga aacaacacgg 3780  
 gcatgtttcc tttgccgtcc ggttcgttac ctataaagac agggtaggtc tggtcgggaa 3840  
 aaagacacaa tcagcgcta tcccgctcgt cgaagtctat tgccataccc tatcacggat 3900

catcagactc ataaca

3916

&lt;210&gt; 58

&lt;211&gt; 1443

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 58

atgcatctcc cacagcgtct cgttacagca gcgtgtcttt gcgccagtgc cacggctttc	60
atcccatata ccatcaaaact cgatacgtcg gacgacatct cagcccgta ttcattagct	120
cgtcgtttcc tgccagtacc aaaaccaagc gatgctctag cagacgattc cacctcatct	180
gccagcgatg agtcctgtc actgaacatc aaaaggattc ccgttcgtcg tgacaatgat	240
ttcaagattg tggtagcggg aactccctct tgggtctaaca ccgccgtctc cgatcaagat	300
ggtagcgaca tttcatacat ctctgtcgtc aacattgggt ctgatgagaa atctatgtac	360
atggtgctcg acacaggcgg ctctgatacc tgggttttcg gttccaactg cacgtccaca	420
ccctgcacga tgcacaatac cttcggttcg gacgattctt cgacccttga aatgacatcg	480
gaagagtgga gtgtgggcta tgggaactggg tctgtcagcg gcttgctagg aaaagacaag	540
ctcacgattg caaatgtcac tgtacgcatg actttcggac ttgcttccaa cgcacggat	600
aacttcgagt cgtacccaat ggacggcatt ctcggtctcg gtcgaaccaa cgatagtctc	660
tacgacaacc caacattcat ggatgccgtt gcagaaaagta acgttttcaa gtcgaatata	720
gttggttcg ccttttcacg tagccccgcc aaggatggca cggtcagctt tggcactact	780
gacaaggaca agtacaccgg cgatatcacc tacaccgata ccgtcggatc ggacagctat	840
tggcgcatc ccgtggacga tgtctatgtt ggcggcactt catgcgattt ctccaacaâa	900
tcagccatca tcgataccgg aacttcttat gctatgctgc cttcaagcga ctcgaagacg	960
ctgcacagtc tcattcccgg cgccaaatct tcggggagct accacattat tccgtgcaac	1020
acaactacta agctacaagt ggcatctctt ggtgtgaatt acaccatctc gccgaaggac	1080
tacgtgggag caacttcagg ttctggatgc gtttcgaaca ttatcagcta cgacttattt	1140
ggtgatgaca tctggctcct ggggtgacacg tttctcaaaa atgtgtatgc tgtgtttgac	1200
tacgatgagt tacgggtcgg atttgcagag cgttcctcga acaccacctc tgcgtcgaac	1260
tctacgagct ctggaacaag cagcacctcg ggatccacta caacgggcag ctcaacgact	1320
acgacgagct ctgctagctc tagtagttca tctgatgctg aatcaggaag tagcatgacc	1380
attcccgtc ctcagtattt cttctctgct ctggcgattg ctctcttcat gctttggctc	1440

tag 1443

<210> 59  
 <211> 3300  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 59  
 atgcttcgtg gtcttcgtga tgcgtatta ttacaatttg caatccccctt gttcttgcta 60  
 ttgcatttta gattatcgct acgggggtgtg atcacaggat ttgggttctaa atcacatttc 120  
 cagagaccat tgagcaaaat gtcacttact caaaagagcc atttcaagct actccagaag 180  
 ttcaaaccgg agtactcgcc tagcgagttt gtcagtatg agtcggagag aacaggcatg 240  
 agggtagtgg tcattgacca aaaaggaccc aaagtcacag gttattttgt tctagccaca 300  
 gagattctcg atgattcagg tgctcctcac acgttggagc acttggtgctt tatgggctcg 360  
 cggaactata gatataaggg cttccttgac aagctagcaa cacgtgttta ttcgagcacc 420  
 aatgcctgga cggccacaga ccacacggcc tacaccttgg acacagcagg ctgggaaggg 480  
 ttcgctcaaa tcttgcccggt gtacctagag catgttatag ctccaacact gacagatgaa 540  
 ggggtgctata ccgaagtgca tcatattgat ggcgctggag acgacgctgg agtcgtctac 600  
 tcggagatgc aggggtgtgca gaataactct gcagaggttaa tcgatctaac cgctcgtcga 660  
 ttgacttacc cgcattggtgt aggttttcgc tacgagacag gcggtatgat ggagcagctc 720  
 cgcgtcctca ccgcggaccg tatccgagcg ttccatcgtg agatgtacca gcccaagaac 780  
 ttatgcctaa tcatcacagg cgaagtagat caccagaaca tgctggagac cttggacaag 840  
 ttcgaagata ctattctaga tgtcattccc agtcctgatt cacctttcaa gaggccgtgg 900  
 gtagattcca agcaggcgcc gccattggag aagtcattg tccagactgt ggaatttccg 960  
 gaagaagatg aatcttttcgg ggagatagaa attagattcc tcgggtccgga ctgtaccgac 1020  
 cctgttcaaa ccggggctgt caatgttgca ttgctgtatc tggcgggttc atctgcttct 1080  
 ctattggata acatcctggt tgagaaggag cagctcgcca gtgctgtcta ttatgctacc 1140  
 gaagatcatc ccagcattga gatccgcttc acattaacca gtgtggagac agagaaactc 1200  
 gcgaaggtag agcaacgggt tttcgaagtg ctcaaggacg ctatggagaa agatttagac 1260  
 atgaggata tcaaggagtg cattgaccgg caaagacgga cctggaagtt ctctaccgaa 1320  
 agctccgcct cttcctttgc ggagtagtg atctcggtt ttcttttcgg aaagagagac 1380  
 ggatcgacta tgcttgatgt tgcgacctg caagagtacg acgtgctgga gaagtggagt 1440

gaagaacagt	ggcgagttt	tatcaaaaca	tggatttctg	atgccaacca	tgtcactatc	1500
cttgggtgttc	cgtccgtaa	gatgtctgac	acattaaaga	aggaggagga	agctagagtc	1560
gcagagcaaa	agaagcgctt	gggtgatgag	gggctgaaga	agttggccga	caagctggaa	1620
aaagctaaag	ctgaaaatga	caaggagatc	cccaaggaga	tgctggagag	gttccaaatc	1680
cctggaatag	agtctatcca	tttcgtggac	actactacag	ccaggctctg	tgcagccctc	1740
gatgccgggc	gcccattcca	caaggcgcaa	aaactgggtg	atgctgatgg	ctctgatctg	1800
cccttgttca	tccatttcga	gcataatccc	agtagcttcg	tgcagctctc	cctcctcatc	1860
tcggcacagg	cgtacctgt	gcagcttcgt	ccactgctgt	ctgtgtatac	tgaggcattc	1920
ttcaacctgc	ctgtcaaccg	gaacggggaa	accatcaact	ttgagcaggt	ggttgtcgag	1980
ttggaaagg	atactgttgg	ctactccatg	gaaggagcta	gaagcctagg	aaactcggag	2040
atgttgcgga	tctcattcca	ggtggagctt	gagaagtatc	acacggcgat	cgcatggatc	2100
caggaacttt	cctggaactc	gattttcgat	gtcgagcgac	tccgagcgat	taccagtcga	2160
ctgctctccg	atgtgcccga	ttccaagcgt	agtggcgacg	acatgctcgc	ggctgttcat	2220
gtgatggtcc	actatgcagc	agagtctatt	gttcgggctc	ggagcacctt	ggtgaaggcg	2280
cgttatttga	aacggatcaa	gaagcaatta	gcagaagagc	cgaagtctgt	cgttgcgcgg	2340
atggaagaaa	tcagagatgc	gcttttccgt	ttcagaaca	tgcgagtctt	agttatcgct	2400
gacctggaga	aacttcaaaa	ccctgtgtca	gcatggaaac	catttgctga	gcgtttgggt	2460
gcaggtgccc	ctctacagcc	tatcacgact	agaagaccgt	tgctcagtga	ggcaggccag	2520
aagttgggcg	gtaagtcgta	tgtggttctt	atgccgacga	ttgattcatc	gttcgcatat	2580
gctaccgcac	gtggtttgga	ttcttatgat	gatccaagac	ttcctgcctt	aatggttgca	2640
attgcataca	tgaacgcggt	tgagggtccc	ctctgggttg	cagttcgagg	caagggtttg	2700
gcatatggca	cgaactttgc	ctataacatt	gataccggat	tcgtcaactt	cgacgtttac	2760
cgctccccca	acgccataa	agccttcgac	tccagcaagc	agattgttga	ggatcacctc	2820
tctgggtgca	tgcccttcga	tcccttgatg	ctggagggtt	ccattagcag	cattgtggta	2880
agctttgcga	atgaacagtc	gacaattggt	agcgcagcct	caggcagttt	catccgacag	2940
gtgattcggc	gcctgcctag	cgactacaag	gagcgggtgc	tcaagcaggt	gcgggctact	3000
agcgttgatg	acgtgaaagg	cgctctgaag	gacatcattc	tgcttttgtt	taaccgctcc	3060
acggccaata	tcgtgggttac	ctgcgctaca	gtgcttgagg	agactatcaa	ggaaggctctc	3120

caggcatcgg gattcacgcc tgcggtgcag ccactcaaag aattcgaaga tgactatggg 3180  
 ctgaaggctc gcgatgacga ggacgaggag tccgacgatg acgacgatga gtatgaaacc 3240  
 ggatctgaag atgaagatga cagtgatgaa gacatggagg atgacgaaga tgatgagtga 3300

<210> 60

<211> 2181

<212> DNA

<213> *Aspergillus niger*

<400> 60

atgggagctc ttcagtggct gtccatcacg gctgctgcgg cctccgcagt gtcagccttg 60  
 accccggagc agatgatcgg tgccccacgg agaaccgaag ttataccaaa cccctccggt 120  
 gacaccggtc tattctcgac ctcccaatgg tcgtttgaca ctattctga gagcacctgg 180  
 tggagcttga tcgacctcca atcgggcaag accaccactc tcaccgatga tagcgatatc 240  
 gaggagatca tctggcttgg ctctgacaat tctacgctcc tctacatcaa cagcaccaac 300  
 gcgcaggctc ccggtggcgt ggagctgtgg attgcccact cttctgactt tgcaaagtct 360  
 tacaaggcag cctctctctc cgccggtttt ctcggcatca aatcaaccgt gacagattcc 420  
 ggcgacgtgc atttcacctc tcgtggaaag tcctatccca acggaacggc atacaatgat 480  
 cagctcgccg agacctatcc cagtacagcc cgcactctac acagcatctt tgtgcggcac 540  
 tgggacactt acctgaccac cgcctcccac gctgtattct ccggtaccct gcaaagctcg 600  
 accagcgacg acggcaatgt tcaatatacc tcttcagggg gattgaccaa cctggttaac 660  
 ccagtcaagg gtgccgaaag cccattccct ccttttggag gcaacgacga ctatgacctc 720  
 tcgcctgacg gcaaagtggg taccttcaag agcaaagcgc cagagctgcc tcttgctaac 780  
 aacacggctg cctatgtcta tctcgcccca cacgacggct ctgcgactgc ctttgccgtc 840  
 aacggccctg atagtcctgc aaccccgagg ggagttgaag gagaatccaa caatcccggtg 900  
 ttctcccctg atagcgacaa aatagcgtac ttccaaatgg ctactaatac atacgagtgc 960  
 gaccgcaacg tgctatacgt atactccatc gccgatgaca ccatcactcc ccttgcaaag 1020  
 gactgggacc gatcgccctag ctccgtgaca tgggtcgatg gagacaacct cgtcgtggca 1080  
 agccaagatc taggacgaac cagacttttc gccatcccag gcgatgcagg ggacgacttc 1140  
 aagcccacga acttcaccga cggcggctcc gtgtcggctc aatacgtcct atccaactct 1200  
 accctcctcg tcacgtccag cgccttctgg acaagctgga gcgtctacac cgccagccct 1260  
 gacgagggcg tgatcaaacac actggcctca gccaacgaga tcgaccccga gcttagcggc 1320

cttagttcct cggactttga agagttctac tttgacggca actggactac cctccaagga	1380
tggatcacct accccaaga cttcgactca tccaagaaat accccctcgc cttcctcatc	1440
cacggcggcc ccgaagacgc ctgggcggat gaatggaacc tgaaatggca ctccaaggtc	1500
ttcgccgacc agggatacgt cgtcgtccag ccaaacccca caggaagcac cgggttcggc	1560
cagcagctca cagacgctat ccaacttaac tggaccggcg ccgcctacga cgacctaac	1620
aaagcctggc aatacgtgca cgatacctac gacttcatcg acacggacaa cggcgctgcc	1680
gcgggtccca gcttcggcgc gttcatgac acctggatcc agggcgatga ctttggacgc	1740
aagttcaagg cgctggtag ccatgatggt ccgttcattg gcgatgcgtg ggtcgagacg	1800
gatgagttat ggtttgttga gcatgagttc aacggcacct tctggcaagc gcgcgacgca	1860
ttccacaaca cggatccatc cggccccagc cgcgtcctcg catacagcac cccccagtc	1920
gtcatccaca gtgacaagga ttatcgcata cctgtggcaa atgggattgg actgtttaat	1980
acgctgcagg agaggggctg gccagtcgg tttttgaatt tcccggatga ggatcattgg	2040
gtcaccgggc aagaaaacag cctcgtctgg tatcagcagg tgctgggatg gattaatcgg	2100
tattctgggg tgggagggtc gaatcctgat gcgattgctt tggaggatac ggtgaatccg	2160
gtggtggatt tgaatccttg a	2181

&lt;210&gt; 61

&lt;211&gt; 1695

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 61

atgacgaggc agacttctct cgttcccagg ctactaacgc tagcctcact agctgcactt	60
tcacaagcag agctaggcaa gatccaatgg aaaggatctt gcaacttgac cacttatccg	120
gcattgatct gtggaacact agacgtgcc aacgactaca cggagtcaaa ttccagcaag	180
acactgactc tcgacatcgc caagtggcca gcgaccaaga aaccagtctc ggagcccac	240
atatttaact ttggaggacc tgggtgcaat tcgttcgagg gccttgggct ttatggagag	300
gaatttcagg ctattcttgg aggtcacaat gatttgatag cttttaacaa ccgaggcggt	360
ggaaacacca tcccgttctc ctgctacagc gatgacgcca cccgtgaact cgtcgccctt	420
caagctccta acgacggcag agcgtccagc acggctttgg gagaaatctg ggcccagaac	480
gcaaacatcg cacaggcatg ctatgctacg aacaatcaaa ctggtagtct tattggaact	540
agctttgctg caagggacat catgcaggct gctgatgcgc tcagtggaaa ggatagtttg	600

gtcaactact ggggattctc atacggcact acaatcgggtg ctgttctcgc agccatgttc 660  
 ccggatcgaa tggggaatgt cgcgcttgac ggagtggaca accccagaga ggctctttat 720  
 ggatacaacg cacaagcggg tgtggacgtc gacaaagttt tcgaaggatt ctgcacgggc 780  
 tgcattggccg caccggacct ctgccctatc gccaaaggagt acaccagcgc cgccaacttg 840  
 gaagccgcaa ttacctgat gctggaaaac ctcaagtaca acccgattgc cattcccga 900  
 accgggtggaa tcgtaacttg gagcgacgtc aagtcgacca tttttgaggc catgtacctg 960  
 ccaagctctt ggcccttgac ctctgagctt ctttactacg tgcaaaccgc caacacaacg 1020  
 atccttggca actctgaagt atacgacacc atcaaactct acgggtcaatc ggcttctttg 1080  
 acttcggctt ccgatgaggt cggcacggcc attacatgct ccgacaagca tcgatctgcc 1140  
 accattaaag aggtcctccc gtacgtcaaa gccagacagg ctctgaccaa gatcggaagt 1200  
 gatggctcgg acggcgacat gagatgcgcg cagtggaaac cgaagatgtt cgccaaggag 1260  
 cgctactccg gtgactttga agtcaagaca gccaaaccgc tgttgattct gagcaacact 1320  
 tacgatccag cgactcctct tcccgcagcg aagaacctga cagagacctt tgagggaagt 1380  
 gtcttgctcg agcagaacgg atacggatc actaccctgt ctatgccatc tctttgcact 1440  
 gccaaaggccg tccgggctta cttcaccaat ggacattgc ccgctgacgg aacgatctgc 1500  
 cagggtggacg tgccctctgtt cacgaacttg acctacaagg atgtgtggcc gaagagtttc 1560  
 caacggagcg ttgagtcgag ggatgatgcg actatcctca aggctttgat gtcggtcctg 1620  
 gataagatgt cgcgacgcag gatgtgtatt tatttgtaca ccaacagcgc ttcattggaga 1680  
 ccggaacttc cctga 1695

<210> 62

<211> 1581

<212> DNA

<213> *Aspergillus niger*

<400> 62

atgtactact ctctctgggt tgctgccttg gtggccgcgc tgcccgtctc ccgggcccag 60  
 tttgtggctc cggccacgga tctcattccc accaagggat atctcgacat ccccgctccg 120  
 tacaacagg tccccaccgg catttgtgag actgatccca gtgtcaagag cttctccggt 180  
 tacgtcgatg tcgctgagca tgagcacatc ttcttctggt tcttcgaggc gcgcaaccaa 240  
 gatcccaccg aggtccctt gaccgtctgg atcaatggag gcatgtctga ccccggtcct 300  
 ggttctctct ccatgatcgg cttgttccaa gagcacggcc catgcggcat tgacgccaat 360



ggctccgtct acaacaaccc ctactcctgg aacaacgcca gcaacatgct ctacatcgac 420  
 cagcccgtgc agaccggctt ctcctacagc attccgggtc ccggctatgt ggattcttcc 480  
 acagacaatg gttttatggg cgcatttcct cagtactcgc gcgaaacctt ccacttcacc 540  
 acggagagtt atggcggcca ctacggggcc gtcttcaacg agtacatcga ggagcagaac 600  
 gcccatctcc agccgggagc caagaagatc caactgggca gtgtgatgat cggcaatggc 660  
 tggatatgacc cgattattca ataccaggcc tactacaact ttacgggtata tccgggcaac 720  
 acatacgact acctgccatt caacaagtcc atcagctcgc tgatgtacaa caacctctat 780  
 ggccccggaa actgcctcga ccagctctac gactgcgccg cccgaggcat cgacgagatc 840  
 tgcagcactg ccgacgattt ttgcgccaac gaggtcgaaa acgtctacga c'atttactcc 900  
 ggtcgggatg agtatgactt tctggaactc actccggacc cgttcctta cgagttctac 960  
 gttgactacc tgaacaaagc gtccgtgcag gccgccatcg gcgcatacat caattacacg 1020  
 gagagcaaca acgctgttgg actcgccctt tctgccaccg gtgacgacgg gcgactcatg 1080  
 aacaccatcc aggatgtggg caagctgctc aaacagggtg tcacgggtggt catgtacgcc 1140  
 ggggatgccg actataactg caactggctg ggtggggaag ccgtgtcgtt gcaggtcaag 1200  
 gccgccaact tcagtagtgc ggggttacacc aacattgtca cctcggatgg agtgacacac 1260  
 ggccaggtgc gccaggcggg gcaatttgcc tttgtgcgag tgatagagag tggacatgag 1320  
 gttcccttct atcaaccctt gcttgcgctg gagatgtttg agcgcgtcat tggcggaag 1380  
 gatgtggcga cgggaaagat tcccatctcg tgcagtttac agacgggtggg caccgccaag 1440  
 agttactacc gggagggcaa cagcacgatt cagtgggagg tggtggattc tctggcgacg 1500  
 tacaacacaa ccacgaatgc tccgaaccgg gtgagccgga ggctgaagcg gatgggacca 1560  
 gctttgcggt ttcagatgta g 1581

<210> 63

<211> 3471

<212> DNA

<213> *Aspergillus niger*

<400> 63

atgtcttgcg tctggctcca catccacaaa aggagcctac tgtctgtcgc tacgaacaat 60  
 tctgttgcca gggccgctgc ctctacctcc gccgcgccg cgccgccgtc atcgccgccg 120  
 cctggttcta atacttattc gcctctttat cggcccatca ccaatcccat cggatttact 180  
 ttgtcgctcg cgaggtcact agtttctcgc aatcctaaat ttctgccta tcggcgctct 240

```

agtcgacact tttctttgtg cccggccgct gcaacgcccg gtgtcaccac gagcatctgc 300
cctggtcagg cggcgcgccg ctctctcagc tcgctcatta tacactctac gagaccccg 360
gctatacgta tccgtaccga ccagatggat ttgaatggag acgcaggcgc caagcgcaag 420
cgcagctcca tcaccacacc cggcgaacgg cccgtaaagg accttcgccc cgaatcgagc 480
gcattgacac cgggggattc gacgcctgcc aatgggactg tatacgatgt ggaggatgat 540
gaagatgcga gtcgtctgct gcctgtaggg cctgctcagg ccgactcacc ggaatggcaa 600
gctaccatag aggaggttgt gaaaagcgta gtgtctatcc acttctgtca gacctgctcc 660
ttcgacacgg agctgtccat gagtagtcag gctactgggt ttgtggtaga tgcagagaat 720
gggtacatat tgacaaaccg acacgtggtt tgcccgggac ctttctgggg atactgcatc 780
tttgataacc atgaggaatg cgacgttcgt cctgtgtatc gggaccctgt tcacgacttt 840
ggaattttga aattcgaccc gaaggctatt cgatatatga aattgagggg actgaaactg 900
cagccggatg cagctaaagt gggatcagaa attcgcgttg tgggtaatga tgcaggagaa 960
aaactgagta ttctgtctgg tgtcattagt cggctggata gaaacgcgcc cgaatacggc 1020
gatggctaca gtgacttcaa tacgaattac atccaggccg ccgcagcagc tagcgggtga 1080
agttccggca gtcctgtagt taacattgat ggccatgcga ttgctctgca ggccggtggt 1140
cgtgcagacg gtgcagcgac ggattacttc ctccctctgg accgaccgct acgcgcactg 1200
gaatgcatcc gtcgcggaga gcctgtcacg cgtggaacga ttcagacgca gtggatcttg 1260
aagccgttcg acgagtgtcg tcggttgggc ttgacgcctg agtgggaggc gaccgtgcgt 1320
aaagcagcgc ccacggaaac cagcatgctg gtggccgaga tcatectgcc tgaaggcccc 1380
gcggacggaa agctcgagga aggagacgtg ctcttcagg tcaacggggg gcttctcacc 1440
caattcatcc ggttgatga catcctggat tcgagtgttg ggcagacagt gcgtctgctt 1500
gtccaaagag gcggtcagaa tgtggagatt gagtgccagg ttggcgacct gcatgccatc 1560
acgcccgacc ggttcgtgac ggtggctgga ggacggttc ataacctgtc ttaccagcag 1620
tcgcggtgt atgccatcgc tactcgcggt gtctacgtct gcgaggctgc cggctccttc 1680
aaactggaaa acacactgtc aggatggatc atcgactcg tggacaagcg gccactcgc 1740
aatctggatg agttcgtgga ggtgatgcga acgattcccc atcgttcgcg cgtggtcac 1800
tcgtatcggc atattcgcga tctccacacc cgaggcacca gcatcgtcta tatcgatcga 1860
cactggcacc ccaagatgcg actggctgtg cgcaacgacg acaccggtct gtgggacttt 1920
tcggacctcg cggaccctat ccagctctt cctccggttc cgaggaaagc cgatttcatt 1980

```

```

caactcgatg gtgttagcca gcctgctgcg gccgacattg tgcgcagctt cgtacgagta 2040
tcctgtacga tgccctgaa gctggacggc taccctcagg ccaagaagac tgggttcgga 2100
ttggtcgtcg atgcagagaa ggggttggtg gttgtgtcgc gagcgatcgt gccgtacgac 2160
ctctgcgaca tcaacgtcac ggtggccgac tccatcatcg tgaacgctaa agtagttttc 2220
ctgcatccgc tccaaaacta cagcatcatc cagtacgacc caagcctggg gcaggcgccg 2280
gttcagagtg ccaaactcgc caccgactac atcaagcagg gacaggacac gatctttgtg 2340
ggattcaacc agaacttccg gattgtcgtg gccaaagacc cgttaaccga catcaccact 2400
gtttctatc cagccaacgc gtccgcaccg cgctaccgcg cgatcaacct ggacgccatc 2460
actgtggaca cgggactcag cgggcagtgt tctaacggtg tcctgattgg cgaggacgga 2520
gtggtgcagg cattgtggtt gaactatctt ggagaacgca catctaattc gcataaggat 2580
gtggaatacc atctaggatt tgcgactcca tctcttcttc ctgtcctgtc gaaggtgcag 2640
cagggagaga tgccggaatt gcggttctg aacatggaga gctacgtggg ccagatgagt 2700
caagctcgta tcatgggctg gtcggaggaa tggatcgaga aggtgacgca agctaaccga 2760
tcgcgccatc agctcttcat ggtgcgcaag gtcgattgcc caccgcctgg gttcaactca 2820
gcggccgaca cgttcgagga ggggtgatatc atcctgacct tggacggaca gctgatcacc 2880
cgcgtctcgg agttggatat catgtacgag aaggatacgc tggaaacctt gattgttcga 2940
aatggacaag aaatgcggat ccaggtgccg actgttccaa cagaggacct agagactgac 3000
cgtgcggtcg tgttctgtgg tgctgtgttg cagaaaccac accatgcggg ccgtcagcag 3060
atttctaagc tacacagcga agtctacgtc agcgcagaa gtcgcggatc cccctcctac 3120
caatacggct tggccccaac caatttcac accgccgtaa acggcggttc aacccgaac 3180
ctggaccgct tctccgaaga agtgagcaaa atccccgaca acacatattt ccgcctacgg 3240
gcggtgacat tcgacaatgt gccgtgggta gtgaccgtga agaagaacga tcattacttc 3300
cccatgtccg agtatatcaa agaccagtcc cagccttccg gttggcggac cgtgtctcac 3360
gacaaggata aatataaaga cggcattgca ccggatgctg cgaacttgaa cccggatgct 3420
atggacgaag ggtttgatgg agtcagtgat attgagccgg atttggagtg a 3471

```

&lt;210&gt; 64

&lt;211&gt; 1611

&lt;212&gt; DNA

<213> *Aspergillus niger*

<400> 64  
 atgagagtcc ttccagctgc tatgctgggt ggagcggcca cggcggccgt tcctcccttc 60  
 cagcaggtcc ttggaggtaa cggtgccaag cacggtgccg accatgcggc cgaggtccct 120  
 gcggatcaca gtgccgacgg gttctccaag ccgctgcacg cattccagga ggaactgaag 180  
 tctctctctg acgaggctcg taagctttgg gatgaggtgg ccagcttctt cccggagagc 240  
 atggatcaga accctctctt ttcctcccc aagaagcaca accgccgtcc cgactcgac 300  
 tgggaccaca tcgtcgatgg caagctggaa gcctatgatc tcagggtaa gaagaccgat 360  
 cctggctctc ttggcatcga ccccgccgtg aagcagtaca ccggttatct cgatgacaac 420  
 gagaatgata agcatttggt ctactgggtc ttcgagtctc gcaatgacct cgagaatgat 480  
 cccgttggtc tgtggctgaa cggtgccctt ggtgctctt ccctcaccgg tctcttcattg 540  
 gagcttggtc ctagcagcat caacaagaag atccagccgg tctacaatga ctacgcttgg 600  
 aactccaacg cgtccgtgat cttccttgac cagcctgtca atgtcgggta ctctacagt 660  
 aactctgctg tcagcgacac ggtcgtgct ggcaaggacg tctatgcctt gcttaccctc 720  
 ttcttcaaac aattccccga gtatgctaag caggacttcc acattgccgg tgaatcttat 780  
 gctggctact atatccccgt cttcgcttcg gagatcctgt ctcaacaaga gcgcaacatc 840  
 aacctgcagt ccgttctcat tggcaacggt ctaccgacg gatacaccca gtacgagtac 900  
 taccgtccca tggcctgcgg tgacggcggg taccagctg tcttgacga gagctcctgc 960  
 cagtccatgg acaacgctct tcctcgctgc cagtctatga ttgagtcttg ctacagttcc 1020  
 gagagcgctt gggtttggtt cccggcctcc atctactgta acaacgccct ccttgcccct 1080  
 taccagcgca ctgggcagaa cgtctatgat gtccgtggta agtgcgagga tagctctaac 1140  
 ctttgctact cggctatggg ctacgtcagc gactacctga acaagcccga agtcatcgag 1200  
 gctgttggtc ctgaggtcaa cggctacgac tcgtgcaact ttgacatcaa ccgcaacttc 1260  
 ctcttccacg gtgactggat gaagccctac caccgcctcg ttccgggact cctggagcag 1320  
 atccctgtct tgatctatgc cggatgatgt gatttcattt gcaactggct gggcaacaag 1380  
 gcctggactg aagccctgga gtggcccga caggctgaat atgcctccgc tgagctggag 1440  
 gatctgggtc ttgtcgacaa tgagcacacg ggcaagaaga ttggccaggt taagtcccat 1500  
 ggcaacttca ccttcatgcg tctctatggt ggtggccaca tgggtccgat ggaccagccc 1560  
 gagtcgagtc tcgagttctt caaccgctgg ttgggaggtg aatggttcta a 1611

<210> 65

<211> 840  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 65  
 atgaagttca caaattatct cttgacgact gcaacgctcg caagcagtggt cctagcgggt 60  
 cctgctcccc gcaccgggtt ggaggacaga ctccgtgccc ggtcattgca gcgtcaatca 120  
 catcctctgg cacctattcc acttgacaca tccaccaaag agaattccag actcctcgaa 180  
 gccgacgaga ataccaccca tggtacatac agcagtaact gggcgggccc agtgcgcgag 240  
 caaccacctc cgcaaggcac gtattctgcc gtgtcggcaa cctttcgtgt accagaaccc 300  
 acggcgcaag gggggagcgg aacgcagggt gggtcggcct gggtcgggat agatggcgac 360  
 acatacagca acgccattct acagacagga gtcgacttct acgtggaaaa cgggcagacg 420  
 tacaacgatg cctggtatga gtggtaccca gactatgcat atgacttcga cctagatgta 480  
 agcacagggg acacgatcgt cgccaagggt gaagccatct cgccaagtca aggtgtagcc 540  
 actattgaga acatatcgac ggggaagaag gccacgcaga cgatcagagc cccagctgcy 600  
 acagctaccc ttgccggcca gaatgccgac tggatcggtg aggatttcca gtctggcgac 660  
 tcaatggtcg atctggctgg ctttggcgag atcagcttct ggggcgtgca agcacaagga 720  
 ggagggctca catgggggtgt agatgatgcy actattgtcg aactgaagca gggcaacgaa 780  
 gtgttgacag acgtggaggt gcaaagtgat tcggccttta cggtgaaata tacgagctga 840

<210> 66  
 <211> 1722  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 66  
 atgatatatg tcaactatat cctgggactt ctgtccctct tacacaccgc tgtagccaca 60  
 gtccttgatt atgtcgtggt agaccaactg aacagcatcc ccgacggatg gacaaaaggc 120  
 gcagctcccc cgccatttac tccgatgaag ttctggttgt cgatgcatca cgagtacaag 180  
 gcggacttcg agcagaaagt catcgatata tcgacacccg gtcaccggga ttatggacgg 240  
 catatgaaac gcaacgatgt catggccttt atgcgcccat ccgatcaggt ctcaaagatc 300  
 atcttctctt ggcttgagtc ggagcatggt ccaccaaagt ccatcgaaga tcgcggggat 360  
 tgggtcgctt tcacagtccc gttggcccaa gcacaatcaa tgatgaagac cgatttttac 420  
 aacttccacc acctggaaac aaacacaacc caaattagga ccctcaagta ctccgttccc 480  
 gagcaagtcg atgctcatct gcaaagtatc cagccaacga ctcgcttcgg ccgacctaa 540

```

acacaaacca gcctaccgag cctcatgcca gtgtcgggta acattgatga aataagcgaa 600
gactgcttga caggcgtgac gccatttgc cttcgccagc tctatggttt acctagcacc 660
aaggcaagcc ccgactcgag aaacgtcctc ggaatttccg gctatctgga ccagtacgcg 720
cgctacagtg acctcgacga gtttctagcc gtatactctc caaacagegt agacgcccag 780
ttctccgtag tatcgatcaa cggaggccaa aaccacaaa actcacaaga gggaagcaca 840
gaggccagtc tcgacatcca atacgccctc tccatggcat ttgacgctaa cgcgactttc 900
tacactaccg ccggacgtgc gccatccccg tatctcgaa agctccagta tctgggtgggt 960
cttccggacg aggatcttcc tgcagtgtt agcacgtctt acggcgagga tgagcaaagt 1020
ctgccggagg aatacacaga agccacgtgc aatttatattg cccaattagg tgcacgctgg 1080
gtctcgggta tcttcagcag cggagactcg ggcgtcggag gatcgtgtgt atctaacgac 1140
ggaagccaga ggaccgctt tcagcctatc tccccggcgt cgtgcccggt tgttacatcc 1200
gtgggtggga ctgagggcgt cgggccggaa aaggctgtgg acttttcgag tggaggggtc 1260
tccgagcgct ttgctcgccc gtcgtaccag aatgcgagtg tggaagcata ccttgcccg 1320
ttaggagata aatgggatgg attgtataat ccagacggac ggggtattcc tgatgtgtcg 1380
gcccaggcta gcaactatgt aatcagggac catgggcaat ggctacaaac tgcgggaaca 1440
agtgtctccg cccctgtctt tgcagcagtc atctctcgac tgaacgctgc acgtctcgag 1500
cagggtaaac ctacactagg gtttctgaat ccttggtgtg actcactcga ccagcaagga 1560
tttacggata ttgtagacgg cggatcagtg ggttgtagcg ggtcaaatgg aggagctctt 1620
gtcccgtatg ccagttggaa tgccaccaag gtaggggacg cggttactgg gctggggaca 1680
cctctgtatc agactctgga gcagttggcg cagtctgctt ag 1722

```

&lt;210&gt; 67

&lt;211&gt; 1758

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 67

```

atgcgttctt ccggtctcta cacagcactc ctgtgtctcc tggccgcctc gaccaacgcg 60
attgtccatg aaaagctcgc cgcggtcccc tccggtggc atcatgtcga agatgctggc 120
tccgaccacc agataagctt gtcgatcgcg ctggcacgca agaacctcga tcagcttgaa 180
tccaagctga aagacttgtc aacacctggc gaatcgcaat acggccagtg gctggaccag 240
gaggatgtcg acacgctgtt cccggtggcc agcgacaagg ctgtgattaa ctggctgcgc 300

```

```

agcgccaaca tcacccatat ttcccgccag ggcagcttgg tgaactttgc gaccacggtc 360
gataagggtga acaagcttct caacgccacc tttgcctact accaaagcgg ctcttcccag 420
agattgcgca caacagagta ctccatcccg gatgatctgg tcgactcaat cgacctcatc 480
tccccaacga ccttcttcgg caaggaaaag accactgctg gtctgaacca gcgggcgcaa 540
aagattgaca cccatgtggc caaacgctcc aacagctcgt cctgtgccga tgtcatcacg 600
ctgtcctgcc tgaaggagat gtacaatttt ggcaactaca ctcccagcgc ctcgtcgggc 660
agcaagctgg gcttcggcag cttcctgaac gaatccgcct cgtattctga ccttgccaag 720
ttcgagaagc tgtttaacct gccctcccag agcttttccg tggagttagt caacggcggt 780
gtcaatgatc agaatcaatc gacggcttcc ttgaccgagg cggacctcga tgtggaattg 840
ctcgtcggag ttgctcatcc cctcccgttg actgagttca tcacttctgg cgaacctgcc 900
gccgacaacg agaacgagcc ttacctccag tactatgagt accttctctc caagcccaac 960
tcggctctgc cccaagtgat ttccaactcc tatggtgacg acgaacagac cgttccagag 1020
tactacgcca agcgagtctg caacctgacg ggacttggtg gcctgcgcgg catcagtgtc 1080
ctcgagtcgt ccggtgacga aggtatcgga tctggctgcc gaaccaccga cggcaccaac 1140
cgaaccaat tcaaccccat cttcccgccc acctgtccct acgtgactgc cgtgggagga 1200
acaatgtcct atgccccga aatcgctgg gaagccagtt ccggcggatt cagcaactac 1260
ttcgagcggg cgtggttcca gaaggaagct gtgcagaact acctggcgca ccacatcacc 1320
aacgagacca agcagtacta ctcgcaattc gccaaacttta gcggtcgcgg atttcctgac 1380
gttgctgccc atagctttga gccttcatat gaggttatct tctacggcgc ccgctacggc 1440
tccggcggta cctcagccgc gtgtcccctt ttctctgcgc tagtgggcat gctgaacgat 1500
gctcgtctgc gggcgggcaa gtccacgctg gggttcttga accccctgct ctatagcaag 1560
gggtacagag cgttgactga tgtgacgggg ggccagtcga tcggatgcaa tggcattgat 1620
ccgcagaatg atgagactgt tgccggcgcg ggcattatcc cgtgggcgca ctggaatgcc 1680
acggtcggat gggatccggt gactggattg ggacttcctg actttgagaa gttgaggcag 1740
ttggtgctgt cgtttagtag 1758

```

```

<210> 68
<211> 798
<212> DNA
<213> Aspergillus niger

```

&lt;400&gt; 68

```

atgaagacta ctgctctctt gaccgccggc ctgctggcca ccaactgctat ggccgctcct    60
ctgacggcca agcgccaggc tgctcgggccc aagcgctcca cgaaccgcca gagcaaccct    120
cccttcaagc ctggcaccaa cgaggtcctc gcccttaacg gcaccaagaa tgtggagtac    180
agctccaact gggccggtgc cgtcctcatt ggcactgggt acaactgccgt gaccgccgag    240
ttcgctgtgc ccacccctc cgtgccctcc ggtggctcga gccgcgagga gtactgtgcc    300
tccgcctggg tgggcattga cggtagacacc tgtgacactg ctatcctcca gaccggtgtg    360
gacttttgtg tccagggcag cgaggtgagc ttcgatgcct ggtacgagtg gtaccccgac    420
tacgcctacg acttcagcgg catctccatc tcggccggtg ataccatcaa ggtcaccgtc    480
gatgccagca gcgacaccac cggtagtgc accgattgaga acgtgagcac tggtagcacg    540
gtcaccacac gcttcacggg cgggtgtgat ggtgatctgt gtgagtacaa cgctgagtgg    600
atcgtcgagg acttcgagga ggatgactcc ctcgctccct ttgccgactt tggcaccgtg    660
actttcacca gctgctccgc taccaaggat ggttcctctg ttggccctga ggatgctacc    720
atcatcgaca tcgagcagaa tgaggtgctg acctccgttt ccgtctccag tagcgaggtc    780
gttgtcaagt acgtctaa                                     798

```

&lt;210&gt; 69

&lt;211&gt; 1743

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 69

```

atggctgcct tttcccgcat ctccgagggc ttcccccctg ccgccctgc cctggccagc    60
gtcgctctgg agaccgtcaa gtctgttccc agcgactgga agctcgtgga ggctgctgat    120
accagctcca caatttcttt gtccgttgct ctggcgcgtc agaacctgga ccagttggag    180
gagaagctcc tggccgtgtc caccctggc aaggacacct acggccagtt cttggatctg    240
gacgacatca atgagcagtt tcctctcgca gatgacgctg ctgttggtggc ttggctgaag    300
aaggcaggcg tcaccagat ccataaggag ggtggtctgc tgaactttgc gaccactgtg    360
ggcacagcca accagcttct caacaccacc ttctcgggtg acaagagcgg atctaccag    420
aagctgcgca caacgcaata ctctgttccg gatgagctga ccgggtccat tgatctcatc    480
tcgccgactg ttttctttgg aaagtccaac gctgcgcgct cggcgccgt gcgtgcttcg    540
cagactacca aggagaccag cagaaagaag agcagtaatg tgtgcgagta catcactccg    600
gattgcctca aagagcagta tagcattgac tatacgcccg aggcacgctc gggaagtcgt    660

```



```

gttggggtttg gcagtttctt gaacgagtcg gccttgtagt cggattttgga tctgttcacc 720
cagtacttttg acattcccca gcagagtctt actgttgaga ctatcaacgg gggaatcaac 780
aaccaggaga atgatccgga tgggtgaagcc gatctcgatg tccagaacat cgtgggcatc 840
tcgcatccct tgccggtgac ggagtagatt accggaggat ctctccatt cattcccgac 900
gtcgagacta ctaccgacga gaacgagcct tacctgcagt actacgagta tctgctggcc 960
aagaccaacg acgagctgcc actggttatc agcaactcgt acggcgatga cgaagatacc 1020
gttcccattg cctacgccac ccgcgtatgc aacctcatcg gcctgatggg cacacgtggg 1080
atctccatcc tcgagtcttc cggcgactct ggtgtgggcg gcgcatgcat gtccaacgac 1140
ggcaccgaca agaccgaatt ccccccatg ttcccaggaa catgcccgta catcaccgag 1200
gtcggcggca cccaagacgt gcccgaagtc gcctgggtgg acagctccgg cggcttcagc 1260
aactacttct cgcagccgtc gtaccagtcg gatcagggtg agacctacct ggacaagtac 1320
atctctgcct cgacgaagaa gtactacgag cagtacacca acttcagcgg tcgcgcgttc 1380
cctgacgtgt ctgcgtttgc aggttctcct tactacgaaa cttatattga tggtcagctc 1440
ggccttggtg cgggtacttc tggcgctagc cctgtgtttg cggggatcgt cgcgctgctg 1500
aacgatgccc gtctgcgggc caacaagaca tccttgggct tcctgaacce ttggctgtac 1560
tcgagcggct acaagagcct gaatgacatt accagtggcg aggcagtggg ctgccaaggc 1620
gatgtggagg gcgctggagt cattccttgg gcgagctgga atgccacgac gggatgggat 1680
ccggcgacag ggctgggaac gcctaatttt gccaaagtga aggaggcggg tcttgcgttg 1740
taa 1743

```

```

<210> 70
<211> 1896
<212> DNA
<213> Aspergillus niger

```

```

<400> 70
atgcatggtc tgccgctagt atgcagcata gggacattgc ctttggttat cctggcatat 60
ccggcggttt cattgcatac aacttcagca gccgtggact tggactccct tcgtctgacc 120
tctaactccg aatacgtcaa ttctgtccat gtacacagca atcgatcagt cgcagtgtcc 180
gctgaagaac attataccga tacagcagct cgactgggtc agaacattgt tcctggagcg 240
agctttctgc tcatcgatga ccactttgtc ggcgacaatg gagttgcaca tgtatacttc 300
cgccaaacgc tccatggtat tgacattgac aatgcggatt tcaatgttaa tattggaaaa 360

```

gatggactgg tcttgtcttt cggacattcg ttcttcacag gcgcggtgcc gagcagccat 420  
ctggacaata ccaacgtttt gagtccggag gctgcactta gaggagcaag ggacgctata 480  
cagcttccac tgactattga caatgtttct actgaagctg cagaggggcg gaacgagtac 540  
atattcagag aggcagtggg agcggtatct gaccccaaag ctaagctagt ctaccttgtc 600  
aagccagaag ggactctggc gctcacctgg aggatagaaa cagacatgta tgagcactgg 660  
ctactgacat acattgatgc agagactacc actgtccacg gcgtggttga ctatgtcgca 720  
gacgcgacat atcaagttta tccctggggc acaaacgac cagcagaagg acatcgcacc 780  
attgtcaccg acccctggga cctatccgca tccgcataca cctggataag cgatggacgg 840  
gacaactaca ccacaaccag aggcaacaat gccatcgcac actggaatcc gaccggcggt 900  
ggctcctatc tctacaacct acgtccatcc gaccccaact tgaatttcca atggccatac 960  
tccccaaaca tgtccccacc ccgatcatac atcaacgcct ccatcgcca actcttctac 1020  
acagcaaacg cctaccacga cctcctctat aactcggct tcaccgaatc cgctggcaac 1080  
ttccaatgga ataacagcgc ccacggcggc cgagacaaag actacgtgat cctcaacgca 1140  
caagacggct cggggttcag caacgcaaac tttgcaacc caccgatgg tatccccggc 1200  
cgtatgcgca tgtacatctg gatcgagtct actccgtcgc gtgatggaag ttttgacgcg 1260  
ggcattgtaa ttcacgaata cactcacggt gtatccaatc gtctcaccgg cggctccac 1320  
aacgccggat gcctcagcgc cctcgaatcg ggtggcatgg gcgaaggctg gggcgacttt 1380  
atggcgacgg ccatccgaat caagcccaac gatacacgca caacgtctta cactatgggt 1440  
gcatgggcag ataatgataa atgtggtgtc cgggactatc cttattctac ctcttttact 1500  
gagaaccctt tgaactatac gagcgtgaat accatgaacg gcgtgcacgc catcggaact 1560  
gtctgggcaa ccatgctata cgaggtcttg tggaaacctc tcgacaagta cgggaagaat 1620  
gatgggtcga ggccggtgtt tagaaacggg gtgcctacag atggaaagta cttgatgatg 1680  
aagttggtgg tggatgggat ggcactgcaa ccatgtaatc cgaacttcgt gcaagccagg 1740  
gacgcgatcc ttgacgcaga cattgtgttg actggcggga agaactcgtg tgagatctgg 1800  
agggggtttg cgaagagagg attggggcaa ggagcggctc atagtagttt aaattggatg 1860  
cggaggggga gtacacttct tcctacggga tggttag 1896

<210> 71  
<211> 1185  
<212> DNA

<213> *Aspergillus niger*

<400> 71

```

atggtcgtct tcagcaaaac cgctgccctc gttctgggtc tgcctccgc cgtctctgcg      60
gcgcgggtc ctactcgcaa gggcttcacc atcaaccaga ttgcccgcc tgccaacaag      120
accgcacca tcaacctgcc aggcatttac gcccgttccc tggccaagtt tggcggtagc      180
gtgccccaga gcgtgaagga ggctgccagc aagggtagt ccgtgaccac gccccagaac      240
aatgacgagg agtacctgac tcccgctact gtcggaaagt ccaccctcca tctggacttt      300
gacaccggat ctgcagatct ctgggtcttc tcggacgagc tcccttcttc ggagcagacc      360
ggtcacgata tgtacacgcc tagctccagc gcgaccaagc tgagcggcta cacttgggac      420
atctcctacg gtgacggcag ctcgccagc ggagacgtgt accgggatac tgtcactgtc      480
ggcgggtgtca ccaccaacaa gcaggctgtt gaagcagcca gcaagatcag ctccgagttc      540
gttcagaaca cggccaatga cggccttttg ggactggcct ttagctccat caacactgtc      600
cagcccaagg cgcagaccac cttcttcgac accgtcaagt cccagctgga ctctcccctt      660
ttcgccgtgc agctgaagca cgacgcccc ggtgtttacg actttggcta catcgatgac      720
tccaagtaca ccggttctat cacctacacg gatgccgata gctcccaggg ttactggggc      780
ttcagcaccg acggctacag tatcggtgac ggcagctcca gctccagcgg cttcagcgcc      840
attgctgaca ccggtaccac cctcatctc ctcgatgacg aaatcgtctc cgctactac      900
gagcagggtt ctggcgctca ggagagcgag gaagccggtg gctacgtttt ctcttgctcg      960
accaaccccc ctgacttcac tgtcgtgatt ggcgactaca aggcggttgt tccgggcaag      1020
tacatcaact acgctcccat ctcgactggc agctccacct gctttggcgg tatccagagc      1080
aacagcggtc tgggactgtc catcctgggt gatgttttct tgaagagcca gtacgtggtc      1140
ttcaactctg agggccctaa gctgggattc gccgctcagg cttag                          1185

```

<210> 72

<211> 1197

<212> DNA

<213> *Aspergillus niger*

<400> 72

```

atgaagtcag cctccttgct cacagcatcc gtgctgttgg gctgtgcctc cgccgaggtt      60
cacaagctca agcttaacaa ggtgcctctg gaagagcagc ttacacgca taacatcgac      120
gcccatgtcc gcgctctggg ccagaagtac atgggtatcc gcccgccat ccacaaagag      180
ctggtcgagg agaaccctat caatgacatg agccgtcatg atgttctggt ggacaacttc      240

```

ctgaacgcac agtactttctc tgagatcgag ctgggtactc cccccagaa gttcaagggt	300
gtcctggaca ctggcagctc gaaccttttg gttccttcga gcgaatgcag ctctatcgcc	360
tgctacctcc acaacaagta tgattcgtct gcctccagta cgtatcacia gaatggcagt	420
gaattcgcca tcaagtacgg ctctggcagc cttagcggat tcattttctca ggacaccctg	480
aagattggcg acctgaaggt caagggacag gacttcgctg aggcgaccaa tgagcctggc	540
cttgcccttg ccttcggccg gttcgatggc attctcggct tgggttatga caccatctcc	600
gtgaacaaga ttgttcctcc cttctacaac atgcttgacc agggactcct cgacgagccg	660
gtctttgcct tctaccttgg agataccaac aaggagggtg acgagtcctg ggcgaccttc	720
ggtggtgtcg acaaggacca ctacaccggc gagctgatca agattccct cctgcaag	780
gcttactggg aggttgagct tgacgccatt gctcttggcg atgatgttgc tgagatggag	840
aacaccggtg tcattctgga cactggtacc tccctgattg ctctgcctgc tgacctggct	900
gagatgatca atgctcagat cggtgctaag aagggtgga ccggccagta caccgttgac	960
tgcgacaagc gctcgtccct gccgatgtt actttcacc ttgccggcca caacttcacc	1020
atctcctcgt atgactacac cttggagggtg cagggtctct gcgtcagtgc cttcatgggc	1080
atggacttcc ctgagccggt tgggtcccttg gccatttttg gcgatgcgtt cctgcaag	1140
tggtagcgcg tgtatgacct gggcaacagc gctgttggtc tggccaaggc caagtaa	1197

&lt;210&gt; 73

&lt;211&gt; 1182

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 73

atgcgcaagt accgcttcca tcccaccaag cctgggtccct acactctcag cagctccatc	60
caacagaccg gtcgtccgta cactgaaaag cccatcgggg gtcggggcca tatccggcag	120
ctggtgcgga agaagagcac caccagcagat gaggttggcg aggttccggc cgaagatgtg	180
cagaacgact ccatgtatct ggcgaccgtg gggatcgga ccccggcga gaacctgaag	240
ttggactttg aactgggtc agctgatctt tgggtctggt ccaacaaact cccctcaacc	300
cttctatccg agaacaagac ccatgcgac ttcgactcgt ccaaatcgag cacttcaag	360
accttgaag gtgaatcctg gcaaactctc tacggagatg gatcctccgc atcaggaggt	420
gtgggcaccg acgacgtcaa cattggcggc gtagtcgtca agaaccaagc cggtgagctg	480
gcagagaaga tgtccagcac attcgcccaa ggcgaagggg acggattgct cggctagca	540

```

ttcagcaaca tcaacacggt acagccaaag tccgtgaaaa cggccgtcga gaacatgac 600
ctgcaggatg acattcccaa gtcggctgag ctgttcacgg ccaagctgga tacctggcgg 660
gacactgatg acgagtcggt ttacaccttt ggcttcattg accaggatct ggtgaagacg 720
gcagggtgaag aggtctacta caccctgtc gataacagtc aaggcttctg gctattcaac 780
tcgacctccg cgacggtaaa tggaaagacc attaaccggt cgggtaacac cgccattgct 840
gataccggta cgacgctggc cttgggtggac gatgacacgt gtgaggccat ttatagtga 900
attgacggcg cctattatga tcaggaagta cagggtgga tctatccgac cgatacggcg 960
caggataagc taccactgt gtcgtttgcc gtgggtgaaa agcagttcgt ggtgcagaag 1020
gaggacctgg cgttttcggg ggcgaagacg ggctatgtct atggaggaat ccaaagtcgt 1080
ggtgatatga ccatggacat cttgggagac acatttttga agagtattta tgctgtaagt 1140
gcattgctgt tggcgtaaag gggatgatatc gaagctcact aa 1182

```

<210> 74

<211> 849

<212> DNA

<213> *Aspergillus niger*

<400> 74

```

atgaagttct ctaccatect taccggctcc ctcttcgcca ctgccgtctt ggtgctcct 60
ctcactgaga agcgccgtgc tcgcaaggag gcccgcgccg ctggcaagcg ccacagcaac 120
cctccctaca tccctgggtc cgacaaggag atcctcaagc tgaacggcac ctccaacgag 180
gattacagct ccaactgggc tgggtgccgtc ctgateggcg acggctacac caaggctcact 240
ggcgagttca ctgtccccag tgtctctgct ggatctagca gctccagtgg ctacggcggt 300
ggctacggct actacaagaa caagagacaa tccgaggagt actgcgcctc cgcttgggtt 360
ggtatcgacg gtgacacctg cgagaccgct attctccaga ctggtgtcga cttctgctac 420
gaggatggcc agacttccta cgatgcctgg tacgagtggg accccgacta cgcctacgac 480
ttcaacgaca tcaccatctc cgagggtgac accatcaagg tcaactgtcga ggccaccagc 540
aagagcagcg gtagcgccac cgttgagaac ctgaccactg gccagtcgt caccacacc 600
ttcagcggca acgtcgaggg tgacctttgc gagaccaacg ccgagtggat cgtcgaggac 660
ttcgagtctg gtgactctct tgtggcttgc gctgacttcg gctccgttac cttcaccaat 720
gctgaggcta ccagcgacgg ttccactgtc ggccctctg acgctaccgt tatggacatt 780
gagcaggatg gcaccgtcct caccgagacc tccgtctctg gcgacagcgt cactgtcacc 840

```

tacgtttaa 849

<210> 75

<211> 822

<212> DNA

<213> *Aspergillus niger*

<400> 75

atgggagatt acggccccgg agtgtcgtca ctcacggcac agctacctgg aaatccgcct	60
gtctctgaaa cagatcagga tgagatctca gtacttgtaa cgggctttgg gccattcaag	120
tctaattctag tgaacgcctc atatctgata gcctcgtccc taccaccctc tttcacattc	180
tcacctgcat cttcagacgg ctctgatgct gttccccgtc gagtttcgat aaatgtccat	240
ccttcaccca taccggtgc atattcatcg gtgcggacga ccctccccgt cattctcgat	300
gactatgcca agacgcacgg aggccgaagc ccagacatcg tcatacacat tggcatagca	360
gcaatgagga actactattc cgtggagacg caggctcacc gtgatgggta tctgatgtcc	420
gacatcaaag gcagatccgg gtacgaggat ggcgagaagc tgtggaggga gctcgacttg	480
ccactggtgc ttagggctgg cccttcagag ggacacgcct cggagaagaa acatctcagc	540
ccccgtccac cggacgaaga tttcctagca gcatggaaga cattttgccc tccagaaacc	600
gatgcgcgga tctccactga tgccggacgt tatctctgcy agttcatcct gtacaccagc	660
ttggcactgg cataccaggc ggggtgaggat cgcaatgtca ccttcttcca tgttccccgcg	720
tcatgcttgg atgaggatat agagacgggc aaggagggtg ccgtcgcgct aatcaaggct	780
cttgtgacta gctggagtga gcagcagcac agcggtccct ag	822

<210> 76

<211> 1629

<212> DNA

<213> *Aspergillus niger*

<400> 76

atgggctcaa ggcagggaaa ggcccccttt ggctggggta ctcagtcact tgctcacttt	60
ggatatcaacc cagaccttgg gttgcacaac cagcagaacc tcaactccct catttcacat	120
tcagcgatgg ccactgcgtt ggagacggaa tatgccacca tccctattga ccataacaac	180
gcatcggttg gcacttatca aaatcggttc tgggtcagcg atgaattcta tcagcctggc	240
aacccgatat ttgtgtacga taccggggag tcggatggcg gatcgatagc ccagtcctac	300
ctaacctcca ctctctcctt cttcagagaa ttcctgatcg aattcaacgc catgggaatc	360

gcctgggagc acagatacta tggaaactcg accccggctc ccgtatccta tgaaactcca 420  
 cccgagggcat ggcaatacct caccaccaag caggcgctcg cggaccttcc gtactttgct 480  
 agtaacttta gccgcgagaa gtatcctgac atggacctga cgccgcaggg cacgccgtgg 540  
 atcatgggtgg gcggctcgta cgcagggtt cgtgctgcat taactcgcaa ggagtaccca 600  
 gagacgatat tcgcagcctt ttcctcatcg tctccgggtg aagcacaggc caatatgagc 660  
 gcgtattacg accaagtcta tcgtggcatg gttgccagcg gatggaccaa ctgctcggca 720  
 gatatccacg ctgctctgga atatattgac gatcaacttt cggatgaaga tacagctacc 780  
 tcggtcaaac aacttttctt cggatctggc gccgagacca actccaacgg tgatttcact 840  
 gcagcgctaa ctgccatcta cggctacttc caaagttatg gtatggcggg aggtattgga 900  
 ggtctaggcg cattctcgga gtatctcgaa attgatccca agacgaacgg gactacagga 960  
 ccggatggcc ttgccctac gtatggcggc cagtatgtcg ccgaacgatg ggccgcatgg 1020  
 ccaacctttc tcgagctggt caatctgaat atggggacca actgcggggc tcaggacgcg 1080  
 tctcagccaa ttgactgtga cttttccaag ccatacggcg atccctcggc catcacttgg 1140  
 acttggcaat actgcagcga atgggggttc ttccaggcga acaacgatg gccgcactcg 1200  
 ctggcctcgc gatatcagtc ggtggaatac cagcaagaag tatgtaaccg gcagttcccc 1260  
 gatgcagtgg acaagggact gctgcctcgc tcgccgaggg cggatgatgt caaccaagag 1320  
 tttgggggat ggacgatccg cccgtccaat gtttacttca gcggaggaga attcgatccg 1380  
 tggcgatcat tgtccattct gtcgacagaa gatttcgcac ctcaaggggt ggagtttacg 1440  
 agcgcgatcc cagcctgtgg ggtgcagacc aatgaggaca ccgtctttgg atacgtcatg 1500  
 cagaactcgg aacattgctt tgactttcaa gcgacgccga ccgtggggaa gttatcacgc 1560  
 ggcattctca catccgcctt gttgcaatgg ctcgatgtt ttggacagaa ctcaagccaa 1620  
 tccaggtga 1629

<210> 77  
 <211> 1176  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 77  
 atgaagctct caatagctct tgcactcggc gcaacggctt cgacgggggt gttggctgct 60  
 gttgtaccgc agcaagaacc gctgataacc cccaagatc cccaactca tcatcatcag 120  
 gagaagttct tgatcgagtt ggctccttat cagacgagat gggttaccga ggaagaaaag 180

tgggacttaa aactggatgg cgtgaacttc atcgatatta ctgaagaacg aaacactggg 240  
 ttctacccaa cgttgcatgc tggtagctat gttcactatc cgccgacgat gaagcatgcg 300  
 gagaaggtgg ttcccccttct gcgggggtctc tccaaggaca acatggagca aaacctcaac 360  
 aaatttacct catttcacac tcgctactat aggtcgctca ctggtattga gtccgcaaag 420  
 tggctataca gtaggggttc ggatgtcatt gagcagtcgg gtgcagcaga gtacggcgcc 480  
 actgtggagc agttcgctca ctcatggggc caattcagta tcattgctcg gatcccaggc 540  
 cagactaaca aaactgttgt cctgggcgca catcaggaca gcatcaatct ttctctcccc 600  
 tccatcctag ctgcacctgg tgccgatgat gacggaagtg gaaccgtgac tatactcgaa 660  
 gctttgcgtg gtctgctgca gtcagacgcc attgtccggg gcaacgcttc caacacaatc 720  
 gaattccact ggtactcggc agaggaaggt ggtatgcttg gttcgcaagc catattctct 780  
 caatataaga gagataagcg agacatcaag gcgatgcttc aacaggatat gactggttat 840  
 acccagggag ctctggacgc cggtcgtcaa gaagccattg ggattatggt tgactacgtt 900  
 gatgagggac tgacacaatt cctcaaagat gtcactactg agtattgtgg tattggctac 960  
 atcgaaacca gatgtggcta cgctgttcg gaccacacgt ccgcaagcaa atatggctat 1020  
 cccgcagcta tggcgacgga atccgaaatg gaaaacagca acaagaggat ccacacgact 1080  
 gatgacagca tccggtatct aagcttcgat catatgctgg agcatgcgag gttgacactt 1140  
 ggcttcgctt acgagctggc ctttgctcaa ttctag 1176

<210> 78

<211> 1329

<212> DNA

<213> *Aspergillus niger*

<400> 78

atgagaacta ctacgtcttt tgctaggctt gcattggcag tggcctcagt tggattgtc 60  
 tttgctagtc caacaaaaaa taacgatggg aaactggat atggctcacc agaatccgtc 120  
 ggcatgatat ccgccccttt gcaccaaagt gtccaaaatg ttagcgcata tacacatgct 180  
 gccaaactata gcaagttctc gtacgacaaa gtccatccca tcgagccagg gtctgttacc 240  
 ctggtggctc tcgacgggtg catcgtcagc gaatttgctt tgggcaagag aaatctctac 300  
 gccgatgtca acggcaccaa ttacctcga tacctgcagg aagacaccac cctggataca 360  
 gtctacgata tggcaagcct cacgaagctg ttcaccacgg tagctgcttt acgggaactt 420  
 gacgctggtc gaattgcgct taatgtaact gttgcaactt atataccgga ctttgcgacg 480



```

aatgggaagg agaataattac tatcttggag ctgttcacgc atacaagcgg ttctgcttct 540
gatccatcgc caccactttt ctctgcttat tatacgacgt atgatgaacg cattaaagca 600
atcttgacgc aaaaaattat caataccccc ggcagcacat acctctactt agatctcaac 660
tttatgtcgc tgggcctcgt tatcgagacc gtaacgggac gtgccctgga tgatcttatt 720
tatgacttca ccagaccgct tgaaatgaca tctaccttct tcaaccgcgg gaatatcgaa 780
ggctctacac ccagtcacc caactacgac cgcacagccg tacaagaatt tcagatcgca 840
gccctcggac cctcagaacc acagcgtcca caaccagtgc gcggcacagt tcacgacgag 900
aacgcatggc ccctagacgg cgtatcaggc catgcaggtc tattctccac tgtgcgcgat 960
acagcgacat tctgccagat gatcctcaac aacggcacat atgcaggcca acggatcctt 1020
tctcgaaacg cggtagacat gattttcaca aacttcaatg ccagggttcc gggggatgct 1080
cgtagtttag ggtttgagtt ggatcagtat tctactgcgg gaccgatggc gagtttgcaa 1140
actgcgagtc aactggatt tactgggact acgttggtga tggataggac gtataacgcc 1200
ttttggttgc attttagtaa ccgggtgcat ccgtctaggg catggtctag / caatactatt 1260
gtgagagagg ctattgggta ttgggttggg aagagcttgg ggttggtatg tgcgtttgct 1320
ctggttataa 1329

```

&lt;210&gt; 79

&lt;211&gt; 1839

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 79

```

atggcgctct gggtgctctc gacgctcctt tttctgagcc cgtccttggg gtcagccaaa 60
tcggccgcag actattatgt tcaactccttg cccggtgccc ccgaggggcc cttgctgaag 120
atgcatgccg gccatattga ggtggatcca cagaacaatg gaaatctttt cttctggcac 180
taccagaatc gccatattgc caaccgccag cggactgtga tctggttgaa cgggtggctcc 240
ggatgtagtt ccatggacgg cgcgttgatg gaggtcggtc cgtatcgctt gaaggacaat 300
gaaaccttga cctataatga gggttcctgg gacgaattcg ccaatttggt gttcgtcgat 360
cagccagtcg gaaccgggtt cagttatgtc aacacggaca gctatcttca tgagctcgat 420
gagatgtcgg ctcaattcat tgtctttctg gaagagtggg tcagattatt tccggagtat 480
gaacgcgatg atatctacat tgccggcgag tcttacgccg gtcagcatat tccatacatc 540
gccaaagcca tccaggaacg gaacaagaac gttcaagggg agaccatcgc ttcgtggaat 600

```

```

ctaaaaggcc tattgattgg caatgggttg atttctccta atgaacagta catgtcctac 660
ttgccctacg catatgaaga aggccttata aaggaaggca gccggaccgc gaaggaactc 720
gaagttttac agtcagtctg taagtccagg ctggaaactg gcaagaacaa ggtccacctc 780
aacgactgcg agaagggtcat gaatgctctg ttggataaga cggtcgaaga caacaaatgt 840
ctcaacatgt atgacatccg ccttcgtgac accaccgatg catgcggtat gaactggccc 900
accgacctgg aggacgtgaa gccctatctg cagcgggaag atgtgggttaa agcgcttaac 960
atcaatccgg agaagaagtc tggctgggtg gagtggtcag gtgcagttag cagcgcttcc 1020
aatccgcaaa agtccccgcc ctcggttcaa ctacttcccg gcttgctgga atcgggactt 1080
caaatcctcc ttttcagcgg agacaaggac ctgatttgca accatgttgg aacggaacag 1140
ctcatcaata acatgaagtg gaacggaggc acgggtttcg agacctcacc tggcgtctgg 1200
gctcctcgac acgactggag tttcgaaggc gagccggcgg gtatctatca atatgccaga 1260
aacctgactt acgtgctcat ctacaacgca agccatatgg ttccctacga ccttcctcgt 1320
cagagccggg acatgctaga tcgcttcctg aatgtcgata tcgcgagcat cggaggcagc 1380
cccgccgact cgcgcatgta cggcgagaag ctgccccaga cgtcgggtggg cggccatccc 1440
aacagcaccg cggcggagga gcaggagaag gagaggatca aggagacgga atggaaagcc 1500
tacgccaaat caggcgaagc cgttctcctc gtcgtcatta tcggtgtatt agtttggggc 1560
ttcttcatct ggcgcagccg ccggcgtcac cagggatacc ggggcgtctg gcataaggac 1620
atgagcggaa gctctgttct cgagcgggtc cacaacaagc gcacgggagg cgcagacgtc 1680
gaagcggggg atttcgacga ggcggagctc gatgaccttc attctccaga cctcgaaaga 1740
gaacactacg ccgtgggcga ggacagcgac gaggatgata tttcacgaca gcattctcaa 1800
caggcctccc gagccggggg cagtcataat ctatcctag 1839

```

<210> 80

<211> 1596

<212> DNA

<213> *Aspergillus niger*

<400> 80

```

atgtttctga tttcacctgc agtgacagtt gcggtgcac ttctgctgat caacggcgca 60
ggagcaactc aatctgaacg aagtcgggct gccgtcatt ttccaaacg tcatccgacg 120
taccgtgctg cgaccagagc ccagtcgagc aacacttccg actaccgatt cttcaataat 180
aggaccaagc cccacttggt ggaaagctta cccgatgtgc acttcgatgt tggggagatg 240

```

```

tactcggggt cgatccctat cgatgacagc aacaatggat ctcgatccct gttttatata 300
ttccaaccta agataggcga accttcagac gaccttacca tttacctcaa tggagggccca 360
ggctgttcct ccgaacaggg attctttcag gaaaatggca ggttcacatg gcagcctgggt 420
acctatgcac ccgtcatcaa cgaatattct tgggtcaatt tgacgaacat gctatggggt 480
gaccaaccag tcggaaccgg attttccggt ggaaatgtta cagccaccaa cgaagaagag 540
attgccgccc attttctcga cttctttgaa aagtttgaag atctatacgg gataaagaac 600
tttcgcattt tcatgaccgg tgagagctac gccggtcgct atgttcccta tatctcgtcg 660
gcaatgctag acaagaacga caccacgctt ttcaatctga gcggagccct tctttatgac 720
gcctgcatcg gccaatggga ctacatccag gccgaactcc ctgcctaccc cttcgtcaag 780
cagcacgctt cactattcaa cttcaatcag tcctacatga acgagcttga aaccacctac 840
gaagaatgcg gctacaaggc ctacttcgat gagtactttg cctttccacc aagcggcatc 900
caacccccaa aatacatgaa ctactccgag tgcgacatct ataacatgat ctactacgaa 960
gcctataacc cgaacccatg cttcaatccc taccgctca ttgatgagtg tccacttctc 1020
tgggacgtcc tgggctggcc gacagacttg gcatacgagc ctgcgcccac cacatacttc 1080
aaccgtatcg atgtcaagaa ggccctgcac gccccatgg atgtggaatg ggagctctgc 1140
agctacgacc tcgtcttcgc tggaggcgac gctgaccgg gtccggagca gcaaggggat 1200
gactcaccca accccaccga ggggtgcctc ccgcgtgtta ttgaggcgac caaccgcgtg 1260
ctcattgcca acggtgactg ggactacctg attatcacca acggcaccct cctcgccatc 1320
cagaatatga cctggaacgg ccagctgggc ttccagtcg cacctgccac accgatcgat 1380
attcagatgc ccgatctcca gtgggttgag atttttgagg cccaggaggg atatggaggg 1440
ctggatggcc ctcagggggg tatgggtgta caacattatg agcgcggttt gatgtgggcg 1500
gagacatatc agtcggggca taagcaggct caggatcagg gccgtgtctc gtatcgccat 1560
ctgcagtggc tgttggggca agttgagatt ctttag 1596

```

```

<210> 81
<211> 1596
<212> DNA
<213> Aspergillus niger

```

```

<400> 81
atgctgtttc gcagtctgtt gtcgacggct gtccatagccg tctcgctgtg cacggataat 60
gcttcagctg ctaaaccatgg tcgatttggc caaaaagctc gcgacgccat gaacatcgcg 120

```

```

aagcgttccg ctaacgccgt gaaacactcg ttgaagatcc ctgtcgagga ctatcagttc 180
ttgaacaaca agactaagcc ttaccgcgtg gaaagcctgc ctgatgttca cttcgatctg 240
ggcgagatgt attccggctt ggtccctatt gagaagggca acgtgtcacg gtcccttttc 300
tttgtcttcc agcccactat tggcgagcct gtggatgaga tcaccatctg gctgaatggt 360
ggccctgggt gcagttccct tgaggccttt ctccaggaga atggttagatt cgtgtggcag 420
cctggaacct accagcctgt tgagaaccca tactcgtggg tgaatctcac caatgttctg 480
tgggttgacc aacctgtggg aacgggatcc tctctgggtg tcccaaccgc tacgtccgag 540
gaggagattg ctgaagactt tgtgaagttc ttcaagaact ggcagcagat ctttgggatc 600
aaaaacttca agatctatgt tactggagaa agttatgcgg gccgttatgt tccttacata 660
tccgctgctt tccatgatca gaatgatata gaacacttca acctaaaagg tgcactggca 720
tatgatccct gtattggtca gtttgactac gtgcaggagg aagcacctgt tgttcccttt 780
gtccagaaga acaatgccct cttcaatttc aatgcaagct ttttggcgga actagagagc 840
atccatgagc aatgtggata caaggatttc atcgaccagt atctagtctt cccagcatcc 900
gggtgccagc cgccaaaggc tatgaactgg agcgatccca actgtgatgt ttatgacatc 960
gttaataacg ccgtcctgga tcccaaccgg tgcttcaacc cctacgaaat caacgagatg 1020
tgccccattc tctgggacgt tcttggattc cccaccgaag tcgactatct ccctgcgggc 1080
gccagcatct actttgaccg cgctgatggt aagcgtgcc aagcacgtcc taacatcacc 1140
tgggtccgag gctcgggtgga gagcgtcttt gtcgggggcg acggcggtcc cgagcaggag 1200
ggcgactact cggccaaccc catcgagcat gtcttgcccc aggtcatcga aggcaccaac 1260
cgagttctga tcggtaacgg tgattatgac atggtcatcc ttaccaacgg cacccttctc 1320
tcgatccaga acatgacatg gaatggaaag cttggattcg acacggcccc cagcaccccc 1380
atcaacatcg acatccctga cctgatgtac aatgaagtgt tcattgagaa cggtatgac 1440
ccacaagggt gtcagggtgt catgggcata cagcactatg agcgtggtct tatgtgggct 1500
gagaccttcc agagcggaca catgcagccc caattccaac ccagagtgtc ataccgtcac 1560
cttgagtggc tgcttggccg gcgggatacc ctgtaa 1596

```

```

<210> 82
<211> 1479
<212> DNA
<213> Aspergillus niger

<400> 82

```

```

atgaaaggtg cggcgctaata tctctcttgcg gcgggcattc cttttgccc tggcctgtct      60
ctccataaac gcgacggggc tgcgctcggt cgtatgccc ttgagcgag gagcgcccag      120
tccttgcaga aacgagattc tacggtcggt gtgactttgc agaactggga tgcgacctat      180
tacgcagtca acctgacgtt aggaacacct gcgcaaaagg tatcattagc tttggacact      240
ggcagcagcg acctctgggt gaacaccggc aactcaactt actgctcaat cgacaatcta      300
tgcaccctt atggcttgta caatgccagc gaatcgctta ctgtaaagac cgtgggcaca      360
cacctcaacg atacatatgc ggacggcaca aacctttacg gtccttatgt gaccgataag      420
ctcagatcg gcaacacaac aatcgataat atgcagtttg ggatcgccga gtcaacgact      480
agtaaacgcg ggatcgccgg cgtcggttac aagatttcga cctaccaagc cgagcatgac      540
gacaaagtct acgccaacct ccctcaggcc ctcgctgaca gcggtgccat taagtctgct      600
gcgtacagca tatggctaga tagtttgag gcgtcgactg gtcctcctt tttcggaggt      660
gtcaatacag ccaagtacaa gggcgatctg cagactcttc cgatcattcc tgtgtatggc      720
aaatactact ccctcgccat cgcccttacg gagctcagcg ttgcgaccga ctccaactcc      780
agtagcttca ccgacagtct cccctctct gtgtcactcg atactggcac caccatgacg      840
gcactgccc gcgacctggt caacaaggtc tacgatgcgc tcaacgcaac ctacgacaag      900
acatacgaca tggcctacat cgactcgac actagagagg cggattacaa tgtaacatac      960
agtttctccg gggcaacgat caccgtgagc atgagtgagc tgattatccc cgcaacggag     1020
ccggggtggc ccgacaacac gtgtgtcttg ggcctcgtgc ctagccagcc gggcgtgaac     1080
ctgctcggtg atacattcct gcgcagtgcg tacgtcgtgt atgatctcga gaacaacgaa     1140
atctctctcg ccaataccaa tttcaatcca ggcgacgatg atatcctcga aatcggaacg     1200
ggaacgtctg ctgtgccagg agccacaccg gttccctctg ctgtctcttc tgcaactgga     1260
aatggactga tctcgtctgg caccgcagtg cccacgctgt cgggtgtcac aataactgct     1320
acagccacag caaccggctc aaccggcact ggctctagcg gtggttcgtc ggctgaagcc     1380
acgagtactt cctcggaggg cgctcgggcg caagctacga gcaaccgat gaacctgctc     1440
ccaggacttg cgggtatcgg cctacttctc gctctgtaa                                1479

```

&lt;210&gt; 83

&lt;211&gt; 1836

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 83

atgctgtcgt ctctccttag ccagggagca gccgtatccc tcgcggtggt gtcgctgctc	60
ccttcgcctg tagccgcgga gatcttcgaa aagctatccg gcgtcccca tggctggaga	120
tacgccaaca atcctcaagg caacgaggtc attcgcttgc aaatcgccct tcagcagcat	180
gatgtcgtg gtttcgaaca agccgtgatg gatatgtcca cccccggaca cgccgactat	240
ggaaagcatt tccgcacca cgatgagatg aagcgcatgt tgctccccag cgagactgcc	300
gtcgactcag tccgcgactg gctggaatcc gccggtgtcc acaatatcca ggtcgacgcc	360
gactgggtca agttccatac caccgtaaag aaggccaatg ccctgctgga tgccgacttc	420
aagtgggatg tcagcgacgc caagcatatt cgtcgtctgc gcaccctgca ataactccatc	480
cccgaagccc tgggtctgca catcaacatg atccagcccc ccaccgctt tggccagatc	540
cagcccaacc gtgccaccat gcgcagcaag cccaagcacg ccgatgagac attcctcacc	600
gcagccaccc tggcccagaa cacctcccac tgcgactcca tcatcacacc gcaactgtctg	660
aagcagctgt acaacatcgg tgactaccag gccgatcccc agtccggcag caagatcggc	720
tttgccagct accttgagga atacgcccg tatgccgatc tcgagaggtt cgagcagcac	780
ctggctccca atgccatcgg ccagaacttc agcgtcgtcc aattcaacgg cggcctcaac	840
gatcagcttt catcgagtga cagcggcgaa gccaacctcg acctgcagta catcctgggc	900
gtcagcgctc ccgtcccat caccgagtac agcaccggcg gacgcggcga actagtcccc	960
gacctgagct ccccgaccc caacgacaac agcaacgagc cctacctga ctctcttcag	1020
ggaatcctca agcttaacaa ctccgacctc ccacaagtca tctctacctc ctacggtgaa	1080
gacgaacaga ctatccccgt cccctacgcc cgcaccgtct gcaacctcta cgcccaactc	1140
ggcagccgcg gcgtctctgt aatcttctcc agcggcgact ccggcgctcg cgccgcctgc	1200
ctcaccaacg acggcaccaa ccgcacgcac ttccctctc aattccccgc ctctgcccc	1260
tgggtaacct ccgtcggcgc aacctccaag acctccccg agcaagccgt ctcttctcc	1320
tccggcggct tctccgacct ctggccccgc cctcctacc aacacgccgc cgtgcaaacc	1380
tacctacca agcacctggg caacaagttc tcggggcttt tcaacgcctc cggccgcgcc	1440
ttccccgacg tctccgcgca gggcgtaaac tacgctgttt acgacaaggg catgcttggc	1500
cagttcgacg ggacgagttg ctccgcgccg acgttcagtg gcgtcatcgc gttgttgaac	1560
gatgcgagac tgagggccgg gttgcctgtg atggggttct tgaatccgtt cctgtatggt	1620
gtcgggaagtg agaaggggtg gttgaatgat attgtgaacg gcgggagtg gggttgtgat	1680
gggaggaatc gggtcggggg cagcctaata gtagtcctg ttgtgccgtt tgctagtggg	1740

aatgccacga ccgggtggga tcctgtgtcg gggttgggaa cgccggattt tgcgaagttg 1800  
 aaaggggtgg cgttgggtga ggagggtggt aattaa 1836

<210> 84  
 <211> 1437  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 84  
 atgtggctct ttctcgtgtg cagtatcctg ctgccacttg gagtagtcaa cgcacagtct 60  
 caatacttca acaacaaaac caaagaattc gtcgtcaatg gctctgctat tccttttgtc 120  
 gatttcgaca ttggcgagtc ctatgcgggc tacctacca acacgccttc tggaatctcg 180  
 agtctatact tctggttctt tccatcttct gatcctgatg cgtctgatga gatcaccgtc 240  
 tggctgaatg ggggcccagg atgcagctct ctggcaggca tcatgctcga gaacggcccc 300  
 tttctatggc aacctggtac ctaccgaccc gtgcgcaacc cttatgcctg gaacaacctc 360  
 acaaatatgg tgtacattga tcagcctgct ggaacgggat tctcgcttgg ccggtctacg 420  
 gtggtctcag aatttgatgt agccagacag tttatggact tctggaggcg gtcatgaaa 480  
 acattcgatc tgcagaatcg aaagatatat ctactggcg agagctatgc gggccagtac 540  
 atcccataca tcgctcgca gatgcttgac caggatgatg atgagtattt ccgggttgcc 600  
 ggcattccaga tcaatgatcc ctacatcaat gagctgccag ttttgcaaga tgttgcgacc 660  
 gtcaatcagc accgctccct ctttcccttt aatgacacct tcatgagtca aatcaccaag 720  
 ctttccgacg attgtggcta cacttcgttt cttgacgatg cccttacctt tccaccccg 780  
 tctcaattcc catcagtgcc ctataatgct agctgcaaca tctgggatat cataaacaac 840  
 gcttctctag ctctcaaccc atgcttcaac cgctaccata tccccgacgc ctgccccacc 900  
 ccctggaacc cagtcggcgg ccccatcggt ggacttggtc cgaccaacta cttcaaccgc 960  
 agtgacgtcc agaaagccat caacgcgtac ccaacggact atttcgtctg caaggatgga 1020  
 atcttcccgga cggccaacgg actggacaca tccccccaa gctccctggg accgctgccg 1080  
 cgcgtcatcg aacagaccaa caataccatc attgcgcacg gcctgatgga tttcgagctg 1140  
 ctggcgaggg gaaccctgat cagtatccag aatatgacct ggaatgggaa gcaggggttc 1200  
 gagcgggagc cgggtggagcc gttgttcgtg ccgtatgggt gatcatcggg aggaggcgtg 1260  
 ctgggaacgg cacatacaga gcgtggattg acattttcga cagtatttag ttcaggacat 1320  
 gaaatcccgg aatatgcacc gggggcggca tatcgccagc tggagttttt gctggggagg 1380

gttgcaatc tgtcgacaat tattgagcag gtgcagataa cagagcagaa tggttga 1437

<210> 85  
 <211> 633  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 85  
 atgtccaaac tctccgctgc tatctccaag ctctccctct ccaccatagc caccactctg 60  
 ctctctctta ccccccaaac caccgcctac ttctacaaat atcccgcctt cttegtctac 120  
 aaagacacca actgcaccga tatctccttc tcacttgtct acccctccct gggtaactgc 180  
 aacggcggat actacgacta cgcgggctca ttccagatgt tcaatatcga tgctgcgtat 240  
 acctgtaatg gcagtgactc gacactgatg tttgagatgt ataatagctc cggtcggat 300  
 tgtggagatg agagtgattt gttgtttaga cagccggtga cggaggagtg tactgttgcg 360  
 gatgtggaga gtccggggcc gttggagatg ccggtttggt ttgagttggg gtcactattg 420  
 gggaattgtg gtgggatggc tgggtactatg ttgttcggtg tggggattct tgagggtggg 480  
 ttagagacta aattatactg gaaatgttat tcatcaaggc tgaatacaag tgtaaccgtg 540  
 cacagattat ctttgatact gtctatgggc tgtacgagcg tctctgactc ctacaatgag 600  
 ttagcggctg cacattacta tgaggacctg tga 633

<210> 86  
 <211> 1827  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 86  
 atgcgtcacc tcttatcact gctgggtgctt ctgatcgcat cggccgcctt ggtctccgcc 60  
 gtccccgcgc gctccattat cactccacaa ccaccgctcg agcccggtca ccttctctct 120  
 tcccagcctt ctgatccccg aaggccatgg atccgcctcc gtgactggat catcgagtcc 180  
 atatggggca tcgaaaaacc cgcattctctg cgattccac tcaacgattc cccgcgcaat 240  
 cgctctcttc cctcccggat tctggcgcg c tacggtagt acgtcgtact tcgtttcagc 300  
 ctgcgcaatc acgatgaggc cgaggcattg gccaggctg cagacattct attcctggac 360  
 gtatgggcgt ctactccagc attcgtatg atccgactgg ccgaggaagt caccgcatat 420  
 actcccctaa tagacaacct ggcagagaga atctatacga cctatccatc taaaaagccg 480  
 ataggacttg aaggacaatc tggatttgcg tcctcgagtc gacctgcgcc aaagttcggt 540



gacctttttt tccacgagta tcagcctttg tccgtcatta tcccctggat gcggctgctg 600  
 gcttccatgt ttccatccca tgtgcgcatg attagcgttg gagtatctta cgaggggtcgc 660  
 gaaattcccg ccctccgact gagcgcaggc agctccaccg cggcgtcagg ccctcgtaaa 720  
 acaatcatcg ttacgggttg tagccatgcc cgcaaatgga ttggcacctc aaccgtgaac 780  
 catgtaatgt acacgctcat taccaagtat ggcaaatcca aggccgttac ccgccttcta 840  
 caggacttcg actggatcat gatccccacg atcaatcccc acggctatgt ttatacctgg 900  
 gagacggacc gactatggcg caagaatcga cagcggacca gcctacgctt ctgtcccga 960  
 atcgatcttg accgcgcctg gggcttcgaa tgggacggcg gtcggaccgc cgetaacct 1020  
 tgttcagaaa actatgctgg agacgagccc ttcgagggaa tggaagcaca acaattagca 1080  
 cagtgggctc tcaacgagac acaaaacaac aatgccgaca tcgtgagctt ccttgacctt 1140  
 cactcttact ctcaacaat tctctacccc ttctcctact cctgctctc gatccctcca 1200  
 acgctcgaga gcctggaaga gctaggcctt ggcctagcca aggccattcg gtacgcgact 1260  
 cacgaaatct acgatgtcac ttctgcctgc gaaggcatcg tcacggccag tgcggcagat 1320  
 aacaaccccg ggcggttctt ccccatgtgt ggcaactccg gtggcagtcg gttggactgg 1380  
 ttttaccacc aagtgcacgc gacttattca taccagatca agcttcgtga tcgcggaagc 1440  
 tacgggttcc tccttcctgc tgaacacatc atccccaccg gcaaggagat ctacaatgtt 1500  
 gttctgaaat tgggacctt cctcatcgga ggcgactcat ttgacgtcga ttgggaatca 1560  
 gaactcttcg atctgtcaaa ggacgaatcc gatctggata gccgctattc aaaatccaat 1620  
 gaccgctccc cggcgtatct acacaacgcc aacggccccc tgcccaacat tgacgaagac 1680  
 gaagataagg aatgggtaat ggtggaggaa gaagactaca cagacgatga cgacgacgat 1740  
 gatgatgatg atgaagaaga ggaagaggaa gaggaagata catattgggc caccgaacac 1800  
 acatacgaat ttcggcgacg acgctga 1827

&lt;210&gt; 87

&lt;211&gt; 1251

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 87

atggccttcc tcaaacgcat tctcccgtg ctggccctca tcttacctgc agttttcagt 60  
 gccacagaac aggtccctca tccgaccatc cagaccatcc cggggaagta cattgttact 120  
 ttcaagtccg gcattgacaa tgcgaagatt gagtctcatg ccgcatgggt aacggagctc 180

cacaggcgca gcttagaagg ccgcagtaca accgaagatg accttccgc cgggatcgaa 240  
 agaacgtaca gaattgccaa ttttgctggg tacgcggggt ctttcgatga gaaaactatc 300  
 gaggagatcc gcaaacaatga ccatgtagct tatgtggaac aagatcaggt ctggtatctc 360  
 gatacgctag ttaccgaaag gcgagctcct tggggactgg ggagcatttc tcaccgtggt 420  
 gggctctagca ccgactacat ctatgatgac agcgctgggg agggtagata cgcttatgta 480  
 gtggacaccg gcatcttggc tacgcataat gagtttggtg gtcgtgctag cctggcatat 540  
 aatgctgcag ggggtgagca cgttgatgat gttggacatg gtacacatgt agcagggacc 600  
 atcgggggca aaacatacgg ggtttcgaaa aacgctcacc tactgtccgt gaaggtgttt 660  
 gtaggtgaat ccagctcgac atcggtcatt ctggatggct tcaattgggc cgccaatgat 720  
 atttgagca agaaccggac cagtaaggcg gcgataaata tgagtcttgg tggaggctac 780  
 tcctatgcgt ttaacaatgc agttgagaat gcttttgacg aggggtgtgt ctcttggtt 840  
 gccgctggaa atgagaatag agatgcagca cggactagcc cggcttctgc acccgacgcc 900  
 attactgttg ccgctatcaa cagaagcaat gcccgctcgt cattctcaaa ctacggctct 960  
 gtggttgaca tttttgcccc gggagagcaa gtactttctg catggaccgg ctggaactcg 1020  
 gccaccaaca cgatctccgg cacgtccatg gctacacccc atgtgacagg tttgatcctc 1080  
 tatttgatgg gcttgccgga ccttgctacc ccagcggtg caacgaccga gctcaagagg 1140  
 ttggctacgc ggaatgctgt caccaatgtg gcgggtagcc ccaatcttct ggcctacaat 1200  
 ggaaacagcg gcgtgtcaaa agggggtagc gatgatggag atgaggacta g 1251

<210> 88

<211> 1368

<212> DNA

<213> *Aspergillus niger*

<400> 88

atgatcacc ttttgctggc cctgttcggc agcgtagtat atgccgctac gcagaccgtg 60  
 ttagggccag agggggctga tccctttacg gtgtttcgca gccacactc accggcattt 120  
 tcaattcgca tccaggagca gaatgactcg atctgtgatg ctcgctcacc ccaattcact 180  
 ggttggtcgc acattggccc gaagcatctt ttcttttgggt attttgaaag ccagaatgac 240  
 cccttccatg atcccctaac gctatggatg actgggggccc caggagactc gagtatgatt 300  
 ggacttttgc aagaagtgg cccttgccgg attaataagt ttgggaatgg aacagatcac 360  
 aaccctggg cctggacca gaattcatca cttctttttg ttgaccagcc agtcgatgtc 420

```

gggttttcct atatcgatga gggctatgag ctgcctcatg actcacgtga agccgcggtg 480
gacatgcate ggttccttgcg attattcata tccgagattt ttcctcacia acagttcctt 540
cccgttcacc ttcccggtga atcttacgca ggccggtaca ttccttatct ggcgacccaa 600
atcttggaac aaaatgaact gtataaagat agccccagga taccgctgaa atcgtgcttg 660
gtgggtaacg gattcatgtc acccaaggat gcaacgttcg ggtattggga aacactgtgt 720
actactaact caggagtccc atctcctatc ttcaatgaaa ctagggtgca tattatggcg 780
gcgaatatgc cgcactgtat ggatctatat gacatatgca ttcaacactc agaccccgcg 840
atatgtcatg cgccccagtc cgtctgttac gatagtgttg tagggctcat ggccaaatta 900
ttgctaagga tgacgacagt cactgcacct tgtgagatcg acgaaatgtg ctatatcgaa 960
gcggctctaa ttgagagata tttgaattcg ccactctgtt gggaggccct gtcgccaccg 1020
caacaggtta ccgaatacaa attcgtcgct acttctgtta ttgatgcatt tgctcaatca 1080
gcggacggca tgggtgctgag ctggaagcag atcgctttct tactcgcaaa taatgttgac 1140
ttcttagcgt atcaaggcaa ccttgatctc gcctgtaata cggctggcaa cctacgttgg 1200
gcgaactcgc tttcttggaaggccagaca gaatttaccg caaagccctt acttccgtgg 1260
gaaattcagg ttccggtcgg tgaaggagc gacgaaacgt cacgctttgc ctttgtgact 1320
gtggacaacg ctggacacct gttgcggggac tcaaagattt caaactga 1368

```

<210> 89

<211> 2376

<212> DNA

<213> *Aspergillus niger*

<400> 89

```

atgcgggtttc tcacttatct cctgcccttc attgcaagtg ctatctcgct ctttggggtc 60
aatgtacaag ctcgatcaca agctccaagt gccatccgtc atgtgtcgac gcttgaccag 120
cccaccatca agacaccctc acagcgggtc gatcaccttg accactttga catcaccttc 180
aatattcatg acaagcacca gcggataaag ctggagctgg agcccaacca tgacatcctg 240
gcggaagacg catccgtaca gtatctcgac gcggacggga acgtgcgacg gcacgagccc 300
attgctccac atgagcataa ggtcttcaag gggaggagtc tactcgggag aggaaaaggc 360
atgtgggatc cggtcggatg ggcgcggatc tacttgaagc aggatggctc agagccacta 420
tttgaggag tcttcagtat cgacggcgac aaccatcacg ttcagctgaa atcggcatac 480
atggagaaga aacgccccgt ggatgtcgac cttcccgaact cagcgactga ctatatgatc 540

```

ttctaccggg attcggatat ggtgcgtcta catacggaac tcaagcggtc gtcgctcgga	600
tcgacctcgt gtcaagccga tcagctcggc ttcaacta accccaacca ccctgtgcta	660
caaccgtatg gccaggcaga gaccgatacg tggggagcaa ttctattgaa ctctttgttt	720
ggactcaaca agcgccaatc cgatatcgga agtgtgtctg gcaatgcggg cggagtcaat	780
ctggcgctga ccattggtga tacttcgggc tgtccgagta cgaagcaagt agctttgatt	840
gggtgtgcaa cggactgcgc ctttaccggc tcattcaaca acgagactgc cgccaaggaa	900
tgggtcatca gtactgtcaa cagcgcgctc aatgtctacg aaaagtcctt caacattacg	960
attgggctgc ggaatctgac taccacgac agtcatgcc ccgacaacc gcccgcgcc	1020
acggcatgga acatgcctg ctccagcggc aatctcacct cccgactgga tctgttttcc	1080
aagtggcgcg gtgagcaatc ggatgacaat gcttattgga ccctgatgag cgattgcgcg	1140
acgggcaacg aggtcggact gtcattgctt ggccaactct gcaatagcga tgcctcttcg	1200
gatggctcga gcacggtcag tggaactaac gtcgctcgtc ggtcttccgg ctccgattgg	1260
cagatctttg ctcatgaatc tggccacacc tttggcgctg tccacgactg tgactcccag	1320
acctgcggcg aggatctcga agcctcgctc cagtgtgtgc cgttgacctc gagcacctgc	1380
aacgccaacg ggaaatacat catgaatcct acaactggaa cagacatcac tgcgttctcg	1440
caatgcacta tcggaaatat atgcgagcc ctgggccgca acagcggtta gtccagttgt	1500
ctctccgcca accgcgacgt caccacctac actggcagcc agtgcggcaa cggaattgtc	1560
gagtcggcg aagactgcga ttgtggcggg gaagatggtt gcggcgacaa caactgctgc	1620
gacgcgaaga catgcaagtt caagtcggga gctgtgtgtg atgactcaa cgacagctgc	1680
tgttcaagct gccaatctc ctacgctggg acggtatgtc gtgccagtcg cggcgactgc	1740
gacgtggcag agacctgcag cggcaactcc agtacttgtc ctaccgactc gttcaagaag	1800
gacggcacga gctgcggcag cagtggctcg ggacttgct gcgctagtgg ccaatgcacc	1860
agccgcgact accagtgcg cagtgtgatg ggcagtctcc tccacagcaa cgacacctac	1920
gcctgttct ccttcagttc ctctgcgaa ctggtctgca cctccccgaa gatcggcacg	1980
tgctacagcg tcaacaaaaa ctctctcgac ggcaactcct gcggtagtgg cggctactgc	2040
agcaacggcg actgcaaggg ccaaaacgtc gaatcctgga tcaagaacca caaaggatc	2100
gtcattggtg tcgctgcgc cgtaggcgcc ctgaccttt tggccctgat gacctgcatc	2160
gtaaaccgct gtcgccccg tcgcgcgcca aaaccgtcc cgcgtccagt gccttacggg	2220
ccgtggcccc gcgctaggcc tccccgccc ccgcccata accagtggcc ggcgcgaggc	2280

tatcaaggct tagggaatga gccgccgccc ccgtatccag gtgtacctgg tcagccagta 2340  
 ccgcaacata tgcctcccca ggggcggtac gcttga 2376

<210> 90  
 <211> 1446  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 90  
 atgcgtttcc taagcagtgc agccctattc ggcttggcgt atgcctccac ccaggcggtc 60  
 ctccagccag aggaaccatc cgacttccgt acattccaca gcccatattc cccgcaccac 120  
 tcgatccgca tccgccagca gaatgaatca atctgcgctg cccattccgc ccaatacacc 180  
 ggctggctcg acatcgggccg taaacatctc ttcttctggt actttgagag ccagaatgac 240  
 cctgccaatg atccccctac tctctggatg acaggagggc caggggggtc cagcatgac 300  
 ggtctgtttg aagaagtcgg gccatgtctg atcaatgagt acggcaatgg cacttactac 360  
 aatccgtggg gctgggtccc gaactcctcc ctactatttg tcgatcagcc agtcgatgtg 420  
 ggattttcgt acgtcgtatga aggagaggac ctgccgggcg attcgcacatca agctgcaatt 480  
 gacatgcacg ggttcttgca gttgtttgtc tcggagggtt tcccgcaatt gcagactctt 540  
 ccggttcacg tttctggtga atcgtatgct ggtcactatg tcccttacct cggcagtcag 600  
 atcgtccaac agaacaagct ctatcccact gagccccagg tccctctgca ctcatgtctc 660  
 gtaggcaacg gctactattc tcctcgcgac actacctacg gctactggga aaccctctgc 720  
 accactaacc ctggagtccc cgagcccgtc ttcaaccgaa ccagatgcga catcatggcg 780  
 gccaatatgc cgcgatgcat ggaagtatcc gacgtatgtg ttcggaaccc cgatccagct 840  
 atctgccatg ctgcgtcgga ggtatgtac gagggcgtga tcggatggta tgatgacgag 900  
 tctggtgaag gtggtcgga taggtttgat ataaccgctc cctgcgccct tgacggcata 960  
 tgctacatcg aggccgctcg catcgagcag tacctgaaca caccgcagc ttgggctgct 1020  
 ctatcaccac ccaaagaaat caaagaatac aaggttactt ccgacaatgt gtcgcgcgca 1080  
 ttcgatctca cttcagacac gatgacgcca gcgtctgagc aagtcgcgtt cctgcttgcg 1140  
 aatcaggtag atttctggc gtatcagggc aatctcgatc tggcgtgtaa tacggcgggt 1200  
 aatctgcgct gggcgcatc tctgccatgg agaggtcagg tcgagttcgc gtcgaaggcg 1260  
 ctgcggccat ggagttgggt agatgtggta tctggaaaag gtggagtggc tggaacgacg 1320  
 aaggaggagt cgaggtttgc gctagttacg gttgatgggg cgggacattt tcttcctcaa 1380

gatagacctg atatcgcggtt ggatatgatg gtgcgctgga tatccggggc atcgtttact 1440  
gagtga 1446

<210> 91  
<211> 960  
<212> DNA  
<213> *Aspergillus niger*

<400> 91  
atgacattgt tactcaactt ccacgcgctc ttacagtc tttctgttgc caatctttca 60  
accagatgca ggcactgct ctctggacgt gacttttctt ccacgccagc gcccggtgag 120  
tactccgag cggagcatag gaggtgtat gatgtacagg cccaacgtga cagcaccgcc 180  
gaggagagcc gggaggtggt gccttggtt gaaatcgaga catgggttca tattgtaagc 240  
agcaatgaag cagcaaacac agtatcagac gacatgatca ccagccagct ttcctatctt 300  
cagaaggcat atgaaagtgc gactatcacc tatcggttgg agggcataac tcgtcacata 360  
aatgactcgt gggcgcgaaa tgatgatgaa ctggggatga agaatgccct acgaaggggc 420  
aattatggca cattaaatgt ctatttccaa acagatctcc aggcgtcatc cgacgagaat 480  
tctcgggact atccaaatga cggtaacgga cgaacagatg tgcagatca atcatcatca 540  
actgtcctag gcttctgtac gttgcctgac ccgagtgtga attccagcag ccctcgttcc 600  
agctacatca aggatggttg taacgtgtta gcggatatca tgccgggtgg tagtttagcg 660  
cagtacaaca aaggcggcac agcgggtcat gaggttggcc attggaatgg gctgctgcat 720  
acgttcgaag gtgaatcgtg ctcccctgat aatgaaggag attacattga tgacaccccg 780  
gagcaatctg agcctacgag cggatgtccc gccgagaaag attcatgccc cgatcttccct 840  
ggccttgatg ctattcataa ttttatggac tattcatctg atgactgtta tgagagtttt 900  
actccagatc aagcggagag aatgaggagt atgtgggtccg ctatgcggga agggaagtga 960

<210> 92  
<211> 1920  
<212> DNA  
<213> *Aspergillus niger*

<400> 92  
atgcatgtct cacttttccct actcagtgtt acggcagcgt ttgccagccc aacaccccat 60  
aactatgttg ttcattgagcg gcgcgatgca ttgccagtg tctgggtaga agaaagccgg 120  
ctggacaaaag gtgccctact gcctatgcgg atagggtta ctcagtcctaa cctggatcgt 180

ggccatgatt tattgatgga ggtgtctcat ccacaatcgt ctcgctacgg aaagcatctc	240
tccagcgagg aggtgcacga cctatttgcc cgcgcgaatg aggccgtcga gaccgtccga	300
acctggattg aatccgccgg aattgctcca agccgcatct cgcaatcata caacaagcag	360
tggctacagt tcgatgcccc tgcaagcgag gttgagcagc ttctgcagac ggaatactac	420
atctacaccc atgccgacac gggaagtcc catgtgacat gccacgagta ccatgtgccc	480
gaaaccatcc aatcgcacat cgactacata acaccaggag taaagatgct ggaagtgcgc	540
ggcacgccct ccaaaaagag agatgcagag aagcgctctc ttggcagtct gccccaatc	600
ttagcaccac taccaatcaa tatcacgaag attttcgacg acccgctagc aactgcgat	660
ctggcggtaa cccagactg cattcgagcc atgtacaaca tcaccaaagg aacaacagcc	720
acaaagggca acgagctcgg catcttcgag gacctaggag acatctacag ccaagatgac	780
ctcaaccttt tcttcgcaa ctttgccagc gacatcccac agggaacca tccaacctc	840
gactccatcg acggcgccac cgcccaaca gacgtacca acgcccggcc cgaatccgac	900
ctggacttcc aaatcgcta ccaatcatc tggccccaga acaccatcct ctaccaaacc	960
gacgaccca actacgaaga caactacaac ttcaaaggac tcctcaaca cttcctctac	1020
gccatcgacg gctcctattg caacgaaacc tcctctctag accctcaata ccagatccc	1080
tccccaggcg gctactctc cccaagcaa tgcggcgtct acacccccac aaacgtaatc	1140
tccatctcct acggcgagcc cgaagccgac ctccccatcg cctaccaacg ccgccaatgc	1200
cacgagttca tgaactcgg ccttcagggc atcagcgtgg tcgtcgcac gggcgactcc	1260
ggcgtcgcct ccagcacggg c'acctgcttt ggcgatgcag acaacgtctt cgtcccagat	1320
ttcccagcca catgtcccta tctcacgca gtaggaggca catacctccc cctaggcgca	1380
gacgcagcca aggaccagga aatagcagtc acccgcttcc cctccggcgg cggcttcagc	1440
aatatctacg cccgaccatc ctaccagaac cactccgtgg agacctattt ctccactacc	1500
agcgacgacc tcacctacce ttactactcc ggagtaaact acacagactt ctccaacaca	1560
gatggggtat acaaccgcat cggacgagga taccctgatg ttccagctat cgcagacaat	1620
atcatcatct acaaccaggg cgaagcgaca ctgggtgggtg gtacgtctgc cgcggcggc	1680
gcgttcgcgg ccatgttgac gcgcattaac gaggagaggc tggcgaaggg gaagtccacg	1740
gtggggtttg tgaaccgggt gctgtatgaa catcctgagg cgtttaggga tgtgactgtt	1800
gggtcgaatc ccgggtgtgg gactgatggg ttcccggttg ctgggggggtg ggatccgggtg	1860
acgggggttg ggacgccgcg gtttgaggat ttgatggata tatttgtggg tgatgattga	1920

<210> 93  
 <211> 1116  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 93  
 atggcctcca agaccctcct actcattccg gcaactggcca cagccgctct gggaaagtga 60  
 ttggacctag atatcaaggt agaccttgga accccagggtg gcccgtttga tttgatgtac 120  
 gacaccggat catcaacact ctgggtgctt gatagcaatt gtacagatga ttgtccaaat 180  
 gttagcgggt actcccgaca cggtacaaac ctcacctcta ctggtgtcaa cttagggtgtc 240  
 aacgacagca ttgcttacag cggaggcact gtcagcggct tcaactgccac ggatattctc 300  
 acggttcccg acaccaacgt ctcatatcgc cagagctttg ccgtcattac cgacagtacc 360  
 tgggcggcct tagcagccga tgggttcata ggcctggcat cgtctacat cgcatccaag 420  
 aatactacga cagccgtcga acagatgatg caggatggac ttttggatga acctcgattc 480  
 gccatatatg cagggttcagg ggaatcgacc gtgaccaacc ctaatccgga gaataatggc 540  
 gtgttcacct ttggtggcag ccatgaggaa acctatgcgg acggggaact gcaatggatg 600  
 aagatgctct ccccttttga aatatacaaa acaaactctc ttggaattca gggacacaac 660  
 aactccgatg gccaggccct gtcaagcgac gtcctgaact ggtacggcca gactaatcta 720  
 ttcaacgtcg cagggtgctt atcgataagc attcccaacg accagattga ggcgatgtat 780  
 gccctaacgc ctttctcata cgctgacatc tcacttggat accgacctct gtgctccgat 840  
 ttcaatgata catggctgat ctcttttaca atgggcttct atggcgaggg tgtcaccttc 900  
 aatttgaccg gtgatcagct ggccgtgcct ggctatcagg acgacgacca ctgcttcctc 960  
 cccttcaatc catgggacag ctacaacacg attattgggtc agcattgggt gagcaatttc 1020  
 tatgctgtat tcgacttcgg atcattcgac ccggagacat acgatatacg tgttgggctg 1080  
 gtccttttga agaaggaata cctgccgagc gcttga 1116

<210> 94  
 <211> 1245  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 94  
 atgtttccct gctctcgtat ttggtctctg ctcgttgca cgcaccgc tagtgctgta 60  
 cccaccagtc tggccaccac gcacctgcaa tcggttgact tgcttctgac tcgcagttct 120



tacgggtttc ttactgacat agcccttga actccgggtc agagcctgcc gtatctggtt	180
gactggacct ggaccggcca ctatgtggtg accaccttgt gctacaacga tcccaccgcc	240
acctacgatt gtctcaacgt cgatcagaaa attttcaacc agactttgtc atccactttt	300
atcaacaaa ctgaccagta tggctatctt tactgggata ccaaccactt ctactttacg	360
gagcccgag cagccgatgt ggcgacggac atgctgcgca tcggtccac cgcggtgaac	420
accaccatcc aagcagccaa tttcgtcttc aacgagacta ttagcgcatc ccctttctcg	480
ggagtatatg gactctcacc tgtttttcag ggtgacaatc gatccgtgca agcgtccttc	540
taccaaggat ggaggagcgg cgctggcac tctccaattg tctcttttat ctactgccac	600
gacaatgcca ccaaagcggg atgcagtggg tacgacggcc ttcagacact aggcggatac	660
aacacctctc acgtccaggg agatatcacc tggtagcaca tcattgtcac ggagggcgtc	720
aacacgctgg actttgtcta tgcgccagcc gtgattaatt attgggcgtt gaacctcacg	780
cgcttctcta tcggagacga agagcaagag ctcaacaaga ccactactct ggatggaaag	840
caagccgccc ttgccgcgtt cgaccacgct tcgtatgggc gcggtgcccc agtgtctgtg	900
tacggttacc agcgtctagt cgagctgggc ggggcaaaag ccgtcacgct ttccgatcct	960
caaataacg gtgagcaggg attctatcag ttcgattgcc ggaactcgag ttacttgcca	1020
ccgtgcggt atgagtttgc cgggtcagag cgggcgtggg agattgtgcc cgagaactat	1080
gtggagggtg tggcgaacgg aaccaataag tgcaccttta atgtacgcac cctgggagat	1140
ggagcgatgg taatgggaaa ttttggcgag acatttgcca ttgataagta tgtcatgttt	1200
gactttgaga agttgcaggg ggggattgca gacttcgcgt ggtaa	1245

&lt;210&gt; 95

&lt;211&gt; 1443

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 95

atgcatctcc cacagcgtct cgttacagca gcgtgtcttt gcgccagtgc cacggctttc	60
atcccataca ccatcaact cgatagctcg gacgacatct cagcccgta ttcattagct	120
cgtcgtttcc tgccagtacc aaaaccaagc gatgctctag cagacgattc cacctcatct	180
gccagcgatg agtcctgtc actgaacatc aaaaggattc ccgttcgtcg tgacaatgat	240
ttcaagattg tggtagcgga aactccctct tggcttaaca ccgccgtct cgatcaagat	300
ggtagcgaca tttcatacat ctctgtcgtc aacattgggt ctgatgagaa atctatgtac	360

```

atgttgctcg acacaggcgg ctctgatacc tgggttttcg gttccaactg cacgtccaca 420
ccctgcacga tgcacaatac cttcgggttcg gacgattctt cgacccttga aatgacatcg 480
gaagagtgga gtgtgggcta tggaactggg tctgtcagcg gcttgctagg aaaagacaag 540
ctcagcattg caaatgtcac tgtacgcatt actttcggac ttgcttccaa cgcacggat 600
aacttcgagt cgtaccaat ggacggcatt ctcgggtctcg gtcgaaccaa cgatagttcc 660
tacgacaacc caacattcat ggatgccgtt gcagaaagta acgttttcaa gtcgaatac 720
gttggttcg ccctttcacg tagccccgcc aaggatggca cggtcagctt tggcactact 780
gacaaggaca agtacaccgg cgatatcacc tacaccgata ccgtcggatc ggacagctat 840
tggcgcatte ccgtggacga tgtctatgtt ggcggcactt catgcgattt ctccaacaaa 900
tcagccatca tcgataccgg aacttcttat gctatgctgc cttcaagcga ctogaagacg 960
ctgcacagtc tcattcccgg cgccaaatct tcggggagct accacattat tccgtgcaac 1020
acaactacta agctacaagt ggcattctct ggtgtgaatt acaccatctc gccgaaggac 1080
tacgtgggag caacttcagg ttctggatgc gtttcgaaca ttatcagcta cgacttattt 1140
ggtgatgaca tctggctcct ggggtgacacg tttctcaaaa atgtgtatgc tgtgtttgac 1200
tacgatgagt tacgggtcgg atttgacagag cgttcctcga acaccacctc tgcgtcgaac 1260
tctacgagct ctggaacaag cagcacctcg ggatccacta caacgggcag ctcaacgact 1320
acgacgagct ctgctagctc tagtagttca tctgatgctg aatcaggaag tagcatgacc 1380
attcccgtc ctcagtattt cttctctgct ctggcgattg cttccttcac gctttggctc 1440
tag 1443

```

&lt;210&gt; 96

&lt;211&gt; 1401

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 96

```

atgacgtctt ctaccttgcg ccttgccgtc gcgttggtt tgtcaacttg cagcagtgcc 60
ctatcgagcc agcgagatga ttcacttggt gttccatttc cttttggcaa tcttgaggat 120
gtccatattg ccaagcggga tagctccaag acagtagaag ctctctagt gatatatggc 180
gacagctact ggatgaacgc ctcaattgga acccctgcgc agtcactaag ttctactacta 240
gatcttacgc gctcaagggt cgagcccgcac tacaccctcg atgagaatta cgaatgttct 300
gacgatgaac tctgctccga attcggcttc tacaaacca ccgattcatc cacttatcag 360

```

catctcacct acacacagag acacgatgca ggtgtcgact actcctacct tgataccata 420  
 actcttggag atcacgcaac cgacaatgtc ccactggaca tgtatctttt gtcctacatt 480  
 tectacagct cctcgggtct ctctccgtc aacaccagct tcccctacat cctggtcgat 540  
 cgcggcctca ccacctcccc atccttcage ctaatcggcg acaacggaaa caccaccacc 600  
 ccagcatca tctttggagg catcaacacc tccaaattca acgggcccct gcaagccttc 660  
 tccttcgag accacagcat caccaacaat ccattcgta ccgtcgaagc tgactccctc 720  
 caactaacca ccaacaccaa cgataattcc acctacccta ttccctcctc caccctcatg 780  
 atgtcagaa ccgaagaact aatcacctac ctcccaact cgaccgtcca atccctctac 840  
 accgacctta acataaccat ggacggcggtg atctccactt caagattcta cggggtcctt 900  
 ccctgcgccc gccaggaaac cgaatctcac acaatctctc tagccatcgg caacatgacc 960  
 ttctctgtgt cctgggatga gctcttcgtc ccgtggacgc gtgacggact atgcaagttc 1020  
 ggcattcagg ccagagattc agattacaaa actcgtgcgg agctgggtgt tccctttctg 1080  
 agacggatgt atgtcgtgt ggattataat aatcagtttg tgggcgttgc gacgctgaag 1140  
 gatgatgatg atcagaatgg aggtgaagat gagattgtgg agattggcac tgggacggcg 1200  
 ttgcctagtg ctgtcgggga ttggccggt agtggtacgg cgtatacgcc tgctgcttct 1260  
 acagggacgg cggctgcgac gttgacattc acgacggcga cgtctagcgg gggaggtgtg 1320  
 gtgccgacgg gtctatcaga gttgggtagg gcgtttttgg tgccgggggt gctggggatg 1380  
 gctgttttgc aggtgttta g 1401

<210> 97

<211> 1632

<212> DNA

<213> *Aspergillus niger*

<400> 97

atgatgcgac cgatacttct cccctactg ggggtatttc tgcagacctc ctcggcaccc 60  
 aatccctatg taatgagctg gtcttcccaa gcctacggtc cagatggccc gtggcaggcc 120  
 gtatccatcg acgtgggcag caaccagcag acggtcgatc ttatccccgg agccaactat 180  
 gctagcacga tctgatgag cactctctgc acgaacaaaa cctgtcatc cacctgctac 240  
 gctgccgaag caggcacgtt caaccaaacc acctccacca ctgcctacac caccgccagc 300  
 tcgtgggaaa caacttactg ggccgtcgag ggtggaagcc aagaggctgt gctcggcgat 360  
 gaggtcacct tagggtcgtt tgctgtcccc aatgtgagct tcgaagccat ctaccagacc 420

```

taccagacct atcccaatgg catcgccctat cctgtctcgg tcggcagttc ggccctgggg 480
ggtcctgtact tgtcggatac cgtctccaat tcgacgggtcc tgaacatgat cgcaggatgg 540
ctttactcgt ccaacgacat tccgtcctac tcgtacggca tgcataatcgg gtcggtagac 600
cccaaatcc caggctccct gatcttgggg ggctacgata agagccgagt gatcggagac 660
gtgagtgcgc agggagtagt gtcttcgagt ggtcttttgg aacttgaatt aaaggatatt 720
gggctgggtg ttgcgggcggg ttcctctccc ttcagcttca acaacgaaag tggcttgttt 780
ctccaaagca gtggttcggt tcaggccaag accgtccaga ttgatccaac caagccctac 840
atgtaccttc cccaggcgac atgcatgcc atcacctcca ccatgccgat ctccctcaat 900
tccagcttgg ggctatactt ctgggacacc acgagcgatg attatctgaa tatcacgtct 960
tccgcgcgat acctctcctt tgtgttcaac atgaatgggg tcaacaacaa gaacattacc 1020
atcaagattc ccttttccca gctcaatctt acgctgcaag aaccgctggg cgatcaaac 1080
gtcacctact tccgtgctt cctcactacc tccaccccgg tgctcggtcg agcctttctc 1140
cagtcgcgat tcgttggggg gaactggttc aacgggaaca actcgggcac atggtttctg 1200
gcacaggccc cgggcccggg ttacgccagt gaagacatca eccggatcgc agtgagtgc 1260
acgtcgcttt ctgcctctaa cggctacctg gaagagacct gggctacgta ctggggcatc 1320
aaaacatccg acaactcgag cagctccaag agtggcctgt cttccggtgc caaaattgga 1380
attggcgctc ggggtgggtg cgggtggagca gtgttgatcg cagcaggat agccattgca 1440
ttctgtcttc gccgtcgccg cggggcgagt caagaggcgg ctggagagca acggaggctc 1500
atgttttagg gctttgcgga gctaccggga ggtgctcaca gtgaaccggc gaaggagtgt 1560
gatacgaaga tgcataagcc gccgcaggaa atgatggctt cgcaggaggt agagcgatac 1620
gagctggggg ga 1632

```

```

<210> 98
<211> 2535
<212> DNA
<213> Aspergillus niger

```

```

<400> 98
atgcgtctta cagggtggtg cgctgcggct ctgggcctct gcgctgctgc ctccgcttct 60
ctccatcccc atcgttccta cgagacccat gattacttcg ctctacacct tgatgaatcc 120
acctcgccgg ccgacgtcgc ccaacgacta ggtgctcgcc acgaaggccc cgtcggagaa 180
ttaccctcac atcatacctt ctcgataccc cgtgaaaaca gtgacgatgt ccatgcgctg 240

```

ctggatcaat tgcgcgatcg tcggagggtta cgccgccgct ccggagatga cgccgctgtc	300
cttccctcct tggtcggggcg agacgaaggt ctaggtggca ttctttggtc cgagaagctg	360
gtccccaga gaaagctcca taaaagagtg ccgccgacag gatatgctgc cagatcgccc	420
gtcaacactc agaatgacct ccaagcgctt gcggcgacaga aacgcattgc ctcggaattg	480
ggcatcgcgg accccatctt cggcgaacaa tggcatttgt ataatactgt tcagttgggc	540
catgatctta acgtgacggg tatctggctg gagggcggtta cagggcaggg tgtcacgacg	600
gctattgtcg atgacggttt ggacatgtac agcaacgac ttaggccgaa ctattttgcg	660
gcgggttctt atgactataa cgacaaagta ccagagccga ggccgcgctt gagcgatgac	720
cgccacggta ctagatgcgc gggtgaaatc ggtgcggcga agaacgacgt gtgcgggggt	780
ggtgttgctg atgatatgct catcgctggg attcggattc tctccgcacc cattgatgac	840
actgatgagg ctgcggctat taactacgcc tatcaggaga acgatatcta ctcggtttcc	900
tggggtcctt atgacgatgg cgccacaatg gaagccccgg gcaccctgat caagcggggc	960
atggtcaatg gtatccaaaa tggtcgtggg ggaagggtt cggtttttgt gtttgcggct	1020
ggtaacggtg ccattcatga cgataactgt aactttgacg gttacaccaa cagtatctac	1080
agcatcacgg tgggtgccat tgatcgggag ggtaaccatc ctccgtattc ggaatcctgc	1140
tcggcgcaac tgggtggttg ctacagcagc ggcgccagtg atgcaattca taccacggac	1200
gtcggcacag acaagtgtc gactacctat ggtggaactt cggcggccgg cccgctcgct	1260
gcgggaaccg tggcgctggc cctcagtgtg cggccggaac tcacctggcg tgacgttcag	1320
tatttgatga ttgaggcggc agtgccctgt catgaagatg atggaagctg gcaggacact	1380
aagaacggga agaagttcag ccatgactgg ggatatggta aggtcgacac atatacgctg	1440
gtgaaacggg cagagacctg ggatctggtg aagcctcaag cctggctcca tccccctgg	1500
cagcgggttg agcatgagat ccacacgggc gagcagggtt tggctagttc gtacgaggtg	1560
acggaggata tgttgaaggg agccaacctg gaacggctgg agcatgtcac ggtcaccatg	1620
aatgttaacc acaccgccg aggcgatctc agcgtggagt tacggagccc tgacggtcgg	1680
gtcagtcacc tcagtacgcc cggcgggcca gataatcaag aggtgggcta tgttgactgg	1740
accttcatga gcgttgctca ctggggcgag tccgggattg gaaatggac tgtgattgtc	1800
aaggacacca atgtcaacga gcatactggg caattcatcg attggcgact caacttgtgg	1860
ggcgaggcga ttgacggagc cgagcagcct ctccacccca tgctactga acacgatgac	1920
gaccacagct atgaggaagg aaacgtggct accacgagca tcagcgccgt tcccacgaaa	1980

accgagctgc ctgacaagcc cactggtggc gttgategcc cggatgaacgt taagcctaca 2040  
 acatcccgga tgccgaccgg tagtcttaca gagcccatcg atgatgaaga actccagaag 2100  
 acccctagta cagaggcaag ctcaacacca agtccttctc cgaccaccgc gtcagatagt 2160  
 atcctgcctt ccttcttccc cacgttcggt gcgtcgaagc ggacgcaagt ttggatctac 2220  
 gctgcgatcg gctccatcat tgtgttctgc attggcctgg gcgtctactt ccatgtgcag 2280  
 cgccgcaaac gtattcgcga cgacagccgg gatgactacg atttcgagat gatcgaggac 2340  
 gaggatgagc tacaggcaat gaacggacgg tcgaaccggt cacgtcgccg gggaggcgag 2400  
 ctgtacaatg cttttgcggg cgagagcgat gaggaaccgt tattcagtga tgaggatgat 2460  
 gaaccgtatc gggatcgggg gatcagcggc gaacaagaac gggagggcgc agatggagag 2520  
 cattctcgga gatga 2535

<210> 99  
 <211> 450  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 99  
 atgaagacct tctctaccgt cacctctctc ctccgtctct tctctcggc tctggccgca 60  
 cccgttgaca gcgctgaagc cgccggcacc accgtctctg tctcatacga cactgcctac 120  
 gatgtctctg gagcttcctt gaccaccgtc tcctgtctgg acgggtgcaa cggcctgac 180  
 aataagggct actccaactt cggtctccct ccgggcttcc ccaagattgg aggcgcccct 240  
 accattgcag gctggaactc tcccaactgc ggcaagtgt acgccctgac gtacaacggc 300  
 cagacagtca acattctggc cattgattcc gcacctgggt gcttcaacat cgctctggag 360  
 gccatgaaca ccctaccaa caaccaggcc cagcagctgg gtcgtatcga agctacctat 420  
 actgaggtgg atgtcagtct ttgcgcataa 450

<210> 100  
 <211> 891  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 100  
 atggctcaaa tattctggct ttcaactctc ctgcttctct cttgggtcag agccgagtcc 60  
 aaccgcaccg aggtggacct gattttccca agaaatgata cctttgcgcc aatgcctttg 120  
 atgccggttg tattegccgt tcaagcccct tccgtcgccc ataaagttaa tacatacatc 180

gagtacggct attaccaggt aggccgtcca aatgaaacag ttattggcca gaccgaccat 240  
 gtgtccgact caacaaacga aaccacttat ttcagtgtct ctggtatcgg cagaacgttc 300  
 aataccactg gcagctggga gctgttttgg aggctgagat ggaccaattg ttcaatctca 360  
 gaagactcga gatactacaa ccaatcctac ccctggatat cctccccata catcgacggg 420  
 agcctcaaca tcgacaaggt ctatgagggc tttcactaca cagcatacaa tgtcattgtc 480  
 gacaggggta ccttcagcac tcgcaagat gctagccaac ccaacctcac gacctcacc 540  
 aatagcgaga actgcgataa agtctcgtct cttgctctat tgtcgattgt ggactcccta 600  
 aggattccac ccagttacc ccaagaagat attgataccg tgtcaatgtg cccacaactc 660  
 gccgatgcca ggctaaattc aacttcaact tcaagccct gcagcggttag cattagtccc 720  
 gaggttgagt ctaatatcct ggccaagatc gcagacaatg aatgcaataa cgcacttcac 780  
 cccgctgtga gttgcaccac tgaagaaacc aaggaaggca gcgcgagcag ccatgaccac 840  
 ggccatgctg tatggcttgt cattacgcta gcttttgcct tccttttcta a 891

<210> 101

<211> 933

<212> DNA

<213> *Aspergillus niger*

<400> 101

atgggtggc gagatgtcgc cattctcagc aggcactttg ctgtgacatc ctcacaaagt 60  
 gttaatggcg ttgtctctgg gatgttccaa cacacagtca cctcttcacc cagcttcact 120  
 accaaccaat tcttcaagaa gaagttcact gctgcaattg ctactgccat tttecgcaagc 180  
 gttgccgtcg cagctcccca gcgtggcctc gagggccgcc tcaaggcccg cggcagcagc 240  
 aagggatccc gacctcca ggcagttgct agacctgcat caaccaagaa ccagaccaac 300  
 gttgagtaca gctccaactg gtccggtgcc gtgctggtgg agcctccctc tgetgcagcg 360  
 acctacactg cggtgaccgg caccttcact gtccctgagc ccaccggcaa ctctggaggc 420  
 agtcaggctg catctgcctg ggttggtatc gacggtgata cctatggaaa cgccattctt 480  
 cagaccggtg ttgacttcac cgtgaccgac ggagaggcct cgttcgatgc ctggtatgag 540  
 tggatcccg attacgccta cgacttcagc ggcacgcaca tctcggcagg cgatgagatt 600  
 gttgccattg tggagtccta cacctcgact accggtattg ccattattga gaacaagagc 660  
 accggccaga aggtgtccaa ggagctgtcg tccagctcca gcctcgggtg acagaacgct 720  
 gagtggattg tggaagactt cgaggaaaat ggttcgctcg tcaacctggt ggactttggc 780

accgtcacct tcaactggtgc tgttgccaag gcggcgggtg gtgagagtgt tggacttacc 840  
 gatgcgacca tcatcgagat tgaggagaat ggccagggtg tcaactgacgt taccatcgac 900  
 agcgactctg aggtgacat cacctacgag taa 933

<210> 102

<211> 2046

<212> DNA

<213> *Aspergillus niger*

<400> 102

atgcgctgct ccctcatctc ccttctaggc ctggcggcca tcccgccct tggaggctgt 60  
 cccttcgcac aactgcgaa catgggcatt gataacatgg tgaaagcaca cgctcacatg 120  
 tcccgaccgt tgattgcctc caagagcagc cctcaactg ttctacctc ctctagcacc 180  
 ccttctgtcg ggcagaaagg cgtgttcatg atgaaccgca ttgctcctgg cacatccgag 240  
 ctctacattg ccaacacaga tggcagtaat gaacgccac tcctctcaa cccgctctac 300  
 gagtaccatg cctccttctc cccggatgta gaatggatca ccttcaccag cgagcgcaat 360  
 ggtgacggta actctgacat ctaccgcgta cggaccaacg gctccgatct ccaggaattg 420  
 gttgccacgc ctgcagtga agactccgtt gttatctctc ccaacggccg cctggcagcc 480  
 tacgtctcca ccgccaacaa catgaaggca aacatctgga tccttgatct tcagaccggc 540  
 gcgcagtga acctcacaaa tacaccacc actgccgcca actcctccct catggagagc 600  
 tatctccgtc ctgcctggtc tcctgatggc gaatggatcg ccttctcttc ggaccgcaac 660  
 acccaatggg acggacacgg cgtaccgacc ttctcggcc gcacgggctg ggagacgacg 720  
 caagaactct ctctctacgc catccgtccc aatggctctg acttccgtca gatcatctcc 780  
 aagccatact actctcttgg atctccgaaa tggtcagcag acggtaaacg catcgtctac 840  
 tacgaaatga cccgggaaga cacctacaac gcccatcgtc cagaaacat taccacagcc 900  
 aactcgacga tcatgtccgt agacttcgag acaggcaccg atgtgcgctg ggaagtgcgc 960  
 ggctccggtg tcaagcaatt ccctcagtac ctggacaaga acggcaccat cgctacacc 1020  
 ctcaaaggcg gcaccagcga gggcttctac acgaccgagg gactctacgt caacacgacc 1080  
 tcggcgaccc tcaggtcccc ggcgtggtct cccgacggca agcaagtagt ctacgaaaag 1140  
 agcacctgga gcatccgctc ggggtacaag cagctctaca gctgggacag tgactgggac 1200  
 taccgttca cggacgtctt ccctcaggtc tcgcaccagg agcgcgctgc catcacacag 1260  
 aagcagctgg gcaattcgtc catcgtgacg ttgaacacaa ccggaggcga cttgcaactc 1320



gtctacgacc ccagcacggc ggactttgtc agcgatgacg aaaccacagg actgagcgct 1380  
 taccagccca gctggtcacc ctgcggcgag tggctcgtct tcggcgctcg attctgggtc 1440  
 gagacgagag aagcctcagg cggatggatc gtgcggggcca ccgccaacgg gagctactcg 1500  
 gaggttctcg tgaacagcag ctactccatc accgaggatg gagccctgaa cagcgggttc 1560  
 ccgagtttct cgccggatgg caagaaagtg gtgtatcggg ttgggggagc cgacactgca 1620  
 acctacggca acgccagcga gatcgggctg cgggtgctgg acctcgagac gcgaaagaca 1680  
 accgtcctaa ccacagaatg ggacaatctg ccccgattct ctcccgatgg agagctcatc 1740  
 ctattcacac gcaaaaccag cacgtacaat tacgatgtgt gcacgatccg gccggatggg 1800  
 acagatctcc gcgtgttgac gagcagcggg gctaatagat gcgatgcggg ctggctcgag 1860  
 gatggacgga ttatgtggtc taccggcatg tatgggttcc ggtttgagtg tgcgctgtat 1920  
 ggtgatacgt tccagccgta tgggcaggtt atgattatgg atgcggatgg gggaaataag 1980  
 aagttgatga ccaactcgat gtgggaagat tcgatgccgt tgttcttgcc gagggaggta 2040  
 ctttag 2046

<210> 103  
 <211> 1875  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 103  
 atgcctccgg atgcaaaatc gcctggctac cagcctggta tggcagtatt accatctagg 60  
 ccacatcctg ccaagggaaa agccattcga ttccctcctt cccttgcatg ggtcgcgttt 120  
 gctattgttc aattatgtgg taatttccac aaaaatagga gcgttgaaca acagcttcag 180  
 agtcaaacac ttgatgatga gtcctttaa tgggaagatg ttactcctac caagcaactc 240  
 gtataccatc catgctttgg tgatcacgaa tgcgctcgct tgcgcttcc aatgaattgg 300  
 aaccgaactg atggtgaagg gtcaaaaatt gccttggcgg ttatcaaact tcctgccaag 360  
 gtacctgtca cagatgcgcg atatgggtgg gccattcttc tgaatccagg tggctcctgg 420  
 ggatccggag tgagcatggg ctttagatac gggaaagcta tccagaccat cgtcgactcc 480  
 ccagaatcac caagtgcaga ttcagcgagc ggaagatatt tcgatgttgt tagctttgat 540  
 ccaagagggg tcaacaacac aacacctaatt ttttctgct tccctgaccc cgcgacgagg 600  
 aaagcgtggg tactgcagtc agaggcagag ggtctacttg ggagttctga aggagtcttc 660  
 gatactcgat gggcaaggta cgaagctttt gagcggctac tttcgacagc tccgaacact 720

```

ttcccagttg gaacaaacgt tgacgccgag aggataaggc tgcacaaccg ttggaaaaaa 780
ggggaggaga agctgctata ctggggcttt tcctatggga caatcctggg ttccacgttt 840
gcggctatgc agcctcatcg cataaacctg gctgtcatag acggagtctg caacgctgat 900
gattattacg ccggcaactg gcttaccaat ttacaagatt cggatgcagc attcaataaa 960
tttttcgagt actgctacac agctggccca tcagcgtgtc cgtttgctg cggcggagat 1020
cccgaagatc tcaagtctcg ttatgagcag attttgacca atcttacatc gagccctatt 1080
gctgtgtctc cttctggaaa taggggcca gagataataa cctatagtga tgtgaagtca 1140
ttggtcgtgc aagctctcta tgtgcctttg aaattattcg atttggtggc taggctatta 1200
gctgagctcg agcaaggtaa cggctcttca ttcgtgact tgaagtatga agccaaacaa 1260
tggccagtac cgctccatg cgattcctcg tccacacaat acaaagtacc tggcgagagt 1320
gatcaggagg ccgggaggaa taccctatgt acagatggc caggcctcga cggaactgcc 1380
aaggaggatt tccggagcta ctggaatatg ctccggggac aaagtaaggc ggttgagat 1440
ttctgggccc aggttcgcat gtcgtgtgtc aaactggaga cgcgacctga gtggcgctat 1500
gatggtatgc gtatccaagg gcccttcgca ggcaatacat cgcacccatt gctgtttatc 1560
gggaataact atgatccagt aacgccgcta cggaatgctc atacgatggc gcgtggattt 1620
cctgagtcaa tcgttctaga gcagaactct gtcggacatt gcacactgag tggcccatcc 1680
ttgtgtacag cgaaagcgat acgccagtat ttccagaccg gagagttacc tgaccccgga 1740
actgtttgcc aggtagagga gcttcccttt cgtcttgccg gatatgagag aagtcaggtc 1800
atgtcgccag gtgacacaga attgatgtcc gccttgcat cgctgagcga gttccgccat 1860
ctgctaggcg cgtga 1875

```

<210> 104

<211> 1665

<212> DNA

<213> *Aspergillus niger*

<400> 104

```

atggtgagta gtctgctgct tgggggtctt ctgggtctag cgaccgctca atttcctccc 60
gagccggaag gcatcactgt gctcaagtcc aagttgcatg agaatgtgac tatttctttc 120
aaagagcctg gaatttgcca aactacgccg ggtgtccgat cttattcggg ctatgtacac 180
cttccccccg cctcaaccag cttcttttgg tttttcgaag cccgcaaaga tcccagcaat 240
gcgcctctgg ccacttggt caatggcggc ccgggtggct cgctgctcat ggggctcctt 300

```

```

gaagaattag gtccttggtc cattgcatca gactccaaga ccacagtcc tcaatccttgg 360
agttggaaca atgaagtcaa tcttctattc cttgaccagc caactcaagt cggcttctca 420
tacgatgtcc caacaaatgg cactttgaca gctaattgga ctgcattcgc ggctcacgct 480
ctatggcatt tcgcgcaaac ctgggtttttc gagttccac actacaagcc aaacgatgat 540
cgtgtcagtc tctgggctga aagttacgga ggccattatg gtccaggcat ctttcgggtc 600
ttccaacagc agaatgacaa aatcgcagag gggactgcag aagacggtgc acagtatttg 660
catctcgaca cgcttgcat tgtgaacggc ttgatggata tgggatcca agaagaggct 720
tacattactt ggccatacaa taacgtaagg ctgccccctt cttcattcaa ctgcgagggc 780
tttcgcatc aggccctcgc ctgcgaagcg gctttgaaag aacgcgattc cggcttgcc 840
cactcaggga agaataatctc tgaaatttgc ggaggccttg cactagaatg gggagatggc 900
cccatcacct actaccacac cttcaatcgc ggggtgtacg acatcgccca tcctaagaac 960
gacccattcc ctgccaagca catgctcggc tatttgacgc aggagtccgt ccttgccgct 1020
cttggggtac cagtcaattt cacatcgtct tcgagtgcg tggctacaca gttcataaaa 1080
acctttgata tcgtccacgg cggcttctct gatgcaattg gctacctcct cgacagtgg 1140
gtaaaagtac acatgatgta cggagatcgt gattacgcct gcaattgggt cgggggcaa 1200
aaagccagcc ttgcagttcc gtattcccgt atcaccgaat ttgccgacac gggatactcc 1260
ccactcctta cgcccgacgg gatcagcggc atgaccgcgc agctgggcaa ctacagcttc 1320
actcgcgtct tccaagccgg gcatgaggtc ccctcctacc agcctgtcgc ggcgtatgag 1380
atcttcatgc gggcgacatt caacaaagat atccctactg gcctcttggc tgttgatgac 1440
gaattccagt cggttggacc taaggatacg tggcatatca agaataatccc tcctattatg 1500
ccaaagccgc agtgctatgt tctaagtccc ggcacgtgta ccccgagggt ttgggagacc 1560
gttttgaacg gatccgcgac ggtaaaggat tggatgtcg tggatgatag cgcgggtgtt 1620
gaggaccacg aggggttcag cattcttggg ggggatgagt tgtag 1665

```

```

<210> 105
<211> 1737
<212> DNA
<213> Aspergillus niger

```

```

<400> 105
atgaccagg ttcaattgct tccccttgc gcagggtgc ttgccccttc aattgcagcc 60
cttagcatcc cttccccgca gcagatcctc gattctctca ctttcggaga gcacaccgac 120

```

ggcttttgtc cgctggcacc caaggttgag gttcctgacg atggtttctt tccagctctc 180  
 aagttcgtag aagatgcctc gttcaagtcg cgccaagtca atcgtctctc cagggcggtt 240  
 caagttccga cgcgaatcga cgactacatg aaggatccct acgacgaaaa gtctgccccca 300  
 ttctctgact tccagaagct cctgcagacc ctctttcccc tcacccactc ctacgcccgc 360  
 gtagatcaca tcaaccgatt tggctctcgtc ttcaccctca atggcacaga tgactcgctc 420  
 aagcccctgc tattcaccgc gcaccaggac gtcgtgcccc tcaacgaccc tgccgactgg 480  
 acctatcccc ccttcgatgg ccactacgac ggcgaatggc tctggggcgc cggtgccagc 540  
 gactgcaaga acgtcctgat cggctctcatg tccgttggtg aagacctact ctcccaaaag 600  
 tgggagccaa cccgcacagt cgtcctggcc ttcggattcg acgaagaatc ccacggcttc 660  
 ctgggcgcgc gatccatcgc caaatcctt gagaagaaat acggaccgga cagcttcgaa 720  
 tttatcctcg acgaaggcgc catgggcctc gaagttctag acgacaacaa caacggcgctc 780  
 gtctacgctc tccccggcgt tggcgaaaag ggcagcatcg acgttggtgt cactctggcc 840  
 gtaccaggcg gccacagctc cgtgccccct ccacacacgg gaatcggcat catcgccgag 900  
 atcatctatg agctagaacg ccaggacctc ttcgtccccg tcctagacac tcaccacccg 960  
 acccgcaaga tgctcgaatg ccaagtccgc cactccccct cgcaagtcca accgtggctc 1020  
 gcctccgccc tccaatcaag cgactacatc tccctagcag agaaaactggc ctctctcgcg 1080  
 ggcgacaagt tccgcttcat cctccaaacc tccaagcag cggacatcat caacggcggc 1140  
 gtcaaatcca acgtctctcc cgagaaaatc aacgccctcg tcaactaccg catcgctctg 1200  
 caccaaacc cagacgatat caagaaccgc gctgtggaga tcatctctcc catcgctcaag 1260  
 aaatataacc tctccctcac ggccctcccg gaaagcgaca ccgttgaccc ctccctcaac 1320  
 aaccacctca cccttactac cctcagcggc gccctcagtc ccgccccggt cagcccaacg 1380  
 gacatcgaca ccgacgccgt ctggggccgt ttctcgggcg tcactcgctc ggtcttcgaa 1440  
 tctgtcccta gtctcgaggg cagaaaggtc gtcgtgagcg gcgacatcat gaccgggaat 1500  
 acggatacga gattctactg ggctttgtcg aggaatattt acaggtggag tccgtcgagg 1560  
 gcgggtaaaag cgctgaatat tcatactgtt gatgagagga tcgatattga tattcatctt 1620  
 gaggcgatga tgctgtatta cgatcttatt cgctctttcg atggacggac cgattcatct 1680  
 gtcatttctg ctgcgtcggc agctgctgat gatgaacttg ctcacgacgt gctgtga 1737

&lt;210&gt; 106

&lt;211&gt; 1371

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 106

```

atgaagagca ccactcttct ttccttggcc tgggctgccc agtccgccta ttccctctct 60
atccacgagc gcatgaacc cgctactctt cagttcaact ttgaacgtcg tcagatcgcc 120
gaccgggtccc gtcggaagcg atcgacggcc tcggccgacc tcgttaacct ggctacgaat 180
cttggctaca cgatgaacct cacactcggc actcccggcc aggaagtcag tgtgacgttg 240
gacaccggca gcagcgatct ctgggtcaat ggggccaaact cgtccgtctg cccctgtacc 300
gattacggct cttacaactc aagcgcttct tccacctaca ccttcgtgaa cgatgagttt 360
tatatccagt atgtcgacgg cagtgaagcc acaggcgact atgtcaacga tactctaaag 420
ttctccaatg tgactttgac gaactttcaa ttgcccgtcg catatgacgg cgactccgag 480
gaggggggtcc tcggtatcgg atacgccagc aatgaagcca gccaggccac cgtcgggtggt 540
ggtgaataca ccaacttccc cgaagccctc gtcgatcaag gcgcgatcaa ctggccggcc 600
tacagtctat ggctcgatga cctcgacgaa ggaaaaggca ccattctgtt cggcggagtc 660
aacaccgcca agtactacgg cagcctgcag accctgccta tcgtctccat cgaagacatg 720
tacgtcgagt tcgcggtcaa cctgacggcc gtgcaccttg agaagaacgg caactccgtc 780
tcggtcaaca acagcgccac gcaattcccc atccccgcg tgctggacag cggcacggcc 840
ctgacctaca tcccgaacct cgccgcagcc agcatctacg aggccgtcgg tgcccaatac 900
ctgagcgagt acgggtacgg agtgatcgag tgcgacgtca aggacgaaga cttcaccttc 960
ctgttcgact ttggatcctt caacatgagc gttgacatca gcgagatgat cctcgaggcc 1020
agttccgaca tgaccgacat gaacgtttgt acgtttggcc tcgcagtgat cgaaaatgag 1080
gccctgctgg gcgatacctt cctgcgcagc gcatacgtcg tctacgatct cggaacaac 1140
gagatctccc tggccaaggc caacttcaac cccggcgagg accacgtcct ggagatcggc 1200
accggatcgg atgccgtgcc caaggcgacg ggggcgacgg cgaccggcgc ggcagccaca 1260
tccacggcct cgagcgacaa gtcggacaag gagagtccgg ctacagtgcc gcgcagccag 1320
attgtctcgc tgggtggcggg agtcttggtc ggtgttttct tggttctgta a 1371

```

&lt;210&gt; 107

&lt;211&gt; 1995

&lt;212&gt; DNA

<213> *Aspergillus niger*

&lt;400&gt; 107

atgttgggtcc gtcagcttgc cctgggtctg gccattgagg ccttgtccga tgccattccg	60
acatccatca agcatgtcct gcacgagaaa cgtcacaagc ccgcatccga ctgggtgaag	120
ggtgcgcgcg ttgagagcga tgcgggtcctg cctatgcgca ttggccttgc ccagaacaac	180
ttggacaagg gctatgactt cctgatggaa gtatcggacc ccaagtcttc caaatacggc	240
cagtactggg cggcagacga ggtgcacgac atcttttcgc catccgagga ggctgttgag	300
gcagtgcgag aatggcttgt cgcctctggg atccatccgt cgcgggtggg gcaactccgac	360
aacaaggggt ggctcgcgtt cgacgcctac gccatgaag ccgagagggt gttcatgacg	420
gaattccacg agcagagag cgaccgaagt gctaagatca gggttggatg cgaccaatac	480
cacgtccccg aacacatcca gaagcacatc gactacatta cccctggagt gaagctcacc	540
caggctcgtg agaggaccaa caaagtcaag cgtgcttccc aactagctca ctcttccaag	600
gccaaagtctg ctgcccaagg tccgcagcca ctccccaaca aggccaagtt cctgcctgaa	660
gacctccgcg gctgcggtta caacatcacc ccctcgtgta tcaaggcctt gtatcagatc	720
ccagacgcta agacggcgac cccgaacaac agcctgggtc tgtacgagca gggtgactac	780
tttgccaagt ccgacctcga cctcttctat aaggagtatg cgcctgggtt tccccagggg	840
acctatccca tcccagccct gattgatggc gccaatctact cggttccttc ctacagctcc	900
ctgaacacgg gtgaatccga cattgacatt gacatggcct actccctgct ctaccctcag	960
caggtgacct tctaccaggt tgacgaccag ctctacgaac cagtcgaggt cgacacaacc	1020
aatctgttca acaccttctt cgacgtcttc gatggctcct actgcacctc cagcgctac	1080
ggcgagaccg gcgatgacct gtcgatcgac cccgtatacc ccgacaccg ccccgggcgg	1140
tacaaaggaa agctccagtg cggcgtctat aagcccacta acgtaatcag cgcctcctac	1200
ggccaatccg aagccgacct ccccgctcagc tacaccaagc gccaatgcaa tgagttcatg	1260
aagctcgggtc tacagggaca ctccatcctc ttcggtcttg gcgactacgg cgctcggtct	1320
ttcgccggcg acggtgacga gaacggctgt ctcggcccag agggcaagat cttcaacccc	1380
cagtaccctt ccaactgccc ctacgtcacc tccgttgag gtacctgct gtacggctac	1440
cagaccgtca acgacagcga gagcgtcatg cacgttaacc ttggcggaac cgcaagtaac	1500
ttcagcactt ctgggtggctt ctcgaaattac ttccccaac cggcatatca gtttgctgct	1560
gtggagcaat acttccagtc tgcgaacctg tcgtatccgt attactcgga gtttgaggct	1620
gatgttaaca cgaccaaggg tctctacaat aggcctgggtc gtgcttatcc ggatgtctcg	1680
gcgaatggag cgcatttccg cgcttatatg gatggatacg attatcattg gtatggatcg	1740

agtttggcgt cgcctttgtt cgcgtcgggt cttactttgc tcaacgagga acgcttcgct 1800  
 atcggcaagg gccccgtggg attcgtgaat cccgtgcttt atgcttatcc gcaagtgtg 1860  
 aacgatatca ctaatggtac taatgctggg tgtggaactt atgggttttag tgctattgag 1920  
 ggatgggatc ccgctagtgg tttgggtacg cctaactacc cattgatgaa ggagctgttc 1980  
 ctctctttgc cttag 1995

<210> 108  
 <211> 1563  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 108  
 atgcggtta ccacggcaat tgcttcatta ctactggtcg gtcggccac cagtctccaa 60  
 aatcctcatc gtcgggctgt tccgcccct ctctcgcatc gcagcgtagc gtctcgctcc 120  
 gtgcccgttg agcgccgaac caccgacttt gagtatttga ctaacaagac tgcaagattc 180  
 ctggtcaatg gcacaagcat ccccgaagtc gatttcgacg tcggcgagtc ctacgccggc 240  
 cttctcccca atacgccac tggcaattct agcctattct tctggttctt cccctcgcaa 300  
 aatccagagg ccagcgatga gatcaccatc tggctcaacg gcggccccgg atgtagctcc 360  
 ctagacggcc tgcttcaaga gaacggccca ttctctggc agcctggcac ttacaagccc 420  
 gttcctaata catactcatg gaccaacctc accaatgtgg ttacatcga ccaaccgcc 480  
 ggcacaggct tctccccggg cccctcgacc gtaaataacg aggaagacgt ggctgcccag 540  
 ttcaacagct ggttcaagca cttcgtcgac accttcgacc tgcaaggccg caaggctctac 600  
 atcaccgttg aaagctacgc gggcatgtac gtcccctaca ttgccgatgc catgctgaac 660  
 gaggaggata caacctactt caacttgaag ggtatccaga tcaacgaccc gtccatcaac 720  
 agcgactcgg tcatgatgta ctccccgcc gtcggccatc tgaaccacta caacaacatc 780  
 ttccagctaa actccacttt cctctcctac atcaacgcca aagccgacaa gtgaggctac 840  
 aacgccttcc tcgacaaagc catcacctac ccacccccca gtcccttccc caccgcccct 900  
 gaaatcaccg aagactgcca agtctgggac gaagtcgtca tggccgccta cgacatcaac 960  
 cctgcttca attactacca cctgatcgac ttctgcccct acctctggga cgtgctcggc 1020  
 ttcccctccc tcgcctccgg cccaacaac tacttcaacc gtcgcgacgt ccagaagatc 1080  
 ctgcacgtcc ctccaacgga ctactccgtg tgctcggaga ccgtcatctt cggaacggc 1140  
 gacggcagcg accccagctc ctggggctcc ctaccagcg tcatcgaacg cactaacaac 1200

actatcatcg gccacggctg gctcgattac ctctcttctt tgaacggctc gctcgccaca 1260  
 atccagaaca tgacctggaa cggtaagcaa gggttccagc gtcctcccgt ggaaccgctc 1320  
 ttcgtccctt accattatgg tctggctgag ctgtactggg gcgatgagcc tgaccctgat 1380  
 aaccttgatg ctggcgctgg atacctgggt acagcgcata ccgagcgagg gttgactttc 1440  
 agctcgggtg atttgtctgg tcatgaaatc ccgcagtatg ttcttggtgc ggcttaccgc 1500  
 cagttggagt tcctgctcgg taggattagt agtctttcgg cgaaggggaa ctatacctct 1560  
 tga 1563

<210> 109  
 <211> 1656  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 109  
 atgcgtggct ctcggttggg gctcttgttg cccttggtg cacttagttg tgctatgccc 60  
 gagaatgaat ggtcatctac gataagaagg cagttaccaa aagcgtccac tggcgtcaaa 120  
 tcgataaaaa ccccaaacaa tgtcactatc aggtataaag aaccaggaac cgaaggaatt 180  
 tgtgagacaa cacctggggg caaatcatat tccggatatg tcgatctttc gccagagtcg 240  
 catactttct tttggttttt cgagtcacgc cgtgaccccc aaaatgatcc agtgactctg 300  
 tggctgaatg gtggccctgg aagcgattcc ttgattgggc tttttgaaga gttgggtccg 360  
 tgtcacatca caccagagta cgaatcaatc atcaatcagt actcctggaa cgaggtcacc 420  
 aatcttcttt tcttgtctca gcccctcggt gtggggttct cttacagtga aaccgaggcc 480  
 gggtccttga atccatttac tggagccgct gagaacgcct cctttgctgg agttcagggt 540  
 cgatacccag ttattgatgc cactatcatc gacacgaccg atatcgctgc acgcgcaacc 600  
 tgggaggtgc ttcagggtct cctcagtggc ctgtcgcagc tagattccga agtcaagtcc 660  
 aaggagtcca acctgtggac agagagttac ggaggacact atggaccagc gttcttcaat 720  
 catttctacg agcaaaatc gaagatcgct agcggggaag tcaatggcgt ccaactgaat 780  
 tttactccc tcgggattat caacggcatc attgatgccg cgattcaggc agactactac 840  
 gcagactttg ccgttaataa tacatatgga atcaaagctg tcaatgacac agtgtacaac 900  
 tatatgaagt tcgccaacac gatgccaat ggatgccagg atcagggttc ttcgtgtaaa 960  
 ttgaccaata ggacctcgct ttctgattat gctatatgta cagaagcagc caatatgtgc 1020  
 agggacaatg tcgaagggcc ttactaccag tttggcggcc gtggcgtgta tgatattcgg 1080



caccctaca atgacccgac cccgccgtcc tactttgttg actacctcaa gaaagactca 1140  
 gtcattggatg ctatcggcgt ggacattaac tacaccgagt ccagcggcga agtatattat 1200  
 gcattccagc agaccggcga ctttgtatgg ccgaatttca ttgaggacct cgaagagatc 1260  
 ctccaactcc ccgtacgcgt gtcgttgatc tacggcgatg ccgactatat ctgtaactgg 1320  
 ttcggcggtc aggccatctc actcgcagtt aactaccccc atgcagctca gttccgtgca 1380  
 gggggataca caccatgac agtagatggg gtcgaatacg gtgagactcg cgagtatggc 1440  
 aacttttcgt tcaccgcgt atatcaggct gggcacgagg ttccatacta tcaaccgatc 1500  
 gcagcgttgc agctgttcaa ccgtacttta tttggatggg atattgcagc ggggtacaact 1560  
 cagatttggc ccgaatatag caccaacggg acatcgcagg ctacacacac ggagtcgttc 1620  
 gtgccactgt ccacggcgtc gagtaccgtc aattag 1656

<210> 110  
 <211> 1872  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 110  
 atgccttttc ccttttcgtc cgctcttctc ggctatatct taactacgag cactactctc 60  
 acctccctag tcgcaggaca gtattacctt ccgacgcctg aggatctcac cgttattcat 120  
 tcggagatat tccctgggtg gaggatctcc tataagcaac ccctcggcat ctgcaccacc 180  
 acccctcca cccccagcta ctccggctac atccacctcc cccacacac ccttaccaat 240  
 ctctccattc caggaatcag catctcgcaa ccatacccta tcaatacctt tttctggtac 300  
 tttccttccc gccatcacca caacaatgat acatccccac tcaccatctg gatgaacggc 360  
 gggcccggcg gatcctccat gattgggcta tttcaagaga acgggccatg tactgtgaat 420  
 acggactcga attccacggc ctataatccc tggtcgtgga atgagtacgt cgatatgttg 480  
 tatattgagc agccggtgca gacgggattt agttatgatg tggtgaggaa tgggacgtta 540  
 gatttgaatg agacgttttt ggtggggacg ttgccgagtc aggatgtgca tgggacggtg 600  
 aatgggacgg ttaatggggg aagggcgctt tgggttgctg tgcaggtttg gttgggtgaa 660  
 ttctctgaat atgtttcttc tgttgacggg aatggtggtg gtgatgacag ggtgagtata 720  
 tggacggagt catatggggg acggtatgga ccggcataca cggcgctctt tcaggagatg 780  
 aatgagagga ttgagagtgg ggaggtaagc accgggaaga agatccattt ggatacgcgtg 840  
 ggcattatca atgggtgtgt ggatttactc gtgcaggctc cttcgttccc tgagcaggcg 900

tataacaata cgtatgggat cgagggaaatc aatcgcacgc tctacgaccg ggctatggat	960
agttggagca agcctggcgg gtgcagggat atgatcatcg agtgtcgca tgctggcgag	1020
ctcggagatc ccctcatcat ctgcgaggag gcgtcggact actgttcgcg ggagatcaag	1080
agcctgtata cgaatacctc cgggcgagga tactacgaca tagcgcattht cacgccggat	1140
gcagctctcg tgccttactt cgtcgggttc ttgaatcgcc catgggtgca aaaggcactt	1200
gggggccggg tgaactatac catgtcgtca gaggcagtg ggaacagtht cgcttcgacg	1260
ggcgattatc cgcgaaatga tccccgcgga atgatcgggg atattggata cttgcttgac	1320
tccggtgtca aggtggctat ggtatatggg gaccgggact atgcttgctc gtggcgcggc	1380
ggggaagatg tcagcctgct ggtggagtac gaggatcgcg agaagttccg tgctgctggg	1440
tatgccgaag tgcagacgaa gtcatacctac gttgggggtc tagtaaggca gtatgggaac	1500
ttctcgttca cgcgtgtctt tcaggcgggc catgaggtgc cattttatca gcccgaacg	1560
gcgtatgaga tttttaatcg cgctcagtht aattgggata ttgcgacggg aggcatttht	1620
ctggagcaga atcagagcta tgggacggag ggaccgtcgt caacgtggca tatcaaaac	1680
gaagtgccgg agagccctga gccgacgtgc tatttggttg cgatggattc gacttgctacg	1740
gatgagcaga gggaaacgggt gctgagtggg gatgcggtgg tgagggattg ggttggtgtt	1800
gatgatattg aggctgaaag ctcgttcagc ggtgttggtg atcagctggc acaggctcct	1860
ttgggacatt ga	1872

<210> 111  
 <211> 1320  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 111	
atgagaacat ctactcttht gtcctcttg agcactgcag gacgagcttht ggcttctccg	60
taccgccttc ccgactcgca agtagtcttc gccgcggatc acgaggtccc gaatacacag	120
ggcaaacacg tcgtggacga ggccatactc tcggcgctga acgctcattht tgaccagtc	180
gctgcaatgg tgtctctacg tcccgaact gcagcttht tagctgaacc tcgtctcttg	240
cacattcggg gcgaagagaa ggcggaatgg atgaccgaag gcgacaagct gcgcctccgc	300
caacgcggaa agaagttcat ggacattacc gagcatcagg acttctacgc agagcaggcg	360
atggcttcgt ttgctgggga tcctaactct cccaagctgt ccataaagg tctcgtcaag	420
ccgctgttct ctcaaatcga gacggaacga atgcacgata tcctgcagca catgacctcc	480

tactacaatc gatactacgg tgattatcac ggcgagatga gctccgaatg gctgcacgac 540  
 tacattgctg cgatcatctc caaatcgccct ttccgcaccc acatctctct cgaatacttc 600  
 acccatcctt tccgccaatc ttcaattatt gcacgcttcg agcctaaagt tcgcagcttc 660  
 tccaacctt tgaccatcat tgggtgcgcac caagattcgg ccaattatct ttttcccctg 720  
 ctgcccgcgc ctggcgctga cgatgactgt tccggcactg tcagtatcct cgaggccttc 780  
 cgcgcttctg cgagagaatg ctacacgccc aaggacgggc ctgttgaatt ccattgggtat 840  
 gcggctgaag aggccgggct actgggcagc caagccatcg cgcggtacaa gaaggagcag 900  
 ggcgctaaaa ttgatgccat gatggagttt gatatgacgg cttttattgc ccgtaacgcc 960  
 accgagacca tcgggtttgt tgcaacccaa gccgatgcag cgctcacaaa ctggggccctc 1020  
 aacctcagtc gagaatacat ctccattccg gcggaagtct atgaacttgg cccaacgct 1080  
 ggatccgact acatgtcata cactaagctc aactaccccg ctgcctttgc atccgaaggc 1140  
 aaccgcctcg ctgggggctc tttcccgggt gaaatggacc cctacgtaca cggcatacag 1200  
 gataggatgg acgttgacga tgaaacgggc gtcttctcta tcgaacacat ggctcgggtc 1260  
 tccgagttgg ctatcgcat tgttgctcag caggctgggt gggataatac atggcggtag 1320

<210> 112

<211> 1581

<212> DNA

<213> *Aspergillus niger*

<400> 112

atgcgttcct tctccgttgt cgctgccgcg tcaactggcg tctcttgggc gtctctggcc 60  
 caggctgctc gccccgtct tgtgcccaag cctatctctc ggccagcttc gagtaagtcg 120  
 gctgcgacta cgggtgaggc ttattttgag cagctgctgg accatcacia cccggagaag 180  
 ggaacgtttt cccagcggta ctggtggagt actgaatact ggggtggacc tgggtcaccg 240  
 gtggtcctct ttaaccctgg agaggtctct gccgatggct atgaggggta tctcaccaac 300  
 gatactctca ctggtgtcta tgcgcaggag atccagggtg ccgtcattct cattgaacac 360  
 cgctactggg gcgactcttc gccttatgag gtgctcaatg ccgaaacact tcagtatctc 420  
 acactggatc agtccattct ggacatgacc tacttcgccg agacggtaaa gctgcagttc 480  
 gataatagca gccgcagcaa tgcgcagaat gctccctggg tcatggctcg tggctcatac 540  
 agcgggtgct tgacggcttg gaccgagtct atcgcgctg gaacgttctg ggcttaccat 600  
 gccaccagtg cgctgtgga ggctatctat gacttttggc aatacttcta cccattcag 660

caaggtatgg cacagaactg cagcaaggat gtgtctctgg tagccgagta tgtcgacaaa 720  
 attggaaga atggaactgc caaggaacag caggagctca aagaattggt tggctctggga 780  
 gctgttgagc attacgatga ctttgccgct gtctgcccac acggaccgta cctctggcaa 840  
 gacaacgact ttgtcacagg atactcttcc ttcttccagt tctgtgatgc tgtcgagggg 900  
 gtcgaagccg gcgcggcagt gacccccggc cccgagggcg tcggacttga aaaggccctg 960  
 gccaaactacg caaactgggt caattcaacc atactcccta actactgcgc aagctacggc 1020  
 tactggaccg acgaatggag cgtcgcctgt ttcgacagct ataatgcctc gagccccatc 1080  
 ttcaccgaca cctccgtggg taaccctgtc gaccgccaat gggaatgggt cctctgcaac 1140  
 gagcctttct tctggtggca ggacggtgcc cccgagggaa cctccactat tgtgccccgg 1200  
 ctctgcagcg cctcctactg gcaacgccaa tgcccgtctc acttcccoga agttaacggc 1260  
 tacacgtacg gcagcgcgaa gggtaaaaac tccgctacgg tgaacagctg gacgggtgga 1320  
 tgggatatga cccgcaacac gacgcggttg atctggacga acgggcaata tgaccctggg 1380  
 cgcgactccg gtgtgtcgag cactttccgg cccggtggtc cgctggttag cacggcgaac 1440  
 gaaccctgac agattattcc gggcggttc cattgctcgg acttgatat ggaggattac 1500  
 tatgcgaatg aggggtgtgag gaagggtggt gataatgagg tgaagcagat taaggagtgg 1560  
 gtggaggagt attatgcttg a 1581

<210> 113  
 <211> 1275  
 <212> DNA  
 <213> *Aspergillus niger*

<400> 113  
 atgcagctcc tccagtcctt cattgttgcc gtttgcttca gctacggcgt cctctcctta 60  
 ccccatggcc cgtcaaacca gcacaaagca cgttccttca aggttgaacg ggtccgtcgt 120  
 ggaaccgggtg ctctgcatgg gcccgctgct ctccgcaaag cataccggaa gtacggaata 180  
 gctcccagca gtttcaacat cgatctggca gactttaaac ccattacgac aaccatgct 240  
 gctgctggga gcgagattgc agagcctgat cagactggcg ctgtcagtgc tacttccgtc 300  
 gagaacgatg ccgagttcgt ttcgcctgtt cttattggcg gccagaagat cgtcatgaca 360  
 tttgacactg gttcttctga cttttgggtg ttcgatacga atctcaatga aaccttgacg 420  
 ggacacacgg agtacaaccc ttcgaactcc tcgaccttca agaagatgga cggatacacc 480  
 ttcgatgtct cgtatggtga cgactcgtac gcctctggcc ccgtcggaaac ggataccgtc 540

```

aacattggcg gcgccattgt caaggagcaa gccttcggtg tccccgacca ggtatcccag 600
tcgttcacgc aggacacgaa ctccaacggc ctggtcgggt tgggcttttc ctccatcaac 660
accatcaaac cggaggcgca agacacgttc ttcgccaatg tcgcaccaag tctggacgag 720
cccgtcatga ccgcctcgct caaggctgac ggagtgggag agtacgagtt cggcacgac 780
gacaaagaca agtaccaggg caacattgcc aacatcagcg tggactcatc gaacggatac 840
tggcagttct ccactcccaa gtactccgtg gcagacggag agctgaagga cattggaagc 900
ttgaacacct cgatcgcgga caccggtacc tcccttatgc tgctggatga agacgtggtt 960
actgcctact atgcgcaagt tcccaactcg gtctacgtga gcagtgccgg tggttacatc 1020
tacccttgca acaccactct tcccagcttc tcgcttgccc tcggcgagtc gagcctggcc 1080
acgatecccc gtaacctgat caatttctcc aagggtggca ccaacaccac caccggacag 1140
gccttgctgt ttggcggcat tcaatccaac ggaaacacct cgctgcagat tctgggcat 1200
atcttctgta aggccttttt cgttgtcttc gacatgcgag gccctcgct tgggtgtgccc 1260
tctcccaaga actag 1275

```

```

<210> 114
<211> 1647
<212> DNA
<213> Aspergillus niger

```

```

<400> 114
atgcgcattg actccgcggc gctacatctg gtcccagtc tcttgggcca ggtcgggtgct 60
ttacaattac ccttgggtcca agactccaat tcacagtggc agaaaccaaa tgcaggtgat 120
aaacccttaa ttagctctcc gttgcttcaa gagcaggtea aggcggagaa tctgttggac 180
agggcccggc agctttacaa gattgcggag ctgggagaag acgagtataa ccaccctact 240
cgcgtcattg gcagtaaagg tcaccttggc acgctcgact acatatactc cacccttacc 300
gacctcggtg attattatac tgtcgtcaat cagtccttcc ctgccgtgag cggtaatgtc 360
ttcagatctc gccttgcctt tggtcacgat gttcccaagt cagctacacc aatgggtctc 420
actcccccaa cgaggaataa ggagccggta tatggctccc tggttgctgt atccaacctc 480
gggtgtgagg cctcggacta ctctccaac ttgaaaggcg ccgttgcatc tatcagtcgg 540
ggaagctgtc cgttcgggac caagtctcaa ttagctggta aagcgggagc tgttgctgcc 600
gtcatctaca acaacgagcg gggtgacctc agcggaactc taggaaaccc aacccccgat 660
catgttgcta cctttggtat ctacagacgag gatgctgccc cagtcctgga gaagttgaat 720

```

```

aaaggcgaga aggtggacgc tatcgctac gttgatgca tagtagagac catccacacc 780
accaatatca tcgcgacagc cacggatggg gacccgaaca attgtgtaat gctgggtggc 840
cacagtgaca gcggtggccga gggcccgggt atcaatgacg acgggtccgg tactctgacc 900
cttttggagc ttgccacatt gctcaccag ttccgtgtca acaactgcgt gcgatttgc 960
tggtgggccc cggaggagga aggccttctc ggatctgact attacgtgtc cgttctcaca 1020
ccggaagaga accgcaagat ccgcttggtc atggactacg acatgctcgg ctgcccgaac 1080
tttgcgtagc aagtttaca tgccactaat gctgtgaacc ccgagggatc tgaggagctt 1140
cgtgatctgt acaccgactt ttacgaagat catgggttca actacacgta cattccgttt 1200
gacggacgca ggcactatga tgccttcatt cggcatggta tcccgggtgg tggcattgcc 1260
acgggagcag agggatatcaa gactgtcgag gaagcggaca tgtttggtgg ggttgctggc 1320
caatggtatg acccgtgtta ccatcagatc tgcgatacgg tggccaatgt gaacttgact 1380
gcgtgggagt ggaacaccaa gctcgttgcc cactccattg cgacttacgc caagtccttt 1440
gacggattcc cggaacggtc cgatgaaccc atcagccctg ctgcttttga ggaaccgaag 1500
taccatggcc acgcgttgca attacttcgc ggtaatacta cagggaacca gagcgtcctg 1560
tggggagccc aaatccagaa tggaacagct gcacgggtgc ttaatctatt gtccatacga 1620
cgcagaggca ctttcagtct aagctaa 1647

```

```

<210> 115
<211> 480
<212> PRT
<213> Aspergillus niger

```

```

<400> 115

```

```

Met His Leu Pro Gln Arg Leu Val Thr Ala Ala Cys Leu Cys Ala Ser
1           5           10           15

```

```

Ala Thr Ala Phe Ile Pro Tyr Thr Ile Lys Leu Asp Thr Ser Asp Asp
          20           25           30

```

```

Ile Ser Ala Arg Asp Ser Leu Ala Arg Arg Phe Leu Pro Val Pro Lys
          35           40           45

```

```

Pro Ser Asp Ala Leu Ala Asp Asp Ser Thr Ser Ser Ala Ser Asp Glu
          50           55           60

```

Ser Leu Ser Leu Asn Ile Lys Arg Ile Pro Val Arg Arg Asp Asn Asp  
 65 70 75 80

Phe Lys Ile Val Val Ala Glu Thr Pro Ser Trp Ser Asn Thr Ala Ala  
 85 90 95

Leu Asp Gln Asp Gly Ser Asp Ile Ser Tyr Ile Ser Val Val Asn Ile  
 100 105 110

Gly Ser Asp Glu Lys Ser Met Tyr Met Leu Leu Asp Thr Gly Gly Ser  
 115 120 125

Asp Thr Trp Val Phe Gly Ser Asn Cys Thr Ser Thr Pro Cys Thr Met  
 130 135 140

His Asn Thr Phe Gly Ser Asp Asp Ser Ser Thr Leu Glu Met Thr Ser  
 145 150 155 160

Glu Glu Trp Ser Val Gly Tyr Gly Thr Gly Ser Val Ser Gly Leu Leu  
 165 170 175

Gly Lys Asp Lys Leu Thr Ile Ala Asn Val Thr Val Arg Met Thr Phe  
 180 185 190

Gly Leu Ala Ser Asn Ala Ser Asp Asn Phe Glu Ser Tyr Pro Met Asp  
 195 200 205

Gly Ile Leu Gly Leu Gly Arg Thr Asn Asp Ser Ser Tyr Asp Asn Pro  
 210 215 220

Thr Phe Met Asp Ala Val Ala Glu Ser Asn Val Phe Lys Ser Asn Ile  
 225 230 235 240

Val Gly Phe Ala Leu Ser Arg Ser Pro Ala Lys Asp Gly Thr Val Ser  
 245 250 255

Phe Gly Thr Thr Asp Lys Asp Lys Tyr Thr Gly Asp Ile Thr Tyr Thr  
 260 265 270

Asp Thr Val Gly Ser Asp Ser Tyr Trp Arg Ile Pro Val Asp Asp Val  
 275 280 285

Tyr Val Gly Gly Thr Ser Cys Asp Phe Ser Asn Lys Ser Ala Ile Ile

290                      295                      300  
 Asp Thr Gly Thr Ser Tyr Ala Met Leu Pro Ser Ser Asp Ser Lys Thr  
 305                      310                      315                      320  
 Leu His Ser Leu Ile Pro Gly Ala Lys Ser Ser Gly Ser Tyr His Ile  
                     325                      330                      335  
 Ile Pro Cys Asn Thr Thr Thr Lys Leu Gln Val Ala Phe Ser Gly Val  
                     340                      345                      350  
 Asn Tyr Thr Ile Ser Pro Lys Asp Tyr Val Gly Ala Thr Ser Gly Ser  
                     355                      360                      365  
 Gly Cys Val Ser Asn Ile Ile Ser Tyr Asp Leu Phe Gly Asp Asp Ile  
                     370                      375                      380  
 Trp Leu Leu Gly Asp Thr Phe Leu Lys Asn Val Tyr Ala Val Phe Asp  
 385                      390                      395                      400  
 Tyr Asp Glu Leu Arg Val Gly Phe Ala Glu Arg Ser Ser Asn Thr Thr  
                     405                      410                      415  
 Ser Ala Ser Asn Ser Thr Ser Ser Gly Thr Ser Ser Thr Ser Gly Ser  
                     420                      425                      430  
 Thr Thr Thr Gly Ser Ser Thr Thr Thr Thr Ser Ser Ala Ser Ser Ser  
                     435                      440                      445  
 Ser Ser Ser Asp Ala Glu Ser Gly Ser Ser Met Thr Ile Pro Ala Pro  
                     450                      455                      460  
 Gln Tyr Phe Phe Ser Ala Leu Ala Ile Ala Ser Phe Met Leu Trp Leu  
 465                      470                      475                      480  
  
 <210> 116  
 <211> 1099  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 116  
 Met Leu Arg Gly Leu Arg Asp Val Val Leu Leu Gln Phe Ala Ile Pro  
 1                      5                      10                      15



Leu Phe Leu Leu Leu His Phe Arg Leu Ser Leu Arg Gly Val Ile Thr  
 20 25 30  
 Gly Phe Gly Ser Lys Ser His Phe Gln Arg Pro Leu Ser Lys Met Ser  
 35 40 45  
 Ser Thr Gln Lys Ser His Phe Lys Leu Leu Gln Lys Phe Lys Pro Glu  
 50 55 60  
 Tyr Ser Pro Ser Glu Phe Ala Gln Tyr Glu Ser Glu Arg Thr Gly Met  
 65 70 75 80  
 Arg Val Val Val Ile Asp Gln Lys Gly Pro Lys Val Thr Gly Tyr Phe  
 85 90 95  
 Val Leu Ala Thr Glu Ile Leu Asp Asp Ser Gly Ala Pro His Thr Leu  
 100 105 110  
 Glu His Leu Cys Phe Met Gly Ser Arg Asn Tyr Arg Tyr Lys Gly Phe  
 115 120 125  
 Leu Asp Lys Leu Ala Thr Arg Val Tyr Ser Ser Thr Asn Ala Trp Thr  
 130 135 140  
 Ala Thr Asp His Thr Ala Tyr Thr Leu Asp Thr Ala Gly Trp Glu Gly  
 145 150 155 160  
 Phe Ala Gln Ile Leu Pro Val Tyr Leu Glu His Val Ile Ala Pro Thr  
 165 170 175  
 Leu Thr Asp Glu Gly Cys Tyr Thr Glu Val His His Ile Asp Gly Ala  
 180 185 190  
 Gly Asp Asp Ala Gly Val Val Tyr Ser Glu Met Gln Gly Val Gln Asn  
 195 200 205  
 Asn Ser Ala Glu Leu Ile Asp Leu Thr Ala Arg Arg Leu Thr Tyr Pro  
 210 215 220  
 His Gly Val Gly Phe Arg Tyr Glu Thr Gly Gly Met Met Glu Gln Leu  
 225 230 235 240

Arg Val Leu Thr Ala Asp Arg Ile Arg Ala Phe His Arg Glu Met Tyr  
 245 250 255  
 Gln Pro Lys Asn Leu Cys Leu Ile Ile Thr Gly Glu Val Asp His Gln  
 260 265 270  
 Asn Met Leu Glu Thr Leu Asp Lys Phe Glu Asp Thr Ile Leu Asp Val  
 275 280 285  
 Ile Pro Ser Pro Asp Ser Pro Phe Lys Arg Pro Trp Val Asp Ser Lys  
 290 295 300  
 Gln Ala Pro Pro Leu Glu Lys Ser Ile Val Gln Thr Val Glu Phe Pro  
 305 310 315 320  
 Glu Glu Asp Glu Ser Phe Gly Glu Ile Glu Ile Arg Phe Leu Gly Pro  
 325 330 335  
 Asp Cys Thr Asp Pro Val Gln Thr Gly Ala Val Asn Val Ala Leu Leu  
 340 345 350  
 Tyr Leu Ala Gly Ser Ser Ala Ser Leu Leu Asp Asn Ile Leu Val Glu  
 355 360 365  
 Lys Glu Gln Leu Ala Ser Ala Val Tyr Tyr Ala Thr Glu Asp His Pro  
 370 375 380  
 Ser Ile Glu Ile Arg Phe Thr Leu Thr Ser Val Glu Thr Glu Lys Leu  
 385 390 395 400  
 Ala Lys Val Glu Gln Arg Phe Phe Glu Val Leu Lys Asp Ala Met Glu  
 405 410 415  
 Lys Asp Leu Asp Met Arg Tyr Ile Lys Glu Cys Ile Asp Arg Gln Arg  
 420 425 430  
 Arg Thr Trp Lys Phe Ser Thr Glu Ser Ser Ala Ser Ser Phe Ala Glu  
 435 440 445  
 Tyr Val Ile Ser Asp Phe Leu Phe Gly Lys Arg Asp Gly Ser Thr Met  
 450 455 460  
 Leu Asp Val Ala Thr Leu Gln Glu Tyr Asp Val Leu Glu Lys Trp Ser

465		470		475		480
Glu Glu Gln Trp	Arg Ser Phe Ile Lys Thr Trp Ile Ser Asp Ala Asn					
	485		490		495	
His Val Thr Ile	Leu Gly Val Pro Ser Val Lys Met Ser Asp Thr Leu					
	500		505		510	
Lys Lys Glu Glu Glu Ala Arg Val Ala Glu Gln Lys Lys Arg Leu Gly						
	515		520		525	
Asp Glu Gly Leu Lys Lys Leu Ala Asp Lys Leu Glu Lys Ala Lys Ala						
	530		535		540	
Glu Asn Asp Lys Glu Ile Pro Lys Glu Met Leu Glu Arg Phe Gln Ile						
	545		550		555	560
Pro Gly Ile Glu Ser Ile His Phe Val Asp Thr Thr Thr Ala Arg Ser						
	565		570		575	
Gly Ala Ala Leu Asp Ala Gly Arg Pro Ser His Lys Ala Gln Lys Leu						
	580		585		590	
Val Asp Ala Asp Gly Ser Asp Leu Pro Leu Phe Ile His Phe Glu His						
	595		600		605	
Ile Pro Ser Ser Phe Val Gln Leu Ser Leu Leu Ile Ser Ala Gln Ala						
	610		615		620	
Val Pro Val Gln Leu Arg Pro Leu Leu Ser Val Tyr Thr Glu Ala Phe						
	625		630		635	640
Phe Asn Leu Pro Val Asn Arg Asn Gly Glu Thr Ile Asn Phe Glu Gln						
	645		650		655	
Val Val Val Glu Leu Glu Arg Asp Thr Val Gly Tyr Ser Met Glu Gly						
	660		665		670	
Ala Arg Ser Leu Gly Asn Ser Glu Met Leu Arg Ile Ser Phe Gln Val						
	675		680		685	
Glu Leu Glu Lys Tyr His Thr Ala Ile Ala Trp Ile Gln Glu Leu Ser						
	690		695		700	

Trp Asn Ser Ile Phe Asp Val Glu Arg Leu Arg Ala Ile Thr Ser Arg  
705 710 715 720

Leu Leu Ser Asp Val Pro Asp Ser Lys Arg Ser Gly Asp Asp Met Leu  
725 730 735

Ala Ala Val His Val Met Val His Tyr Ala Ala Glu Ser Ile Val Arg  
740 745 750

Ala Arg Ser Thr Leu Val Lys Ala Arg Tyr Leu Lys Arg Ile Lys Lys  
755 760 765

Gln Leu Ala Glu Glu Pro Lys Ser Val Val Ala Arg Met Glu Glu Ile  
770 775 780

Arg Asp Ala Leu Phe Arg Phe Glu Asn Met Arg Val Leu Val Ile Ala  
785 790 795 800

Asp Leu Glu Lys Leu Gln Asn Pro Val Ser Ala Trp Lys Pro Phe Ala  
805 810 815

Glu Arg Leu Gly Ala Gly Ala Pro Leu Gln Pro Ile Thr Thr Arg Arg  
820 825 830

Pro Leu Leu Ser Glu Ala Gly Gln Lys Leu Gly Gly Lys Ser Tyr Val  
835 840 845

Val Pro Met Pro Thr Ile Asp Ser Ser Phe Ala Tyr Ala Thr Ala Arg  
850 855 860

Gly Leu Asp Ser Tyr Asp Asp Pro Arg Leu Pro Ala Leu Met Val Ala  
865 870 875 880

Ile Ala Tyr Met Asn Ala Val Glu Gly Pro Leu Trp Val Ala Val Arg  
885 890 895

Gly Lys Gly Leu Ala Tyr Gly Thr Asn Phe Ala Tyr Asn Ile Asp Thr  
900 905 910

Gly Phe Val Asn Phe Asp Val Tyr Arg Ser Pro Asn Ala His Lys Ala  
915 920 925

Phe Asp Ser Ser Lys Gln Ile Val Glu Asp His Leu Ser Gly Ala Met  
 930 935 940

Pro Phe Asp Pro Leu Met Leu Glu Gly Ser Ile Ser Ser Ile Val Val  
 945 950 955 960

Ser Phe Ala Asn Glu Gln Ser Thr Ile Gly Ser Ala Ala Ser Gly Ser  
 965 970 975

Phe Ile Arg Gln Val Ile Arg Arg Leu Pro Ser Asp Tyr Lys Glu Arg  
 980 985 990

Val Leu Lys Gln Val Arg Ala Thr Ser Val Asp Asp Val Lys Gly Ala  
 995 1000 1005

Leu Lys Asp Ile Ile Leu Pro Leu Phe Asn Pro Ser Thr Ala Asn  
 1010 1015 1020

Ile Val Val Thr Cys Ala Thr Val Leu Glu Glu Thr Ile Lys Glu  
 1025 1030 1035

Gly Leu Gln Ala Ser Gly Phe Thr Pro Ala Val Gln Pro Leu Lys  
 1040 1045 1050

Glu Phe Glu Asp Asp Tyr Gly Leu Lys Val Gly Asp Asp Glu Asp  
 1055 1060 1065

Glu Glu Ser Asp Asp Asp Asp Asp Glu Tyr Glu Thr Gly Ser Glu  
 1070 1075 1080

Asp Glu Asp Asp Ser Asp Glu Asp Met Glu Asp Asp Glu Asp Asp  
 1085 1090 1095

Glu

<210> 117  
 <211> 726  
 <212> PRT  
 <213> Aspergillus niger

<400> 117

Met Gly Ala Leu Gln Trp Leu Ser Ile Thr Ala Ala Ala Ala Ser Ala

1	5	10	15
Val	Ser	Ala	Leu
20	Thr	Pro	Glu
		Gln	Met
		25	Ile
		Gly	Ala
		Pro	Arg
		30	Arg
		Thr	
Glu	Val	Ile	Pro
35	Asn	Pro	Ser
		40	Gly
		Asp	Thr
		Gly	Leu
		45	Phe
		Ser	Thr
		Ser	
Gln	Trp	Ser	Phe
50	Asp	Thr	His
		55	Ser
		Glu	Ser
		Thr	Thr
		60	Trp
		Trp	Ser
		Leu	Ile
Asp	Leu	Gln	Ser
65	Gly	Lys	Thr
		70	Thr
		Thr	Leu
		75	Thr
		Asp	Asp
		Ser	Asp
		80	Ile
Glu	Glu	Ile	Ile
		85	Trp
		Leu	Gly
		Ser	Asp
		90	Asn
		Ser	Thr
		Leu	Leu
		95	Tyr
		Ile	
Asn	Ser	Thr	Asn
		100	Ala
		Gln	Val
		Pro	Gly
		105	Gly
		Val	Glu
		Leu	Trp
		110	Ile
		Ala	
Asp	Ser	Ser	Asp
		115	Phe
		Ala	Asn
		120	Ala
		Tyr	Lys
		Ala	Ala
		125	Ser
		Leu	Ser
		Ala	
Gly	Phe	Leu	Gly
130	Ile	Lys	Ser
		135	Thr
		Val	Thr
		Asp	Ser
		140	Gly
		Asp	Val
		His	
Phe	Ile	Leu	Arg
145	Gly	Lys	Ser
		150	Tyr
		Pro	Asn
		155	Gly
		Thr	Ala
		Tyr	Asn
		160	Asp
Gln	Leu	Ala	Glu
		165	Thr
		Tyr	Pro
		Ser	Thr
		170	Ala
		Arg	Ile
		Tyr	Asp
		175	Ser
		Ile	
Phe	Val	Arg	His
		180	Trp
		Asp	Thr
		Tyr	Leu
		185	Thr
		Thr	Ala
		Ser	His
		190	Ala
		Val	
Phe	Ser	Gly	Thr
195	Leu	Gln	Ser
		200	Ser
		Thr	Ser
		Asp	Asp
		205	Gly
		Asn	Val
		Gln	
Tyr	Thr	Ser	Ser
210	Gly	Gly	Leu
		215	Thr
		Asn	Leu
		Val	Asn
		220	Pro
		Val	Lys
		Gly	
Ala	Glu	Ser	Pro
225	Phe	Pro	Pro
		230	Phe
		Gly	Gly
		235	Asn
		Asp	Asp
		Tyr	Asp
		240	Leu

Ser Pro Asp Gly Lys Trp Val Thr Phe Lys Ser Lys Ala Pro Glu Leu  
 245 250 255

Pro Leu Ala Asn Asn Thr Ala Ala Tyr Val Tyr Leu Val Pro His Asp  
 260 265 270

Gly Ser Ala Thr Ala Phe Ala Val Asn Gly Pro Asp Ser Pro Ala Thr  
 275 280 285

Pro Glu Gly Val Glu Gly Glu Ser Asn Asn Pro Val Phe Ser Pro Asp  
 290 295 300

Ser Asp Lys Ile Ala Tyr Phe Gln Met Ala Thr Asn Thr Tyr Glu Ser  
 305 310 315 320

Asp Arg Asn Val Leu Tyr Val Tyr Ser Ile Ala Asp Asp Thr Ile Thr  
 325 330 335

Pro Leu Ala Lys Asp Trp Asp Arg Ser Pro Ser Ser Val Thr Trp Val  
 340 345 350

Asp Gly Asp Asn Leu Val Val Ala Ser Gln Asp Leu Gly Arg Thr Arg  
 355 360 365

Leu Phe Ala Ile Pro Gly Asp Ala Gly Asp Asp Phe Lys Pro Thr Asn  
 370 375 380

Phe Thr Asp Gly Gly Ser Val Ser Ala Gln Tyr Val Leu Ser Asn Ser  
 385 390 395 400

Thr Leu Leu Val Thr Ser Ser Ala Phe Trp Thr Ser Trp Ser Val Tyr  
 405 410 415

Thr Ala Ser Pro Asp Glu Gly Val Ile Asn Thr Leu Ala Ser Ala Asn  
 420 425 430

Glu Ile Asp Pro Glu Leu Ser Gly Leu Ser Ser Ser Asp Phe Glu Glu  
 435 440 445

Phe Tyr Phe Asp Gly Asn Trp Thr Thr Leu Gln Gly Trp Ile Thr Tyr  
 450 455 460

Pro Gln Asp Phe Asp Ser Ser Lys Lys Tyr Pro Leu Ala Phe Leu Ile  
465 470 475 480

His Gly Gly Pro Glu Asp Ala Trp Ala Asp Glu Trp Asn Leu Lys Trp  
485 490 495

His Ser Lys Val Phe Ala Asp Gln Gly Tyr Val Val Val Gln Pro Asn  
500 505 510

Pro Thr Gly Ser Thr Gly Phe Gly Gln Gln Leu Thr Asp Ala Ile Gln  
515 520 525

Leu Asn Trp Thr Gly Ala Ala Tyr Asp Asp Leu Thr Lys Ala Trp Gln  
530 535 540

Tyr Val His Asp Thr Tyr Asp Phe Ile Asp Thr Asp Asn Gly Val Ala  
545 550 555 560

Ala Gly Pro Ser Phe Gly Ala Phe Met Ile Thr Trp Ile Gln Gly Asp  
565 570 575

Asp Phe Gly Arg Lys Phe Lys Ala Leu Val Ser His Asp Gly Pro Phe  
580 585 590

Ile Gly Asp Ala Trp Val Glu Thr Asp Glu Leu Trp Phe Val Glu His  
595 600 605

Glu Phe Asn Gly Thr Phe Trp Gln Ala Arg Asp Ala Phe His Asn Thr  
610 615 620

Asp Pro Ser Gly Pro Ser Arg Val Leu Ala Tyr Ser Thr Pro Gln Leu  
625 630 635 640

Val Ile His Ser Asp Lys Asp Tyr Arg Ile Pro Val Ala Asn Gly Ile  
645 650 655

Gly Leu Phe Asn Thr Leu Gln Glu Arg Gly Val Pro Ser Arg Phe Leu  
660 665 670

Asn Phe Pro Asp Glu Asp His Trp Val Thr Gly Gln Glu Asn Ser Leu  
675 680 685



Val Trp Tyr Gln Gln Val Leu Gly Trp Ile Asn Arg Tyr Ser Gly Val  
 690 695 700

Gly Gly Ser Asn Pro Asp Ala Ile Ala Leu Glu Asp Thr Val Asn Pro  
 705 710 715 720

Val Val Asp Leu Asn Pro  
 725

<210> 118  
 <211> 564  
 <212> PRT  
 <213> Aspergillus niger

<400> 118

Met Thr Arg Gln Thr Ser Leu Val Pro Arg Leu Leu Thr Leu Ala Ser  
 1 5 10 15

Leu Ala Ala Leu Ser Gln Ala Glu Leu Gly Lys Ile Gln Trp Lys Gly  
 20 25 30

Ser Cys Asn Leu Thr Thr Tyr Pro Ala Leu Ile Cys Gly Thr Leu Asp  
 35 40 45

Val Pro Tyr Asp Tyr Thr Glu Ser Asn Ser Ser Lys Thr Leu Thr Leu  
 50 55 60

Asp Ile Ala Lys Trp Pro Ala Thr Lys Lys Pro Val Ser Glu Pro Ile  
 65 70 75 80

Ile Phe Asn Phe Gly Gly Pro Gly Val Asn Ser Phe Glu Gly Leu Gly  
 85 90 95

Leu Tyr Gly Glu Glu Phe Gln Ala Ile Leu Gly Gly His Asn Asp Leu  
 100 105 110

Ile Ala Phe Asn Asn Arg Gly Val Gly Asn Thr Ile Pro Phe Ser Cys  
 115 120 125

Tyr Ser Asp Asp Ala Thr Arg Glu Leu Val Ala Leu Gln Ala Pro Asn  
 130 135 140

Asp Gly Arg Ala Ser Ser Thr Ala Leu Gly Glu Ile Trp Ala Gln Asn  
 145 150 155 160

Ala Asn Ile Ala Gln Ala Cys Tyr Ala Thr Asn Asn Gln Thr Gly Ser  
 165 170 175

Leu Ile Gly Thr Ser Phe Ala Ala Arg Asp Ile Met Gln Val Ala Asp  
 180 185 190

Ala Leu Ser Gly Lys Asp Ser Leu Val Asn Tyr Trp Gly Phe Ser Tyr  
 195 200 205

Gly Thr Thr Ile Gly Ala Val Leu Ala Ala Met Phe Pro Asp Arg Met  
 210 215 220

Gly Asn Val Ala Leu Asp Gly Val Asp Asn Pro Arg Glu Ala Leu Tyr  
 225 230 235 240

Gly Tyr Asn Ala Gln Ala Val Val Asp Val Asp Lys Val Phe Glu Gly  
 245 250 255

Phe Cys Thr Gly Cys Met Ala Ala Pro Asp Leu Cys Pro Ile Ala Lys  
 260 265 270

Glu Tyr Thr Ser Ala Ala Asn Leu Glu Ala Ala Ile Tyr Leu Met Leu  
 275 280 285

Glu Asn Leu Lys Tyr Asn Pro Ile Ala Ile Pro Glu Thr Gly Gly Ile  
 290 295 300

Val Thr Trp Ser Asp Val Lys Ser Thr Ile Phe Glu Ala Met Tyr Leu  
 305 310 315 320

Pro Ser Ser Trp Pro Leu Thr Ser Glu Leu Leu Tyr Tyr Val Gln Thr  
 325 330 335

Arg Asn Thr Thr Ile Leu Gly Asn Ser Glu Val Tyr Asp Thr Ile Lys  
 340 345 350

Ser Tyr Gly Gln Ser Ala Ser Leu Thr Ser Ala Ser Asp Glu Val Gly  
 355 360 365

Thr Ala Ile Thr Cys Ser Asp Lys His Arg Ser Ala Thr Ile Lys Glu  
 370 375 380

Val Leu Pro Tyr Val Lys Ala Arg Gln Ala Leu Thr Lys Ile Gly Ser  
385 390 395 400

Asp Gly Ser Asp Gly Asp Met Arg Cys Ala Gln Trp Asn Pro Lys Met  
405 410 415

Phe Ala Lys Glu Arg Tyr Ser Gly Asp Phe Glu Val Lys Thr Ala Asn  
420 425 430

Pro Val Leu Ile Leu Ser Asn Thr Tyr Asp Pro Ala Thr Pro Leu Pro  
435 440 445

Ala Ala Lys Asn Leu Thr Glu Thr Phe Glu Gly Ser Val Leu Leu Glu  
450 455 460

Gln Asn Gly Tyr Gly His Thr Thr Leu Ser Met Pro Ser Leu Cys Thr  
465 470 475 480

Ala Lys Ala Val Arg Ala Tyr Phe Thr Asn Gly Thr Leu Pro Ala Asp  
485 490 495

Gly Thr Ile Cys Gln Val Asp Val Pro Leu Phe Thr Asn Leu Thr Tyr  
500 505 510

Lys Asp Val Trp Pro Lys Ser Phe Gln Arg Ser Val Glu Ser Arg Asp  
515 520 525

Asp Ala Thr Ile Leu Lys Ala Leu Met Ser Val Arg Asp Lys Met Ser  
530 535 540

Arg Arg Arg Met Cys Ile Tyr Leu Tyr Thr Asn Ser Ala Ser Trp Arg  
545 550 555 560

Pro Glu Leu Pro

<210> 119

<211> 526

<212> PRT

<213> Aspergillus niger

<400> 119

Met Tyr Tyr Ser Leu Trp Val Ala Ala Leu Val Ala Ala Leu Pro Val

1	5	10	15
Ser Arg Ala Gln Phe Val Ala Pro Pro Thr Asp Leu Ile Pro Thr Lys	20	25	30
Gly Tyr Leu Asp Ile Pro Val Arg Tyr Lys Gln Val Pro Thr Gly Ile	35	40	45
Cys Glu Thr Asp Pro Ser Val Lys Ser Phe Ser Gly Tyr Val Asp Val	50	55	60
Ala Glu His Glu His Ile Phe Phe Trp Phe Phe Glu Ala Arg Asn Gln	65	70	75
Asp Pro Thr Glu Ala Pro Leu Thr Val Trp Ile Asn Gly Gly Met Ser	85	90	95
Asp Pro Gly Pro Gly Ser Ser Ser Met Ile Gly Leu Phe Gln Glu His	100	105	110
Gly Pro Cys Gly Ile Asp Ala Asn Gly Ser Val Tyr Asn Asn Pro Tyr	115	120	125
Ser Trp Asn Asn Ala Ser Asn Met Leu Tyr Ile Asp Gln Pro Val Gln	130	135	140
Thr Gly Phe Ser Tyr Ser Ile Pro Val Pro Gly Tyr Val Asp Ser Ser	145	150	155
Thr Asp Asn Gly Phe Met Gly Ala Phe Pro Gln Tyr Ser Arg Glu Thr	165	170	175
Phe His Phe Thr Thr Glu Ser Tyr Gly Gly His Tyr Gly Pro Val Phe	180	185	190
Asn Glu Tyr Ile Glu Glu Gln Asn Ala His Leu Gln Pro Gly Ala Lys	195	200	205
Lys Ile Gln Leu Gly Ser Val Met Ile Gly Asn Gly Trp Tyr Asp Pro	210	215	220
Ile Ile Gln Tyr Gln Ala Tyr Tyr Asn Phe Thr Val Tyr Pro Gly Asn	225	230	235
			240

Thr Tyr Asp Tyr Leu Pro Phe Asn Lys Ser Ile Ser Ser Leu Met Tyr  
 245 250 255

Asn Asn Leu Tyr Gly Pro Gly Asn Cys Leu Asp Gln Leu Tyr Asp Cys  
 260 265 270

Ala Ala Arg Gly Ile Asp Glu Ile Cys Ser Thr Ala Asp Asp Phe Cys  
 275 280 285

Ala Asn Glu Val Glu Asn Val Tyr Asp Ile Tyr Ser Gly Arg Asp Glu  
 290 295 300

Tyr Asp Phe Arg Glu Leu Thr Pro Asp Pro Phe Pro Tyr Glu Phe Tyr  
 305 310 315 320

Val Asp Tyr Leu Asn Lys Ala Ser Val Gln Ala Ala Ile Gly Ala Tyr  
 325 330 335

Ile Asn Tyr Thr Glu Ser Asn Asn Ala Val Gly Leu Ala Phe Ser Ser  
 340 345 350

Thr Gly Asp Asp Gly Arg Leu Met Asn Thr Ile Gln Asp Val Gly Lys  
 355 360 365

Leu Leu Lys Gln Gly Val Thr Val Val Met Tyr Ala Gly Asp Ala Asp  
 370 375 380

Tyr Asn Cys Asn Trp Leu Gly Gly Glu Ala Val Ser Leu Gln Val Lys  
 385 390 395 400

Ala Ala Asn Phe Ser Ser Ala Gly Tyr Thr Asn Ile Val Thr Ser Asp  
 405 410 415

Gly Val Thr His Gly Gln Val Arg Gln Ala Gly Gln Phe Ala Phe Val  
 420 425 430

Arg Val Tyr Glu Ser Gly His Glu Val Pro Phe Tyr Gln Pro Leu Leu  
 435 440 445

Ala Leu Glu Met Phe Glu Arg Val Ile Gly Gly Lys Asp Val Ala Thr  
 450 455 460

Gly Lys Ile Pro Ile Ser Ser Ser Leu Gln Thr Val Gly Thr Pro Lys  
 465 470 475 480

Ser Tyr Tyr Arg Glu Gly Asn Ser Thr Ile Gln Trp Glu Val Leu Asp  
 485 490 495

Ser Leu Ala Thr Tyr Asn Thr Thr Thr Asn Ala Pro Asn Pro Val Ser  
 500 505 510

Arg Arg Leu Lys Arg Met Gly Pro Ala Leu Arg Phe Gln Met  
 515 520 525

<210> 120  
 <211> 1156  
 <212> PRT  
 <213> Aspergillus niger  
 <400> 120

Met Ser Cys Val Trp Leu His Ile His Lys Arg Ser Leu Leu Ser Val  
 1 5 10 15

Ala Thr Asn Asn Ser Val Ala Arg Ala Ala Ala Ser Thr Ser Ala Ala  
 20 25 30

Pro Pro Pro Pro Ser Ser Pro Pro Pro Gly Ser Asn Thr Tyr Ser Pro  
 35 40 45

Leu Tyr Arg Pro Ile Thr Asn Pro Ile Gly Phe Thr Leu Ser Pro Ala  
 50 55 60

Arg Ser Leu Val Ser Arg Asn Pro Lys Phe Pro Ala Tyr Arg Arg Ser  
 65 70 75 80

Ser Arg His Phe Ser Leu Cys Pro Ala Ala Ala Thr Pro Gly Val Thr  
 85 90 95

Thr Ser Ile Cys Pro Gly Gln Ala Pro Val Arg Ser Leu Ser Ser Leu  
 100 105 110

Ile Ile His Ser Thr Arg Pro Arg Ala Ile Arg Ile Arg Thr Asp Gln  
 115 120 125

Met Asp Leu Asn Gly Asp Ala Gly Ala Lys Arg Lys Arg Ser Ser Ile

130                      135                      140  
 Thr Thr Pro Ala Glu Arg Pro Val Lys His Leu Arg Pro Glu Ser Ser  
 145                      150                      155                      160  
 Ala Leu Thr Pro Gly Asp Ser Thr Pro Ala Asn Gly Thr Val Tyr Asp  
 165                      170                      175  
 Val Glu Asp Asp Glu Asp Ala Ser Arg Leu Leu Pro Val Gly Pro Ala  
 180                      185                      190  
 Gln Ala Asp Ser Pro Glu Trp Gln Ala Thr Ile Glu Glu Val Val Lys  
 195                      200                      205  
 Ser Val Val Ser Ile His Phe Cys Gln Thr Cys Ser Phe Asp Thr Glu  
 210                      215                      220  
 Leu Ser Met Ser Ser Gln Ala Thr Gly Phe Val Val Asp Ala Glu Asn  
 225                      230                      235                      240  
 Gly Tyr Ile Leu Thr Asn Arg His Val Val Cys Pro Gly Pro Phe Trp  
 245                      250                      255  
 Gly Tyr Cys Ile Phe Asp Asn His Glu Glu Cys Asp Val Arg Pro Val  
 260                      265                      270  
 Tyr Arg Asp Pro Val His Asp Phe Gly Ile Leu Lys Phe Asp Pro Lys  
 275                      280                      285  
 Ala Ile Arg Tyr Met Lys Leu Arg Glu Leu Lys Leu Gln Pro Asp Ala  
 290                      295                      300  
 Ala Lys Val Gly Ser Glu Ile Arg Val Val Gly Asn Asp Ala Gly Glu  
 305                      310                      315                      320  
 Lys Leu Ser Ile Leu Ser Gly Val Ile Ser Arg Leu Asp Arg Asn Ala  
 325                      330                      335  
 Pro Glu Tyr Gly Asp Gly Tyr Ser Asp Phe Asn Thr Asn Tyr Ile Gln  
 340                      345                      350  
 Ala Ala Ala Ala Ala Ser Gly Gly Ser Ser Gly Ser Pro Val Val Asn  
 355                      360                      365

Ile Asp Gly His Ala Ile Ala Leu Gln Ala Gly Gly Arg Ala Asp Gly  
 370 375 380

Ala Ala Thr Asp Tyr Phe Leu Pro Leu Asp Arg Pro Leu Arg Ala Leu  
 385 390 395 400

Glu Cys Ile Arg Arg Gly Glu Pro Val Thr Arg Gly Thr Ile Gln Thr  
 405 410 415

Gln Trp Ile Leu Lys Pro Phe Asp Glu Cys Arg Arg Leu Gly Leu Thr  
 420 425 430

Pro Glu Trp Glu Ala Thr Val Arg Lys Ala Ala Pro Thr Glu Thr Ser  
 435 440 445

Met Leu Val Ala Glu Ile Ile Leu Pro Glu Gly Pro Ala Asp Gly Lys  
 450 455 460

Leu Glu Glu Gly Asp Val Leu Leu Gln Val Asn Gly Val Leu Leu Thr  
 465 470 475 480

Gln Phe Ile Arg Leu Asp Asp Ile Leu Asp Ser Ser Val Gly Gln Thr  
 485 490 495

Val Arg Leu Leu Val Gln Arg Gly Gly Gln Asn Val Glu Ile Glu Cys  
 500 505 510

Gln Val Gly Asp Leu His Ala Ile Thr Pro Asp Arg Phe Val Thr Val  
 515 520 525

Ala Gly Gly Thr Phe His Asn Leu Ser Tyr Gln Gln Ser Arg Leu Tyr  
 530 535 540

Ala Ile Ala Thr Arg Gly Val Tyr Val Cys Glu Ala Ala Gly Ser Phe  
 545 550 555 560

Lys Leu Glu Asn Thr Leu Ser Gly Trp Ile Ile Asp Ser Val Asp Lys  
 565 570 575

Arg Pro Thr Arg Asn Leu Asp Glu Phe Val Glu Val Met Arg Thr Ile  
 580 585 590



Pro Asp Arg Ser Arg Val-Val Ile Ser Tyr Arg His Ile Arg Asp Leu  
 595 600 605

His Thr Arg Gly Thr Ser Ile Val Tyr Ile Asp Arg His Trp His Pro  
 610 615 620

Lys Met Arg Leu Ala Val Arg Asn Asp Asp Thr Gly Leu Trp Asp Phe  
 625 630 635 640

Ser Asp Leu Ala Asp Pro Ile Pro Ala Leu Pro Pro Val Pro Arg Lys  
 645 650 655

Ala Asp Phe Ile Gln Leu Asp Gly Val Ser Gln Pro Ala Ala Ala Asp  
 660 665 670

Ile Val Arg Ser Phe Val Arg Val Ser Cys Thr Met Pro Leu Lys Leu  
 675 680 685

Asp Gly Tyr Pro Gln Ala Lys Lys Thr Gly Phe Gly Leu Val Val Asp  
 690 695 700

Ala Glu Lys Gly Leu Val Val Val Ser Arg Ala Ile Val Pro Tyr Asp  
 705 710 715 720

Leu Cys Asp Ile Asn Val Thr Val Ala Asp Ser Ile Ile Val Asn Ala  
 725 730 735

Lys Val Val Phe Leu His Pro Leu Gln Asn Tyr Ser Ile Ile Gln Tyr  
 740 745 750

Asp Pro Ser Leu Val Gln Ala Pro Val Gln Ser Ala Lys Leu Ala Thr  
 755 760 765

Asp Tyr Ile Lys Gln Gly Gln Asp Thr Ile Phe Val Gly Phe Asn Gln  
 770 775 780

Asn Phe Arg Ile Val Val Ala Lys Thr Ala Val Thr Asp Ile Thr Thr  
 785 790 795 800

Val Ser Ile Pro Ala Asn Ala Ser Ala Pro Arg Tyr Arg Ala Ile Asn  
 805 810 815

Leu Asp Ala Ile Thr Val Asp Thr Gly Leu Ser Gly Gln Cys Ser Asn  
                   820                  825                  830

Gly Val Leu Ile Gly Glu Asp Gly Val Val Gln Ala Leu Trp Leu Asn  
                   835                  840                  845

Tyr Leu Gly Glu Arg Thr Ser Asn Ser His Lys Asp Val Glu Tyr His  
           850                  855                  860

Leu Gly Phe Ala Thr Pro Ser Leu Leu Pro Val Leu Ser Lys Val Gln  
  865                  870                  875                  880

Gln Gly Glu Met Pro Glu Leu Arg Ile Leu Asn Met Glu Ser Tyr Val  
                   885                  890                  895

Val Gln Met Ser Gln Ala Arg Ile Met Gly Val Ser Glu Glu Trp Ile  
                   900                  905                  910

Glu Lys Val Thr Gln Ala Asn Pro Ser Arg His Gln Leu Phe Met Val  
           915                  920                  925

Arg Lys Val Asp Cys Pro Pro Pro Gly Phe Asn Ser Ala Ala Asp Thr  
  930                  935                  940

Phe Glu Glu Gly Asp Ile Ile Leu Thr Leu Asp Gly Gln Leu Ile Thr  
  945                  950                  955                  960

Arg Val Ser Glu Leu Asp Ile Met Tyr Glu Lys Asp Thr Leu Glu Ala  
                   965                  970                  975

Leu Ile Val Arg Asn Gly Gln Glu Met Arg Ile Gln Val Pro Thr Val  
           980                  985                  990

Pro Thr Glu Asp Leu Glu Thr Asp Arg Ala Val Val Phe Cys Gly Ala  
           995                  1000                  1005

Val Leu Gln Lys Pro His His Ala Val Arg Gln Gln Ile Ser Lys  
  1010                  1015                  1020

Leu His Ser Glu Val Tyr Val Ser Ala Arg Ser Arg Gly Ser Pro  
  1025                  1030                  1035

Ser Tyr Gln Tyr Gly Leu Ala Pro Thr Asn Phe Ile Thr Ala Val

1040                      1045                      1050  
 Asn Gly Val Pro Thr Pro Asn Leu Asp Arg Phe Ser Glu Glu Val  
 1055                      1060                      1065  
 Ser Lys Ile Pro Asp Asn Thr Tyr Phe Arg Leu Arg Ala Val Thr  
 1070                      1075                      1080  
 Phe Asp Asn Val Pro Trp Val Val Thr Val Lys Lys Asn Asp His  
 1085                      1090                      1095  
 Tyr Phe Pro Met Ser Glu Tyr Ile Lys Asp Gln Ser Gln Pro Ser  
 1100                      1105                      1110  
 Gly Trp Arg Thr Val Ser His Asp Lys Asp Lys Tyr Lys Asp Gly  
 1115                      1120                      1125  
 Ile Ala Pro Asp Ala Ala Asn Leu Asn Pro Asp Ala Met Asp Glu  
 1130                      1135                      1140  
 Gly Phe Asp Gly Val Ser Asp Ile Glu Pro Asp Leu Glu  
 1145                      1150                      1155  
  
 <210> 121  
 <211> 536  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 121  
  
 Met Arg Val Leu Pro Ala Ala Met Leu Val Gly Ala Ala Thr Ala Ala  
 1                      5                      10                      15  
  
 Val Pro Pro Phe Gln Gln Val Leu Gly Gly Asn Gly Ala Lys His Gly  
 20                      25                      30  
  
 Ala Asp His Ala Ala Glu Val Pro Ala Asp His Ser Ala Asp Gly Phe  
 35                      40                      45  
  
 Ser Lys Pro Leu His Ala Phe Gln Glu Glu Leu Lys Ser Leu Ser Asp  
 50                      55                      60  
  
 Glu Ala Arg Lys Leu Trp Asp Glu Val Ala Ser Phe Phe Pro Glu Ser  
 65                      70                      75                      80

Met Asp Gln Asn Pro Leu Phe Ser Leu Pro Lys Lys His Asn Arg Arg  
                             85                            90                            95

Pro Asp Ser His Trp Asp His Ile Val Asp Gly Lys Leu Glu Ala Tyr  
                             100                            105                            110

Asp Leu Arg Val Lys Lys Thr Asp Pro Gly Ser Leu Gly Ile Asp Pro  
                             115                            120                            125

Gly Val Lys Gln Tyr Thr Gly Tyr Leu Asp Asp Asn Glu Asn Asp Lys  
                             130                            135                            140

His Leu Phe Tyr Trp Phe Phe Glu Ser Arg Asn Asp Pro Glu Asn Asp  
 145                            150                            155                            160

Pro Val Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Thr  
                             165                            170                            175

Gly Leu Phe Met Glu Leu Gly Pro Ser Ser Ile Asn Lys Lys Ile Gln  
                             180                            185                            190

Pro Val Tyr Asn Asp Tyr Ala Trp Asn Ser Asn Ala Ser Val Ile Phe  
                             195                            200                            205

Leu Asp Gln Pro Val Asn Val Gly Tyr Ser Tyr Ser Asn Ser Ala Val  
                             210                            215                            220

Ser Asp Thr Val Ala Ala Gly Lys Asp Val Tyr Ala Leu Leu Thr Leu  
 225                            230                            235                            240

Phe Phe Lys Gln Phe Pro Glu Tyr Ala Lys Gln Asp Phe His Ile Ala  
                             245                            250                            255

Gly Glu Ser Tyr Ala Gly His Tyr Ile Pro Val Phe Ala Ser Glu Ile  
                             260                            265                            270

Leu Ser His Lys Lys Arg Asn Ile Asn Leu Gln Ser Val Leu Ile Gly  
                             275                            280                            285

Asn Gly Leu Thr Asp Gly Tyr Thr Gln Tyr Glu Tyr Tyr Arg Pro Met  
                             290                            295                            300

Ala Cys Gly Asp Gly Gly Tyr Pro Ala Val Leu Asp Glu Ser Ser Cys  
 305 310 315 320

Gln Ser Met Asp Asn Ala Leu Pro Arg Cys Gln Ser Met Ile Glu Ser  
 325 330 335

Cys Tyr Ser Ser Glu Ser Ala Trp Val Cys Val Pro Ala Ser Ile Tyr  
 340 345 350

Cys Asn Asn Ala Leu Leu Ala Pro Tyr Gln Arg Thr Gly Gln Asn Val  
 355 360 365

Tyr Asp Val Arg Gly Lys Cys Glu Asp Ser Ser Asn Leu Cys Tyr Ser  
 370 375 380

Ala Met Gly Tyr Val Ser Asp Tyr Leu Asn Lys Pro Glu Val Ile Glu  
 385 390 395 400

Ala Val Gly Ala Glu Val Asn Gly Tyr Asp Ser Cys Asn Phe Asp Ile  
 405 410 415

Asn Arg Asn Phe Leu Phe His Gly Asp Trp Met Lys Pro Tyr His Arg  
 420 425 430

Leu Val Pro Gly Leu Leu Glu Gln Ile Pro Val Leu Ile Tyr Ala Gly  
 435 440 445

Asp Ala Asp Phe Ile Cys Asn Trp Leu Gly Asn Lys Ala Trp Thr Glu  
 450 455 460

Ala Leu Glu Trp Pro Gly Gln Ala Glu Tyr Ala Ser Ala Glu Leu Glu  
 465 470 475 480

Asp Leu Val Ile Val Asp Asn Glu His Thr Gly Lys Lys Ile Gly Gln  
 485 490 495

Val Lys Ser His Gly Asn Phe Thr Phe Met Arg Leu Tyr Gly Gly Gly  
 500 505 510

His Met Val Pro Met Asp Gln Pro Glu Ser Ser Leu Glu Phe Phe Asn  
 515 520 525

Arg Trp Leu Gly Gly Glu Trp Phe

530

535

&lt;210&gt; 122

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Aspergillus niger

&lt;400&gt; 122

Met Lys Phe Thr Asn Tyr Leu Leu Thr Thr Ala Thr Leu Ala Ser Ser  
 1 5 10 15

Val Leu Ala Ala Pro Ala Pro Arg Thr Gly Leu Glu Asp Arg Leu Arg  
 20 25 30

Ala Arg Ser Leu Gln Arg Gln Ser His Pro Leu Ala Pro Ile Pro Leu  
 35 40 45

Asp Thr Ser Thr Lys Glu Asn Ser Arg Leu Leu Glu Ala Asp Glu Asn  
 50 55 60

Thr Thr His Val Thr Tyr Ser Ser Asn Trp Ala Gly Ala Val Arg Glu  
 65 70 75 80

Gln Pro Pro Pro Gln Gly Thr Tyr Ser Ala Val Ser Ala Thr Phe Arg  
 85 90 95

Val Pro Glu Pro Thr Ala Gln Gly Gly Ser Gly Thr Gln Ala Gly Ser  
 100 105 110

Ala Trp Val Gly Ile Asp Gly Asp Thr Tyr Ser Asn Ala Ile Leu Gln  
 115 120 125

Thr Gly Val Asp Phe Tyr Val Glu Asn Gly Gln Thr Tyr Asn Asp Ala  
 130 135 140

Trp Tyr Glu Trp Tyr Pro Asp Tyr Ala Tyr Asp Phe Asp Leu Asp Val  
 145 150 155 160

Ser Thr Gly Asp Thr Ile Val Ala Lys Val Glu Ala Ile Ser Pro Ser  
 165 170 175

Gln Gly Val Ala Thr Ile Glu Asn Ile Ser Thr Gly Lys Lys Ala Thr  
 180 185 190

Gln Thr Ile Arg Ala Pro Ala Ala Thr Ala Thr Leu Ala Gly Gln Asn  
 195 200 205

Ala Asp Trp Ile Val Glu Asp Phe Gln Ser Gly Asp Ser Met Val Asp  
 210 215 220

Leu Ala Gly Phe Gly Glu Ile Ser Phe Trp Gly Val Gln Ala Gln Gly  
 225 230 235 240

Gly Gly Ser Thr Trp Gly Val Asp Asp Ala Thr Ile Val Glu Leu Lys  
 245 250 255

Gln Gly Asn Glu Val Leu Thr Asp Val Glu Val Gln Ser Asp Ser Ala  
 260 265 270

Phe Thr Val Lys Tyr Thr Ser  
 275

<210> 123  
 <211> 573  
 <212> PRT  
 <213> Aspergillus niger

<400> 123

Met Ile Tyr Val Asn Tyr Ile Leu Gly Leu Leu Ser Leu Leu His Thr  
 1 5 10 15

Ala Val Ala Thr Ala Pro Asp Tyr Val Val Val Asp Gln Leu Asn Ser  
 20 25 30

Ile Pro Asp Gly Trp Thr Lys Gly Ala Ala Pro Pro Pro Phe Thr Pro  
 35 40 45

Met Lys Phe Trp Leu Ser Met His His Glu Tyr Lys Ala Asp Phe Glu  
 50 55 60

Gln Lys Val Ile Asp Ile Ser Thr Pro Gly His Arg Asp Tyr Gly Arg  
 65 70 75 80

His Met Lys Arg Asn Asp Val Met Ala Phe Met Arg Pro Ser Asp Gln  
 85 90 95

Val Ser Lys Ile Ile Phe Ser Trp Leu Glu Ser Glu His Val Pro Pro

100	105	110
Asn Ala Ile Glu Asp Arg Gly Asp Trp Val Ala Phe Thr Val Pro Leu		
115	120	125
Ala Gln Ala Gln Ser Met Met Lys Thr Asp Phe Tyr Asn Phe His His		
130	135	140
Leu Glu Thr Asn Thr Thr Gln Ile Arg Thr Leu Lys Tyr Ser Val Pro		
145	150	155
Glu Gln Val Asp Ala His Leu Gln Met Ile Gln Pro Thr Thr Arg Phe		
165	170	175
Gly Arg Pro Lys Thr Gln Thr Ser Leu Pro Ser Leu Met Pro Val Ser		
180	185	190
Val Asn Ile Asp Glu Ile Ser Glu Asp Cys Leu Thr Gly Val Thr Pro		
195	200	205
Ile Cys Leu Arg Gln Leu Tyr Gly Leu Pro Ser Thr Lys Ala Ser Pro		
210	215	220
Asp Ser Arg Asn Val Leu Gly Ile Ser Gly Tyr Leu Asp Gln Tyr Ala		
225	230	235
Arg Tyr Ser Asp Leu Asp Glu Phe Leu Ala Val Tyr Ser Pro Asn Ser		
245	250	255
Val Asp Ala Asp Phe Ser Val Val Ser Ile Asn Gly Gly Gln Asn Pro		
260	265	270
Gln Asn Ser Gln Glu Gly Ser Thr Glu Ala Ser Leu Asp Ile Gln Tyr		
275	280	285
Ala Leu Ser Met Ala Phe Asp Ala Asn Ala Thr Phe Tyr Thr Thr Ala		
290	295	300
Gly Arg Ala Pro Ser Pro Tyr Leu Glu Gln Leu Gln Tyr Leu Val Gly		
305	310	315
Leu Pro Asp Glu Asp Leu Pro Ala Val Leu Ser Thr Ser Tyr Gly Glu		
325	330	335



Asp Glu Gln Ser Leu Pro Glu Glu Tyr Thr Glu Ala Thr Cys Asn Leu  
 340 345 350

Phe Ala Gln Leu Gly Ala Arg Gly Val Ser Val Ile Phe Ser Ser Gly  
 355 360 365

Asp Ser Gly Val Gly Gly Ser Cys Val Ser Asn Asp Gly Ser Gln Arg  
 370 375 380

Thr Arg Phe Gln Pro Ile Phe Pro Ala Ser Cys Pro Phe Val Thr Ser  
 385 390 395 400

Val Gly Gly Thr Glu Gly Val Gly Pro Glu Lys Ala Val Asp Phe Ser  
 405 410 415

Ser Gly Gly Phe Ser Glu Arg Phe Ala Arg Pro Ser Tyr Gln Asn Ala  
 420 425 430

Ser Val Glu Ala Tyr Leu Ala Arg Leu Gly Asp Lys Trp Asp Gly Leu  
 435 440 445

Tyr Asn Pro Asp Gly Arg Gly Ile Pro Asp Val Ser Ala Gln Ala Ser  
 450 455 460

Asn Tyr Val Ile Arg Asp His Gly Gln Trp Leu Gln Thr Ala Gly Thr  
 465 470 475 480

Ser Ala Ala Ala Pro Val Phe Ala Ala Val Ile Ser Arg Leu Asn Ala  
 485 490 495

Ala Arg Leu Glu Gln Gly Lys Pro Thr Leu Gly Phe Leu Asn Pro Trp  
 500 505 510

Leu Tyr Ser Leu Asp Gln Gln Gly Phe Thr Asp Ile Val Asp Gly Gly  
 515 520 525

Ser Val Gly Cys Asp Gly Ser Asn Gly Gly Ala Leu Val Pro Tyr Ala  
 530 535 540

Ser Trp Asn Ala Thr Lys Gly Trp Asp Pro Val Thr Gly Leu Gly Thr  
 545 550 555 560

Pro Leu Tyr Gln Thr Leu Glu Gln Leu Ala Gln Ser Ala  
 565 570

<210> 124  
 <211> 585  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 124

Met Arg Ser Ser Gly Leu Tyr Thr Ala Leu Leu Cys Ser Leu Ala Ala  
 1 5 10 15

Ser Thr Asn Ala Ile Val His Glu Lys Leu Ala Ala Val Pro Ser Gly  
 20 25 30

Trp His His Val Glu Asp Ala Gly Ser Asp His Gln Ile Ser Leu Ser  
 35 40 45

Ile Ala Leu Ala Arg Lys Asn Leu Asp Gln Leu Glu Ser Lys Leu Lys  
 50 55 60

Asp Leu Ser Thr Pro Gly Glu Ser Gln Tyr Gly Gln Trp Leu Asp Gln  
 65 70 75 80

Glu Asp Val Asp Thr Leu Phe Pro Val Ala Ser Asp Lys Ala Val Ile  
 85 90 95

Asn Trp Leu Arg Ser Ala Asn Ile Thr His Ile Ser Arg Gln Gly Ser  
 100 105 110

Leu Val Asn Phe Ala Thr Thr Val Asp Lys Val Asn Lys Leu Leu Asn  
 115 120 125

Ala Thr Phe Ala Tyr Tyr Gln Ser Gly Ser Ser Gln Arg Leu Arg Thr  
 130 135 140

Thr Glu Tyr Ser Ile Pro Asp Asp Leu Val Asp Ser Ile Asp Leu Ile  
 145 150 155 160

Ser Pro Thr Thr Phe Phe Gly Lys Glu Lys Thr Thr Ala Gly Leu Asn  
 165 170 175

Gln Arg Ala Gln Lys Ile Asp Thr His Val Ala Lys Arg Ser Asn Ser

180	185	190
Ser Ser Cys Ala Asp Val Ile Thr Leu Ser Cys Leu Lys Glu Met Tyr 195 200 205		
Asn Phe Gly Asn Tyr Thr Pro Ser Ala Ser Ser Gly Ser Lys Leu Gly 210 215 220		
Phe Gly Ser Phe Leu Asn Glu Ser Ala Ser Tyr Ser Asp Leu Ala Lys 225 230 235 240		
Phe Glu Lys Leu Phe Asn Leu Pro Ser Gln Ser Phe Ser Val Glu Leu 245 250 255		
Val Asn Gly Gly Val Asn Asp Gln Asn Gln Ser Thr Ala Ser Leu Thr 260 265 270		
Glu Ala Asp Leu Asp Val Glu Leu Leu Val Gly Val Ala His Pro Leu 275 280 285		
Pro Val Thr Glu Phe Ile Thr Ser Gly Glu Pro Ala Ala Asp Asn Glu 290 295 300		
Asn Glu Pro Tyr Leu Gln Tyr Tyr Glu Tyr Leu Leu Ser Lys Pro Asn 305 310 315 320		
Ser Ala Leu Pro Gln Val Ile Ser Asn Ser Tyr Gly Asp Asp Glu Gln 325 330 335		
Thr Val Pro Glu Tyr Tyr Ala Lys Arg Val Cys Asn Leu Ile Gly Leu 340 345 350		
Val Gly Leu Arg Gly Ile Ser Val Leu Glu Ser Ser Gly Asp Glu Gly 355 360 365		
Ile Gly Ser Gly Cys Arg Thr Thr Asp Gly Thr Asn Arg Thr Gln Phe 370 375 380		
Asn Pro Ile Phe Pro Ala Thr Cys Pro Tyr Val Thr Ala Val Gly Gly 385 390 395 400		
Thr Met Ser Tyr Ala Pro Glu Ile Ala Trp Glu Ala Ser Ser Gly Gly 405 410 415		

Phe Ser Asn Tyr Phe Glu Arg Ala Trp Phe Gln Lys Glu Ala Val Gln  
 420 425 430

Asn Tyr Leu Ala His His Ile Thr Asn Glu Thr Lys Gln Tyr Tyr Ser  
 435 440 445

Gln Phe Ala Asn Phe Ser Gly Arg Gly Phe Pro Asp Val Ala Ala His  
 450 455 460

Ser Phe Glu Pro Ser Tyr Glu Val Ile Phe Tyr Gly Ala Arg Tyr Gly  
 465 470 475 480

Ser Gly Gly Thr Ser Ala Ala Cys Pro Leu Phe Ser Ala Leu Val Gly  
 485 490 495

Met Leu Asn Asp Ala Arg Leu Arg Ala Gly Lys Ser Thr Leu Gly Phe  
 500 505 510

Leu Asn Pro Leu Leu Tyr Ser Lys Gly Tyr Arg Ala Leu Thr Asp Val  
 515 520 525

Thr Gly Gly Gln Ser Ile Gly Cys Asn Gly Ile Asp Pro Gln Asn Asp  
 530 535 540

Glu Thr Val Ala Gly Ala Gly Ile Ile Pro Trp Ala His Trp Asn Ala  
 545 550 555 560

Thr Val Gly Trp Asp Pro Val Thr Gly Leu Gly Leu Pro Asp Phe Glu  
 565 570 575

Lys Leu Arg Gln Leu Val Leu Ser Leu  
 580 585

<210> 125

<211> 265

<212> PRT

<213> *Aspergillus niger*

<400> 125

Met Lys Thr Thr Ala Leu Leu Thr Ala Gly Leu Leu Ala Thr Thr Ala  
 1 5 10 15

Met Ala Ala Pro Leu Thr Ala Lys Arg Gln Ala Ala Arg Ala Lys Arg  
                   20                  25                  30

Ser Thr Asn Arg Gln Ser Asn Pro Pro Phe Lys Pro Gly Thr Asn Glu  
           35                  40                  45

Val Leu Ala Leu Asn Gly Thr Lys Asn Val Glu Tyr Ser Ser Asn Trp  
   50                  55                  60

Ala Gly Ala Val Leu Ile Gly Thr Gly Tyr Thr Ala Val Thr Ala Glu  
 65                  70                  75                  80

Phe Val Val Pro Thr Pro Ser Val Pro Ser Gly Gly Ser Ser Arg Glu  
                   85                  90                  95

Glu Tyr Cys Ala Ser Ala Trp Val Gly Ile Asp Gly Asp Thr Cys Asp  
           100                  105                  110

Thr Ala Ile Leu Gln Thr Gly Val Asp Phe Cys Val Gln Gly Ser Glu  
   115                  120                  125

Val Ser Phe Asp Ala Trp Tyr Glu Trp Tyr Pro Asp Tyr Ala Tyr Asp  
   130                  135                  140

Phe Ser Gly Ile Ser Ile Ser Ala Gly Asp Thr Ile Lys Val Thr Val  
 145                  150                  155                  160

Asp Ala Ser Ser Asp Thr Thr Gly Thr Ala Thr Ile Glu Asn Val Ser  
           165                  170                  175

Thr Gly Thr Thr Val Thr His Ser Phe Thr Gly Gly Val Asp Gly Asp  
   180                  185                  190

Leu Cys Glu Tyr Asn Ala Glu Trp Ile Val Glu Asp Phe Glu Glu Asp  
   195                  200                  205

Asp Ser Leu Val Pro Phe Ala Asp Phe Gly Thr Val Thr Phe Thr Ser  
   210                  215                  220

Cys Ser Ala Thr Lys Asp Gly Ser Ser Val Gly Pro Glu Asp Ala Thr  
 225                  230                  235                  240

Ile Ile Asp Ile Glu Gln Asn Glu Val Leu Thr Ser Val Ser Val Ser

245

250

255

Ser Ser Glu Val Val Val Lys Tyr Val  
260 265

<210> 126  
<211> 580  
<212> PRT  
<213> Aspergillus niger

<400> 126

Met Val Ala Phe Ser Arg Ile Ser Ala Gly Phe Ala Leu Ala Ala Pro  
1 5 10 15

Ala Leu Ala Ser Val Val Leu Glu Thr Val Lys Ser Val Pro Ser Asp  
20 25 30

Trp Lys Leu Val Glu Ala Ala Asp Thr Ser Ser Thr Ile Ser Leu Ser  
35 40 45

Val Ala Leu Ala Arg Gln Asn Leu Asp Gln Leu Glu Glu Lys Leu Leu  
50 55 60

Ala Val Ser Thr Pro Gly Lys Asp Thr Tyr Gly Gln Phe Leu Asp Leu  
65 70 75 80

Asp Asp Ile Asn Glu Gln Phe Pro Leu Ala Asp Asp Ala Ala Val Val  
85 90 95

Ala Trp Leu Lys Lys Ala Gly Val Thr Gln Ile His Lys Glu Gly Gly  
100 105 110

Leu Leu Asn Phe Ala Thr Thr Val Gly Thr Ala Asn Gln Leu Leu Asn  
115 120 125

Thr Thr Phe Ser Val Tyr Lys Ser Gly Ser Thr Gln Lys Leu Arg Thr  
130 135 140

Thr Gln Tyr Ser Val Pro Asp Glu Leu Thr Gly Ser Ile Asp Leu Ile  
145 150 155 160

Ser Pro Thr Val Phe Phe Gly Lys Ser Asn Ala Ala Arg Ser Ala Ala  
165 170 175

Val Arg Ala Ser Gln Thr Thr Lys Glu Thr Ser Arg Lys Lys Ser Ser  
 180 185 190

Asn Val Cys Glu Tyr Ile Thr Pro Asp Cys Leu Lys Glu Gln Tyr Ser  
 195 200 205

Ile Asp Tyr Thr Pro Glu Ala Ser Ser Gly Ser Arg Val Gly Phe Gly  
 210 215 220

Ser Phe Leu Asn Glu Ser Ala Leu Tyr Ser Asp Leu Asp Leu Phe Thr  
 225 230 235 240

Gln Tyr Phe Asp Ile Pro Gln Gln Ser Phe Thr Val Glu Thr Ile Asn  
 245 250 255

Gly Gly Ile Asn Asn Gln Glu Asn Asp Pro Asp Gly Glu Ala Asp Leu  
 260 265 270

Asp Val Gln Asn Ile Val Gly Ile Ser His Pro Leu Pro Val Thr Glu  
 275 280 285

Tyr Ile Thr Gly Gly Ser Pro Pro Phe Ile Pro Asp Val Glu Thr Thr  
 290 295 300

Thr Asp Glu Asn Glu Pro Tyr Leu Gln Tyr Tyr Glu Tyr Leu Leu Ala  
 305 310 315 320

Lys Thr Asn Asp Glu Leu Pro Leu Val Ile Ser Asn Ser Tyr Gly Asp  
 325 330 335

Asp Glu Asp Thr Val Pro Ile Ala Tyr Ala Thr Arg Val Cys Asn Leu  
 340 345 350

Ile Gly Leu Met Gly Thr Arg Gly Ile Ser Ile Leu Glu Ser Ser Gly  
 355 360 365

Asp Ser Gly Val Gly Gly Ala Cys Met Ser Asn Asp Gly Thr Asp Lys  
 370 375 380

Thr Glu Phe Thr Pro Met Phe Pro Gly Thr Cys Pro Tyr Ile Thr Ala  
 385 390 395 400

Val Gly Gly Thr Gln Asp Val Pro Glu Val Ala Trp Val Asp Ser Ser  
 405 410 415

Gly Gly Phe Ser Asn Tyr Phe Ser Gln Pro Ser Tyr Gln Ser Asp Gln  
 420 425 430

Val Glu Thr Tyr Leu Asp Lys Tyr Ile Ser Ala Ser Thr Lys Lys Tyr  
 435 440 445

Tyr Glu Gln Tyr Thr Asn Phe Ser Gly Arg Ala Phe Pro Asp Val Ser  
 450 455 460

Ala Phe Ala Gly Ser Pro Tyr Tyr Glu Thr Tyr Ile Asp Gly Gln Leu  
 465 470 475 480

Gly Leu Val Ala Gly Thr Ser Gly Ala Ser Pro Val Phe Ala Gly Ile  
 485 490 495

Val Ala Leu Leu Asn Asp Ala Arg Leu Arg Ala Asn Lys Thr Ser Leu  
 500 505 510

Gly Phe Leu Asn Pro Trp Leu Tyr Ser Ser Gly Tyr Lys Ser Leu Asn  
 515 520 525

Asp Ile Thr Ser Gly Glu Ala Val Gly Cys Gln Gly Asp Val Glu Gly  
 530 535 540

Ala Gly Val Ile Pro Trp Ala Ser Trp Asn Ala Thr Thr Gly Trp Asp  
 545 550 555 560

Pro Ala Thr Gly Leu Gly Thr Pro Asn Phe Ala Lys Leu Lys Glu Ala  
 565 570 575

Val Leu Ala Leu  
 580

<210> 127

<211> 631

<212> PRT

<213> Aspergillus niger

<400> 127

Met His Gly Leu Arg Leu Val Cys Ser Ile Gly Thr Leu Pro Leu Val  
 1 5 10 15



Ile Leu Ala Tyr Pro Ala Ala Ser Leu His Thr Thr Ser Ala Ala Val  
 20 25 30

Asp Leu Asp Ser Leu Arg Leu Thr Ser Asn Ser Glu Tyr Val Asn Ser  
 35 40 45

Val His Val Asp Thr Asn Arg Ser Val Ala Val Ser Ala Glu Glu His  
 50 55 60

Tyr Thr Asp Thr Ala Ala Arg Leu Val Gln Asn Ile Val Pro Gly Ala  
 65 70 75 80

Ser Phe Arg Leu Ile Asp Asp His Phe Val Gly Asp Asn Gly Val Ala  
 85 90 95

His Val Tyr Phe Arg Gln Thr Leu His Gly Ile Asp Ile Asp Asn Ala  
 100 105 110

Asp Phe Asn Val Asn Ile Gly Lys Asp Gly Leu Val Leu Ser Phe Gly  
 115 120 125

His Ser Phe Phe Thr Gly Ala Leu Pro Ser Ser His Leu Asp Asn Thr  
 130 135 140

Asn Val Leu Ser Pro Glu Ala Ala Leu Arg Gly Ala Arg Asp Ala Ile  
 145 150 155 160

Gln Leu Pro Leu Thr Ile Asp Asn Val Ser Thr Glu Ala Ala Glu Gly  
 165 170 175

Arg Asn Glu Tyr Ile Phe Arg Glu Ala Val Gly Ala Val Ser Asp Pro  
 180 185 190

Lys Ala Lys Leu Val Tyr Leu Val Lys Pro Glu Gly Thr Leu Ala Leu  
 195 200 205

Thr Trp Arg Ile Glu Thr Asp Met Tyr Glu His Trp Leu Leu Thr Tyr  
 210 215 220

Ile Asp Ala Glu Thr Thr Thr Val His Gly Val Val Asp Tyr Val Ala  
 225 230 235 240

Asp Ala Thr Tyr Gln Val Tyr Pro Trp Gly Thr Asn Asp Pro Ala Glu  
 245 250 255

Gly His Arg Thr Ile Val Thr Asp Pro Trp Asp Leu Ser Ala Ser Ala  
 260 265 270

Tyr Thr Trp Ile Ser Asp Gly Arg Asp Asn Tyr Thr Thr Thr Arg Gly  
 275 280 285

Asn Asn Ala Ile Ala His Trp Asn Pro Thr Gly Gly Gly Ser Tyr Leu  
 290 295 300

Tyr Asn Leu Arg Pro Ser Asp Pro Asn Leu Asn Phe Gln Trp Pro Tyr  
 305 310 315 320

Ser Pro Asn Met Ser Pro Pro Arg Ser Tyr Ile Asn Ala Ser Ile Val  
 325 330 335

Gln Leu Phe Tyr Thr Ala Asn Ala Tyr His Asp Leu Leu Tyr Thr Leu  
 340 345 350

Gly Phe Thr Glu Ser Ala Gly Asn Phe Gln Trp Asn Asn Ser Ala His  
 355 360 365

Gly Gly Arg Asp Lys Asp Tyr Val Ile Leu Asn Ala Gln Asp Gly Ser  
 370 375 380

Gly Phe Ser Asn Ala Asn Phe Ala Thr Pro Pro Asp Gly Ile Pro Gly  
 385 390 395 400

Arg Met Arg Met Tyr Ile Trp Ile Glu Ser Thr Pro Ser Arg Asp Gly  
 405 410 415

Ser Phe Asp Ala Gly Ile Val Ile His Glu Tyr Thr His Gly Val Ser  
 420 425 430

Asn Arg Leu Thr Gly Gly Ser His Asn Ala Gly Cys Leu Ser Ala Leu  
 435 440 445

Glu Ser Gly Gly Met Gly Glu Gly Trp Gly Asp Phe Met Ala Thr Ala  
 450 455 460

Ile Arg Ile Lys Pro Asn Asp Thr Arg Thr Thr Ser Tyr Thr Met Gly  
465 470 475 480

Ala Trp Ala Asp Asn Asp Lys Cys Gly Val Arg Asp Tyr Pro Tyr Ser  
485 490 495

Thr Ser Phe Thr Glu Asn Pro Leu Asn Tyr Thr Ser Val Asn Thr Met  
500 505 510

Asn Gly Val His Ala Ile Gly Thr Val Trp Ala Thr Met Leu Tyr Glu  
515 520 525

Val Leu Trp Asn Leu Ile Asp Lys Tyr Gly Lys Asn Asp Gly Ser Arg  
530 535 540

Pro Val Phe Arg Asn Gly Val Pro Thr Asp Gly Lys Tyr Leu Met Met  
545 550 555 560

Lys Leu Val Val Asp Gly Met Ala Leu Gln Pro Cys Asn Pro Asn Phe  
565 570 575

Val Gln Ala Arg Asp Ala Ile Leu Asp Ala Asp Ile Val Leu Thr Gly  
580 585 590

Gly Lys Asn Arg Cys Glu Ile Trp Arg Gly Phe Ala Lys Arg Gly Leu  
595 600 605

Gly Gln Gly Ala Ala His Ser Ser Leu Asn Trp Met Arg Arg Gly Ser  
610 615 620

Thr Leu Leu Pro Thr Gly Cys  
625 630

<210> 128

<211> 394

<212> PRT

<213> Aspergillus niger

<400> 128

Met Val Val Phe Ser Lys Thr Ala Ala Leu Val Leu Gly Leu Ser Ser  
1 5 10 15

Ala Val Ser Ala Ala Pro Ala Pro Thr Arg Lys Gly Phe Thr Ile Asn  
20 25 30

Gln Ile Ala Arg Pro Ala Asn Lys Thr Arg Thr Ile Asn Leu Pro Gly  
 35 40 45  
 Met Tyr Ala Arg Ser Leu Ala Lys Phe Gly Gly Thr Val Pro Gln Ser  
 50 55 60  
 Val Lys Glu Ala Ala Ser Lys Gly Ser Ala Val Thr Thr Pro Gln Asn  
 65 70 75 80  
 Asn Asp Glu Glu Tyr Leu Thr Pro Val Thr Val Gly Lys Ser Thr Leu  
 85 90 95  
 His Leu Asp Phe Asp Thr Gly Ser Ala Asp Leu Trp Val Phe Ser Asp  
 100 105 110  
 Glu Leu Pro Ser Ser Glu Gln Thr Gly His Asp Leu Tyr Thr Pro Ser  
 115 120 125  
 Ser Ser Ala Thr Lys Leu Ser Gly Tyr Thr Trp Asp Ile Ser Tyr Gly  
 130 135 140  
 Asp Gly Ser Ser Ala Ser Gly Asp Val Tyr Arg Asp Thr Val Thr Val  
 145 150 155 160  
 Gly Gly Val Thr Thr Asn Lys Gln Ala Val Glu Ala Ala Ser Lys Ile  
 165 170 175  
 Ser Ser Glu Phe Val Gln Asn Thr Ala Asn Asp Gly Leu Leu Gly Leu  
 180 185 190  
 Ala Phe Ser Ser Ile Asn Thr Val Gln Pro Lys Ala Gln Thr Thr Phe  
 195 200 205  
 Phe Asp Thr Val Lys Ser Gln Leu Asp Ser Pro Leu Phe Ala Val Gln  
 210 215 220  
 Leu Lys His Asp Ala Pro Gly Val Tyr Asp Phe Gly Tyr Ile Asp Asp  
 225 230 235 240  
 Ser Lys Tyr Thr Gly Ser Ile Thr Tyr Thr Asp Ala Asp Ser Ser Gln  
 245 250 255

Gly Tyr Trp Gly Phe Ser Thr Asp Gly Tyr Ser Ile Gly Asp Gly Ser  
 260 265 270

Ser Ser Ser Ser Gly Phe Ser Ala Ile Ala Asp Thr Gly Thr Thr Leu  
 275 280 285

Ile Leu Leu Asp Asp Glu Ile Val Ser Ala Tyr Tyr Glu Gln Val Ser  
 290 295 300

Gly Ala Gln Glu Ser Glu Glu Ala Gly Gly Tyr Val Phe Ser Cys Ser  
 305 310 315 320

Thr Asn Pro Pro Asp Phe Thr Val Val Ile Gly Asp Tyr Lys Ala Val  
 325 330 335

Val Pro Gly Lys Tyr Ile Asn Tyr Ala Pro Ile Ser Thr Gly Ser Ser  
 340 345 350

Thr Cys Phe Gly Gly Ile Gln Ser Asn Ser Gly Leu Gly Leu Ser Ile  
 355 360 365

Leu Gly Asp Val Phe Leu Lys Ser Gln Tyr Val Val Phe Asn Ser Glu  
 370 375 380

Gly Pro Lys Leu Gly Phe Ala Ala Gln Ala  
 385 390

<210> 129

<211> 398

<212> PRT

<213> Aspergillus niger

<400> 129

Met Lys Ser Ala Ser Leu Leu Thr Ala Ser Val Leu Leu Gly Cys Ala  
 1 5 10 15

Ser Ala Glu Val His Lys Leu Lys Leu Asn Lys Val Pro Leu Glu Glu  
 20 25 30

Gln Leu Tyr Thr His Asn Ile Asp Ala His Val Arg Ala Leu Gly Gln  
 35 40 45

Lys Tyr Met Gly Ile Arg Pro Ser Ile His Lys Glu Leu Val Glu Glu

50	55	60																	
Asn	Pro	Ile	Asn	Asp	Met	Ser	Arg	His	Asp	Val	Leu	Val	Asp	Asn	Phe				
65					70					75					80				
Leu	Asn	Ala	Gln	Tyr	Phe	Ser	Glu	Ile	Glu	Leu	Gly	Thr	Pro	Pro	Gln				
				85					90					95					
Lys	Phe	Lys	Val	Val	Leu	Asp	Thr	Gly	Ser	Ser	Asn	Leu	Trp	Val	Pro				
			100					105					110						
Ser	Ser	Glu	Cys	Ser	Ser	Ile	Ala	Cys	Tyr	Leu	His	Asn	Lys	Tyr	Asp				
		115					120					125							
Ser	Ser	Ala	Ser	Ser	Thr	Tyr	His	Lys	Asn	Gly	Ser	Glu	Phe	Ala	Ile				
	130					135					140								
Lys	Tyr	Gly	Ser	Gly	Ser	Leu	Ser	Gly	Phe	Ile	Ser	Gln	Asp	Thr	Leu				
145					150					155					160				
Lys	Ile	Gly	Asp	Leu	Lys	Val	Lys	Gly	Gln	Asp	Phe	Ala	Glu	Ala	Thr				
			165						170					175					
Asn	Glu	Pro	Gly	Leu	Ala	Phe	Ala	Phe	Gly	Arg	Phe	Asp	Gly	Ile	Leu				
			180					185					190						
Gly	Leu	Gly	Tyr	Asp	Thr	Ile	Ser	Val	Asn	Lys	Ile	Val	Pro	Pro	Phe				
	195						200					205							
Tyr	Asn	Met	Leu	Asp	Gln	Gly	Leu	Leu	Asp	Glu	Pro	Val	Phe	Ala	Phe				
	210					215					220								
Tyr	Leu	Gly	Asp	Thr	Asn	Lys	Glu	Gly	Asp	Glu	Ser	Val	Ala	Thr	Phe				
225					230					235					240				
Gly	Gly	Val	Asp	Lys	Asp	His	Tyr	Thr	Gly	Glu	Leu	Ile	Lys	Ile	Pro				
				245					250					255					
Leu	Arg	Arg	Lys	Ala	Tyr	Trp	Glu	Val	Glu	Leu	Asp	Ala	Ile	Ala	Leu				
			260					265					270						
Gly	Asp	Asp	Val	Ala	Glu	Met	Glu	Asn	Thr	Gly	Val	Ile	Leu	Asp	Thr				
	275					280						285							

Gly Thr Ser Leu Ile Ala Leu Pro Ala Asp Leu Ala Glu Met Ile Asn  
 290 295 300

Ala Gln Ile Gly Ala Lys Lys Gly Trp Thr Gly Gln Tyr Thr Val Asp  
 305 310 315 320

Cys Asp Lys Arg Ser Ser Leu Pro Asp Val Thr Phe Thr Leu Ala Gly  
 325 330 335

His Asn Phe Thr Ile Ser Ser Tyr Asp Tyr Thr Leu Glu Val Gln Gly  
 340 345 350

Ser Cys Val Ser Ala Phe Met Gly Met Asp Phe Pro Glu Pro Val Gly  
 355 360 365

Pro Leu Ala Ile Leu Gly Asp Ala Phe Leu Arg Lys Trp Tyr Ser Val  
 370 375 380

Tyr Asp Leu Gly Asn Ser Ala Val Gly Leu Ala Lys Ala Lys  
 385 390 395

<210> 130  
 <211> 393  
 <212> PRT  
 <213> Aspergillus niger

<400> 130

Met Arg Lys Tyr Arg Phe His Pro Thr Lys Pro Gly Pro Tyr Thr Leu  
 1 5 10 15

Ser Ser Ser Ile Gln Gln Thr Gly Arg Pro Tyr Thr Glu Lys Pro Ile  
 20 25 30

Gly Gly Arg Ala His Ile Arg Gln Leu Val Arg Lys Lys Ser Thr Thr  
 35 40 45

Ser Asp Glu Val Gly Glu Val Pro Ala Glu Asp Val Gln Asn Asp Ser  
 50 55 60

Met Tyr Leu Ala Thr Val Gly Ile Gly Thr Pro Ala Gln Asn Leu Lys  
 65 70 75 80

Leu Asp Phe Asp Thr Gly Ser Ala Asp Leu Trp Val Trp Ser Asn Lys  
85 90 95

Leu Pro Ser Thr Leu Leu Ser Glu Asn Lys Thr His Ala Ile Phe Asp  
100 105 110

Ser Ser Lys Ser Ser Thr Phe Lys Thr Leu Glu Gly Glu Ser Trp Gln  
115 120 125

Ile Ser Tyr Gly Asp Gly Ser Ser Ala Ser Gly Ser Val Gly Thr Asp  
130 135 140

Asp Val Asn Ile Gly Gly Val Val Val Lys Asn Gln Ala Val Glu Leu  
145 150 155 160

Ala Glu Lys Met Ser Ser Thr Phe Ala Gln Gly Glu Gly Asp Gly Leu  
165 170 175

Leu Gly Leu Ala Phe Ser Asn Ile Asn Thr Val Gln Pro Lys Ser Val  
180 185 190

Lys Thr Pro Val Glu Asn Met Ile Leu Gln Asp Asp Ile Pro Lys Ser  
195 200 205

Ala Glu Leu Phe Thr Ala Lys Leu Asp Thr Trp Arg Asp Thr Asp Asp  
210 215 220

Glu Ser Phe Tyr Thr Phe Gly Phe Ile Asp Gln Asp Leu Val Lys Thr  
225 230 235 240

Ala Gly Glu Glu Val Tyr Tyr Thr Pro Val Asp Asn Ser Gln Gly Phe  
245 250 255

Trp Leu Phe Asn Ser Thr Ser Ala Thr Val Asn Gly Lys Thr Ile Asn  
260 265 270

Arg Ser Gly Asn Thr Ala Ile Ala Asp Thr Gly Thr Thr Leu Ala Leu  
275 280 285

Val Asp Asp Asp Thr Cys Glu Ala Ile Tyr Ser Ala Ile Asp Gly Ala  
290 295 300

Tyr Tyr Asp Gln Glu Val Gln Gly Trp Ile Tyr Pro Thr Asp Thr Ala



305                      310                      315                      320  
 Gln Asp Lys Leu Pro Thr Val Ser Phe Ala Val Gly Glu Lys Gln Phe  
                                  325                      330                      335  
 Val Val Gln Lys Glu Asp Leu Ala Phe Ser Glu Ala Lys Thr Gly Tyr  
                                  340                      345                      350  
 Val Tyr Gly Gly Ile Gln Ser Arg Gly Asp Met Thr Met Asp Ile Leu  
                                  355                      360                      365  
 Gly Asp Thr Phe Leu Lys Ser Ile Tyr Ala Val Ser Ala Leu Leu Leu  
                                  370                      375                      380  
 Ala Leu Arg Gly Asp Ile Glu Ala His  
 385                      390  
  
 <210> 131  
 <211> 282  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 131  
  
 Met Lys Phe Ser Thr Ile Leu Thr Gly Ser Leu Phe Ala Thr Ala Ala  
 1                      5                      10                      15  
  
 Leu Ala Ala Pro Leu Thr Glu Lys Arg Arg Ala Arg Lys Glu Ala Arg  
                                  20                      25                      30  
  
 Ala Ala Gly Lys Arg His Ser Asn Pro Pro Tyr Ile Pro Gly Ser Asp  
                                  35                      40                      45  
  
 Lys Glu Ile Leu Lys Leu Asn Gly Thr Ser Asn Glu Asp Tyr Ser Ser  
                                  50                      55                      60  
  
 Asn Trp Ala Gly Ala Val Leu Ile Gly Asp Gly Tyr Thr Lys Val Thr  
 65                      70                      75                      80  
  
 Gly Glu Phe Thr Val Pro Ser Val Ser Ala Gly Ser Ser Ser Ser Ser  
                                  85                      90                      95  
  
 Gly Tyr Gly Gly Gly Tyr Gly Tyr Tyr Lys Asn Lys Arg Gln Ser Glu  
                                  100                      105                      110

Glu Tyr Cys Ala Ser Ala Trp Val Gly Ile Asp Gly Asp Thr Cys Glu  
 115 120 125

Thr Ala Ile Leu Gln Thr Gly Val Asp Phe Cys Tyr Glu Asp Gly Gln  
 130 135 140

Thr Ser Tyr Asp Ala Trp Tyr Glu Trp Tyr Pro Asp Tyr Ala Tyr Asp  
 145 150 155 160

Phe Asn Asp Ile Thr Ile Ser Glu Gly Asp Thr Ile Lys Val Thr Val  
 165 170 175

Glu Ala Thr Ser Lys Ser Ser Gly Ser Ala Thr Val Glu Asn Leu Thr  
 180 185 190

Thr Gly Gln Ser Val Thr His Thr Phe Ser Gly Asn Val Glu Gly Asp  
 195 200 205

Leu Cys Glu Thr Asn Ala Glu Trp Ile Val Glu Asp Phe Glu Ser Gly  
 210 215 220

Asp Ser Leu Val Ala Phe Ala Asp Phe Gly Ser Val Thr Phe Thr Asn  
 225 230 235 240

Ala Glu Ala Thr Ser Asp Gly Ser Thr Val Gly Pro Ser Asp Ala Thr  
 245 250 255

Val Met Asp Ile Glu Gln Asp Gly Thr Val Leu Thr Glu Thr Ser Val  
 260 265 270

Ser Gly Asp Ser Val Thr Val Thr Tyr Val  
 275 280

<210> 132

<211> 273

<212> PRT

<213> Aspergillus niger

<400> 132

Met Gly Asp Tyr Gly Pro Gly Val Ser Ser Leu Thr Ala Gln Leu Pro  
 1 5 10 15

Gly Asn Pro Pro Val Ser Glu Thr Asp Gln Asp Glu Ile Ser Val Leu

20	25	30
Val Thr Gly Phe Gly Pro Phe Lys Ser Asn Leu Val Asn Ala Ser Tyr		
35	40	45
Leu Ile Ala Ser Ser Leu Pro Pro Ser Phe Thr Phe Ser Pro Ala Ser		
50	55	60
Ser Asp Gly Ser Asp Ala Val Pro Arg Arg Val Ser Ile Asn Val His		
65	70	75
Pro Ser Pro Ile Pro Val Ala Tyr Ser Ser Val Arg Thr Thr Leu Pro		
85	90	95
Val Ile Leu Asp Asp Tyr Ala Lys Thr His Gly Gly Arg Arg Pro Asp		
100	105	110
Ile Val Ile His Ile Gly Ile Ala Ala Met Arg Asn Tyr Tyr Ser Val		
115	120	125
Glu Thr Gln Ala His Arg Asp Gly Tyr Leu Met Ser Asp Ile Lys Gly		
130	135	140
Arg Ser Gly Tyr Glu Asp Gly Glu Lys Leu Trp Arg Glu Leu Asp Leu		
145	150	155
Pro Leu Val Leu Arg Ala Gly Pro Ser Glu Gly His Ala Ser Glu Lys		
165	170	175
Lys His Leu Ser Pro Arg Pro Pro Asp Glu Asp Phe Leu Ala Ala Trp		
180	185	190
Lys Thr Phe Cys Pro Pro Glu Thr Asp Ala Arg Ile Ser Thr Asp Ala		
195	200	205
Gly Arg Tyr Leu Cys Glu Phe Ile Leu Tyr Thr Ser Leu Ala Leu Ala		
210	215	220
Tyr Gln Ala Gly Glu Asp Arg Asn Val Thr Phe Phe His Val Pro Ala		
225	230	235
Ser Cys Leu Asp Glu Asp Ile Glu Thr Gly Lys Glu Val Ala Val Ala		
245	250	255

Leu Ile Lys Ala Leu Val Thr Ser Trp Ser Glu Gln Gln His Ser Val  
 260 265 270

Pro

<210> 133  
 <211> 542  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 133

Met Gly Ser Arg Gln Gly Lys Ala Pro Phe Gly Trp Gly Thr Gln Ser  
 1 5 10 15

Leu Ala His Phe Gly Ile Asn Pro Asp Leu Gly Leu His Asn Gln Gln  
 20 25 30

Asn Leu Asn Ser Leu Ile Ser His Ser Ala Met Ala Thr Ala Leu Glu  
 35 40 45

Thr Glu Tyr Ala Thr Ile Pro Ile Asp His Asn Asn Ala Ser Ala Gly  
 50 55 60

Thr Tyr Gln Asn Arg Phe Trp Val Ser Asp Glu Phe Tyr Gln Pro Gly  
 65 70 75 80

Asn Pro Ile Phe Val Tyr Asp Thr Gly Glu Ser Asp Gly Gly Ser Ile  
 85 90 95

Ala Gln Ser Tyr Leu Thr Ser Thr Leu Ser Phe Phe Arg Glu Phe Leu  
 100 105 110

Ile Glu Phe Asn Ala Met Gly Ile Ala Trp Glu His Arg Tyr Tyr Gly  
 115 120 125

Asn Ser Thr Pro Ala Pro Val Ser Tyr Glu Thr Pro Pro Glu Ala Trp  
 130 135 140

Gln Tyr Leu Thr Thr Lys Gln Ala Leu Ala Asp Leu Pro Tyr Phe Ala  
 145 150 155 160

Ser Asn Phe Ser Arg Glu Lys Tyr Pro Asp Met Asp Leu Thr Pro Gln  
 165 170 175  
 Gly Thr Pro Trp Ile Met Val Gly Gly Ser Tyr Ala Gly Ile Arg Ala  
 180 185 190  
 Ala Leu Thr Arg Lys Glu Tyr Pro Glu Thr Ile Phe Ala Ala Phe Ser  
 195 200 205  
 Ser Ser Ser Pro Val Glu Ala Gln Val Asn Met Ser Ala Tyr Tyr Asp  
 210 215 220  
 Gln Val Tyr Arg Gly Met Val Ala Ser Gly Trp Thr Asn Cys Ser Ala  
 225 230 235 240  
 Asp Ile His Ala Ala Leu Glu Tyr Ile Asp Asp Gln Leu Ser Asp Glu  
 245 250 255  
 Asp Thr Ala Thr Ser Val Lys Gln Leu Phe Phe Gly Ser Gly Ala Glu  
 260 265 270  
 Thr Asn Ser Asn Gly Asp Phe Thr Ala Ala Leu Thr Ala Ile Tyr Gly  
 275 280 285  
 Tyr Phe Gln Ser Tyr Gly Met Ala Gly Gly Ile Gly Gly Leu Gly Ala  
 290 295 300  
 Phe Cys Glu Tyr Leu Glu Ile Asp Pro Lys Thr Asn Gly Thr Thr Gly  
 305 310 315 320  
 Pro Asp Gly Leu Ala Pro Thr Tyr Gly Gly Gln Tyr Val Ala Glu Arg  
 325 330 335  
 Trp Ala Ala Trp Pro Thr Phe Leu Glu Leu Val Asn Leu Asn Met Gly  
 340 345 350  
 Thr Asn Cys Gly Pro Gln Asp Ala Ser Gln Pro Ile Asp Cys Asp Phe  
 355 360 365  
 Ser Lys Pro Tyr Gly Asp Pro Ser Ala Ile Thr Trp Thr Trp Gln Tyr  
 370 375 380  
 Cys Ser Glu Trp Gly Phe Phe Gln Ala Asn Asn Asp Gly Pro His Ser

385                      390                      395                      400  
 Leu Ala Ser Arg Tyr Gln Ser Val Glu Tyr Gln Gln Glu Val Cys Asn  
                                  405                                   410                                   415  
 Arg Gln Phe Pro Asp Ala Val Asp Lys Gly Leu Leu Pro Pro Ser Pro  
                                  420                                   425                                   430  
 Arg Ala Asp Asp Val Asn Gln Glu Phe Gly Gly Trp Thr Ile Arg Pro  
                                  435                                   440                                   445  
 Ser Asn Val Tyr Phe Ser Gly Gly Glu Phe Asp Pro Trp Arg Ser Leu  
                                  450                                   455                                   460  
 Ser Ile Leu Ser Thr Glu Asp Phe Ala Pro Gln Gly Val Glu Phe Thr  
                                  465                                   470                                   475                                   480  
 Ser Ala Ile Pro Ala Cys Gly Val Gln Thr Asn Glu Asp Thr Val Phe  
                                  485                                   490                                   495  
 Gly Tyr Val Met Gln Asn Ser Glu His Cys Phe Asp Phe Gln Ala Thr  
                                  500                                   505                                   510  
 Pro Thr Val Gly Lys Leu Ser Arg Gly Ile Phe Thr Ser Ala Leu Leu  
                                  515                                   520                                   525  
 Gln Trp Leu Glu Cys Phe Gly Gln Asn Ser Ser Gln Ser Arg  
                                  530                                   535                                   540  
  
 <210> 134  
 <211> 391  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 134  
 Met Lys Leu Ser Ile Ala Leu Ala Leu Gly Ala Thr Ala Ser Thr Gly  
 1                                   5                                   10                                   15  
  
 Val Leu Ala Ala Val Val Pro Gln Gln Glu Pro Leu Ile Thr Pro Gln  
                                  20                                   25                                   30  
  
 Asp Pro Pro Thr His His His Gln Glu Lys Phe Leu Ile Glu Leu Ala  
                                  35                                   40                                   45

Pro Tyr Gln Thr Arg Trp Val Thr Glu Glu Glu Lys Trp Asp Leu Lys  
 50 55 60

Leu Asp Gly Val Asn Phe Ile Asp Ile Thr Glu Glu Arg Asn Thr Gly  
 65 70 75 80

Phe Tyr Pro Thr Leu His Ala Gly Ser Tyr Val His Tyr Pro Pro Thr  
 85 90 95

Met Lys His Ala Glu Lys Val Val Pro Leu Leu Arg Gly Leu Ser Lys  
 100 105 110

Asp Asn Met Glu Gln Asn Leu Asn Lys Phe Thr Ser Phe His Thr Arg  
 115 120 125

Tyr Tyr Arg Ser Ser Thr Gly Ile Glu Ser Ala Lys Trp Leu Tyr Ser  
 130 135 140

Arg Val Ser Asp Val Ile Glu Gln Ser Gly Ala Ala Glu Tyr Gly Ala  
 145 150 155 160

Thr Val Glu Gln Phe Ala His Ser Trp Gly Gln Phe Ser Ile Ile Ala  
 165 170 175

Arg Ile Pro Gly Gln Thr Asn Lys Thr Val Val Leu Gly Ala His Gln  
 180 185 190

Asp Ser Ile Asn Leu Phe Leu Pro Ser Ile Leu Ala Ala Pro Gly Ala  
 195 200 205

Asp Asp Asp Gly Ser Gly Thr Val Thr Ile Leu Glu Ala Leu Arg Gly  
 210 215 220

Leu Leu Gln Ser Asp Ala Ile Val Arg Gly Asn Ala Ser Asn Thr Ile  
 225 230 235 240

Glu Phe His Trp Tyr Ser Ala Glu Glu Gly Gly Met Leu Gly Ser Gln  
 245 250 255

Ala Ile Phe Ser Gln Tyr Lys Arg Asp Lys Arg Asp Ile Lys Ala Met  
 260 265 270

Leu Gln Gln Asp Met Thr Gly Tyr Thr Gln Gly Ala Leu Asp Ala Gly  
 275 280 285

Arg Gln Glu Ala Ile Gly Ile Met Val Asp Tyr Val Asp Glu Gly Leu  
 290 295 300

Thr Gln Phe Leu Lys Asp Val Thr Thr Glu Tyr Cys Gly Ile Gly Tyr  
 305 310 315 320

Ile Glu Thr Arg Cys Gly Tyr Ala Cys Ser Asp His Thr Ser Ala Ser  
 325 330 335

Lys Tyr Gly Tyr Pro Ala Ala Met Ala Thr Glu Ser Glu Met Glu Asn  
 340 345 350

Ser Asn Lys Arg Ile His Thr Thr Asp Asp Ser Ile Arg Tyr Leu Ser  
 355 360 365

Phe Asp His Met Leu Glu His Ala Arg Leu Thr Leu Gly Phe Ala Tyr  
 370 375 380

Glu Leu Ala Phe Ala Gln Phe  
 385 390

<210> 135  
 <211> 442  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 135

Met Arg Thr Thr Thr Ser Phe Ala Arg Leu Ala Leu Ala Val Ala Ser  
 1 5 10 15

Val Gly Ile Val Phe Ala Ser Pro Thr Lys Asn Asn Asp Gly Lys Leu  
 20 25 30

Val Tyr Gly Ser Pro Glu Ser Val Gly Met Ile Ser Ala Pro Leu His  
 35 40 45

Gln Met Val Gln Asn Val Ser Ala Tyr Thr His Ala Ala Asn Tyr Ser  
 50 55 60

Lys Phe Ser Tyr Asp Lys Val His Pro Ile Glu Pro Gly Ser Val Thr  
 65 70 75 80



Leu Val Ala Leu Asp Gly Val Ile Val Ser Glu Phe Ala Leu Gly Lys  
                     85                    90                    95

Arg Asn Leu Tyr Ala Asp Val Asn Gly Thr Asn Leu Pro Arg Tyr Leu  
                     100                    105                    110

Gln Glu Asp Thr Thr Leu Asp Thr Val Tyr Asp Met Ala Ser Leu Thr  
                     115                    120                    125

Lys Leu Phe Thr Thr Val Ala Ala Leu Arg Glu Leu Asp Ala Gly Arg  
                     130                    135                    140

Ile Ala Leu Asn Val Thr Val Ala Thr Tyr Ile Pro Asp Phe Ala Thr  
                     145                    150                    155                    160

Asn Gly Lys Glu Asn Ile Thr Ile Leu Glu Leu Phe Thr His Thr Ser  
                     165                    170                    175

Gly Phe Ala Ser Asp Pro Ser Pro Pro Leu Phe Ser Ala Tyr Tyr Thr  
                     180                    185                    190

Thr Tyr Asp Glu Arg Ile Lys Ala Ile Leu Thr Gln Lys Ile Ile Asn  
                     195                    200                    205

Thr Pro Gly Ser Thr Tyr Leu Tyr Leu Asp Leu Asn Phe Met Ser Leu  
                     210                    215                    220

Gly Leu Val Ile Glu Thr Val Thr Gly Arg Ala Leu Asp Asp Leu Ile  
                     225                    230                    235                    240

Tyr Asp Phe Thr Arg Pro Leu Glu Met Thr Ser Thr Phe Phe Asn Arg  
                     245                    250                    255

Gly Asn Ile Glu Gly Ser Thr Pro Gln Ser Pro Asn Tyr Asp Arg Thr  
                     260                    265                    270

Ala Val Gln Glu Phe Gln Ile Ala Ala Leu Gly Pro Ser Glu Pro Gln  
                     275                    280                    285

Arg Pro Gln Pro Val Arg Gly Thr Val His Asp Glu Asn Ala Trp Ser  
                     290                    295                    300

Leu Asp Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Arg Asp  
 305 310 315 320

Thr Ala Thr Phe Cys Gln Met Ile Leu Asn Asn Gly Thr Tyr Ala Gly  
 325 330 335

Gln Arg Ile Leu Ser Arg Thr Ala Val Asp Met Ile Phe Thr Asn Phe  
 340 345 350

Asn Ala Arg Phe Pro Gly Asp Ala Arg Ser Leu Gly Phe Glu Leu Asp  
 355 360 365

Gln Tyr Ser Thr Ala Gly Pro Met Ala Ser Leu Gln Thr Ala Ser His  
 370 375 380

Thr Gly Phe Thr Gly Thr Thr Leu Val Met Asp Arg Thr Tyr Asn Ala  
 385 390 395 400

Phe Trp Leu His Phe Ser Asn Arg Val His Pro Ser Arg Ala Trp Ser  
 405 410 415

Ser Asn Thr Ile Val Arg Glu Ala Ile Gly Tyr Trp Val Gly Lys Ser  
 420 425 430

Leu Gly Leu Asp Val Ala Phe Ala Leu Leu  
 435 440

<210> 136  
 <211> 612  
 <212> PRT  
 <213> Aspergillus niger

<400> 136

Met Ala Ser Trp Leu Leu Ser Thr Leu Leu Phe Leu Ser Pro Ser Leu  
 1 5 10 15

Val Ser Ala Lys Ser Ala Ala Asp Tyr Tyr Val His Ser Leu Pro Gly  
 20 25 30

Ala Pro Glu Gly Pro Leu Leu Lys Met His Ala Gly His Ile Glu Val  
 35 40 45

Asp Pro Gln Asn Asn Gly Asn Leu Phe Phe Trp His Tyr Gln Asn Arg

50	55	60
His Ile Ala Asn Arg Gln Arg Thr Val Ile Trp Leu Asn Gly Gly Pro		
65	70	75 80
Gly Cys Ser Ser Met Asp Gly Ala Leu Met Glu Val Gly Pro Tyr Arg		
	85	90 95
Leu Lys Asp Asn Glu Thr Leu Thr Tyr Asn Glu Gly Ser Trp Asp Glu		
	100	105 110
Phe Ala Asn Leu Leu Phe Val Asp Gln Pro Val Gly Thr Gly Phe Ser		
	115	120 125
Tyr Val Asn Thr Asp Ser Tyr Leu His Glu Leu Asp Glu Met Ser Ala		
	130	135 140
Gln Phe Ile Val Phe Leu Glu Glu Trp Phe Arg Leu Phe Pro Glu Tyr		
	145	150 155 160
Glu Arg Asp Asp Ile Tyr Ile Ala Gly Glu Ser Tyr Ala Gly Gln His		
	165	170 175
Ile Pro Tyr Ile Ala Lys Ala Ile Gln Glu Arg Asn Lys Asn Val Gln		
	180	185 190
Gly Lys Thr Ile Ala Ser Trp Asn Leu Lys Gly Leu Leu Ile Gly Asn		
	195	200 205
Gly Trp Ile Ser Pro Asn Glu Gln Tyr Met Ser Tyr Leu Pro Tyr Ala		
	210	215 220
Tyr Glu Glu Gly Leu Ile Lys Glu Gly Ser Arg Thr Ala Lys Glu Leu		
	225	230 235 240
Glu Val Leu Gln Ser Val Cys Lys Ser Arg Leu Glu Thr Gly Lys Asn		
	245	250 255
Lys Val His Leu Asn Asp Cys Glu Lys Val Met Asn Ala Leu Leu Asp		
	260	265 270
Lys Thr Val Glu Asp Asn Lys Cys Leu Asn Met Tyr Asp Ile Arg Leu		
	275	280 285

Arg Asp Thr Thr Asp Ala Cys Gly Met Asn Trp Pro Thr Asp Leu Glu  
 290 295 300

Asp Val Lys Pro Tyr Leu Gln Arg Glu Asp Val Val Lys Ala Leu Asn  
 305 310 315 320

Ile Asn Pro Glu Lys Lys Ser Gly Trp Val Glu Cys Ser Gly Ala Val  
 325 330 335

Ser Ser Ala Phe Asn Pro Gln Lys Ser Pro Pro Ser Val Gln Leu Leu  
 340 345 350

Pro Gly Leu Leu Glu Ser Gly Leu Gln Ile Leu Leu Phe Ser Gly Asp  
 355 360 365

Lys Asp Leu Ile Cys Asn His Val Gly Thr Glu Gln Leu Ile Asn Asn  
 370 375 380

Met Lys Trp Asn Gly Gly Thr Gly Phe Glu Thr Ser Pro Gly Val Trp  
 385 390 395 400

Ala Pro Arg His Asp Trp Ser Phe Glu Gly Glu Pro Ala Gly Ile Tyr  
 405 410 415

Gln Tyr Ala Arg Asn Leu Thr Tyr Val Leu Ile Tyr Asn Ala Ser His  
 420 425 430

Met Val Pro Tyr Asp Leu Pro Arg Gln Ser Arg Asp Met Leu Asp Arg  
 435 440 445

Phe Met Asn Val Asp Ile Ala Ser Ile Gly Gly Ser Pro Ala Asp Ser  
 450 455 460

Arg Ile Asp Gly Glu Lys Leu Pro Gln Thr Ser Val Gly Gly His Pro  
 465 470 475 480

Asn Ser Thr Ala Ala Glu Glu Gln Glu Lys Glu Arg Ile Lys Glu Thr  
 485 490 495

Glu Trp Lys Ala Tyr Ala Lys Ser Gly Glu Ala Val Leu Leu Val Val  
 500 505 510

Ile Ile Gly Val Leu Val Trp Gly Phe Phe Ile Trp Arg Ser Arg Arg  
 515 520 525

Arg His Gln Gly Tyr Arg Gly Val Trp His Lys Asp Met Ser Gly Ser  
 530 535 540

Ser Val Leu Glu Arg Phe His Asn Lys Arg Thr Gly Gly Ala Asp Val  
 545 550 555 560

Glu Ala Gly Asp Phe Asp Glu Ala Glu Leu Asp Asp Leu His Ser Pro  
 565 570 575

Asp Leu Glu Arg Glu His Tyr Ala Val Gly Glu Asp Ser Asp Glu Asp  
 580 585 590

Asp Ile Ser Arg Gln His Ser Gln Gln Ala Ser Arg Ala Gly Gly Ser  
 595 600 605

His Asn Leu Ser  
 610

<210> 137  
 <211> 531  
 <212> PRT  
 <213> Aspergillus niger

<400> 137

Met Phe Leu Ile Ser Pro Ala Val Thr Val Ala Ala Ala Leu Leu Leu  
 1 5 10 15

Ile Asn Gly Ala Gly Ala Thr Gln Ser Glu Arg Ser Arg Ala Ala Ala  
 20 25 30

His Phe Ser Lys Arg His Pro Thr Tyr Arg Ala Ala Thr Arg Ala Gln  
 35 40 45

Ser Ser Asn Thr Ser Asp Tyr Arg Phe Phe Asn Asn Arg Thr Lys Pro  
 50 55 60

His Leu Val Glu Ser Leu Pro Asp Val His Phe Asp Val Gly Glu Met  
 65 70 75 80

Tyr Ser Gly Ser Ile Pro Ile Asp Asp Ser Asn Asn Gly Ser Arg Ser

	85		90		95
Leu Phe Tyr Ile Phe Gln Pro Lys Ile Gly Glu Pro Ser Asp Asp Leu	100		105		110
Thr Ile Tyr Leu Asn Gly Gly Pro Gly Cys Ser Ser Glu Gln Gly Phe	115		120		125
Phe Gln Glu Asn Gly Arg Phe Thr Trp Gln Pro Gly Thr Tyr Ala Pro	130		135		140
Val Ile Asn Glu Tyr Ser Trp Val Asn Leu Thr Asn Met Leu Trp Val	145		150		155
Asp Gln Pro Val Gly Thr Gly Phe Ser Val Gly Asn Val Thr Ala Thr	165		170		175
Asn Glu Glu Glu Ile Ala Ala Asp Phe Leu Asp Phe Phe Glu Lys Phe	180		185		190
Glu Asp Leu Tyr Gly Ile Lys Asn Phe Arg Ile Phe Met Thr Gly Glu	195		200		205
Ser Tyr Ala Gly Arg Tyr Val Pro Tyr Ile Ser Ser Ala Met Leu Asp	210		215		220
Lys Asn Asp Thr Thr Arg Phe Asn Leu Ser Gly Ala Leu Leu Tyr Asp	225		230		235
Ala Cys Ile Gly Gln Trp Asp Tyr Ile Gln Ala Glu Leu Pro Ala Tyr	245		250		255
Pro Phe Val Lys Gln His Ala Ser Leu Phe Asn Phe Asn Gln Ser Tyr	260		265		270
Met Asn Glu Leu Glu Thr Thr Tyr Glu Glu Cys Gly Tyr Lys Ala Tyr	275		280		285
Phe Asp Glu Tyr Phe Ala Phe Pro Pro Ser Gly Ile Gln Pro Pro Lys	290		295		300
Tyr Met Asn Tyr Ser Glu Cys Asp Ile Tyr Asn Met Ile Tyr Tyr Glu	305		310		315
					320

Ala Tyr Asn Pro Asn Pro Cys Phe Asn Pro Tyr Arg Val Ile Asp Glu  
325 330 335

Cys Pro Leu Leu Trp Asp Val Leu Gly Trp Pro Thr Asp Leu Ala Tyr  
340 345 350

Glu Pro Ala Pro Thr Thr Tyr Phe Asn Arg Ile Asp Val Lys Lys Ala  
355 360 365

Leu His Ala Pro Met Asp Val Glu Trp Glu Leu Cys Ser Tyr Asp Leu  
370 375 380

Val Phe Ala Gly Gly Asp Ala Asp Pro Gly Pro Glu Gln Gln Gly Asp  
385 390 395 400

Asp Ser Pro Asn Pro Thr Glu Gly Val Leu Pro Arg Val Ile Glu Ala  
405 410 415

Thr Asn Arg Val Leu Ile Ala Asn Gly Asp Trp Asp Tyr Leu Ile Ile  
420 425 430

Thr Asn Gly Thr Leu Leu Ala Ile Gln Asn Met Thr Trp Asn Gly Gln  
435 440 445

Leu Gly Phe Gln Ser Ala Pro Ala Thr Pro Ile Asp Ile Gln Met Pro  
450 455 460

Asp Leu Gln Trp Val Glu Ile Phe Glu Ala Gln Glu Gly Tyr Gly Gly  
465 470 475 480

Leu Asp Gly Pro Gln Gly Val Met Gly Val Gln His Tyr Glu Arg Gly  
485 490 495

Leu Met Trp Ala Glu Thr Tyr Gln Ser Gly His Lys Gln Ala Gln Asp  
500 505 510

Gln Gly Arg Val Ser Tyr Arg His Leu Gln Trp Leu Leu Gly Gln Val  
515 520 525

Glu Ile Leu  
530

<210> 138  
 <211> 531  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 138

Met Leu Phe Arg Ser Leu Leu Ser Thr Ala Val Leu Ala Val Ser Leu  
 1 5 10 15

Cys Thr Asp Asn Ala Ser Ala Ala Lys His Gly Arg Phe Gly Gln Lys  
 20 25 30

Ala Arg Asp Ala Met Asn Ile Ala Lys Arg Ser Ala Asn Ala Val Lys  
 35 40 45

His Ser Leu Lys Ile Pro Val Glu Asp Tyr Gln Phe Leu Asn Asn Lys  
 50 55 60

Thr Lys Pro Tyr Arg Val Glu Ser Leu Pro Asp Val His Phe Asp Leu  
 65 70 75 80

Gly Glu Met Tyr Ser Gly Leu Val Pro Ile Glu Lys Gly Asn Val Ser  
 85 90 95

Arg Ser Leu Phe Phe Val Phe Gln Pro Thr Ile Gly Glu Pro Val Asp  
 100 105 110

Glu Ile Thr Ile Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Glu  
 115 120 125

Ala Phe Leu Gln Glu Asn Gly Arg Phe Val Trp Gln Pro Gly Thr Tyr  
 130 135 140

Gln Pro Val Glu Asn Pro Tyr Ser Trp Val Asn Leu Thr Asn Val Leu  
 145 150 155 160

Trp Val Asp Gln Pro Val Gly Thr Gly Phe Ser Leu Gly Val Pro Thr  
 165 170 175

Ala Thr Ser Glu Glu Glu Ile Ala Glu Asp Phe Val Lys Phe Phe Lys  
 180 185 190

Asn Trp Gln Gln Ile Phe Gly Ile Lys Asn Phe Lys Ile Tyr Val Thr



195	200	205
Gly Glu Ser Tyr Ala Gly Arg Tyr Val Pro Tyr Ile Ser Ala Ala Phe 210 215 220		
Leu Asp Gln Asn Asp Thr Glu His Phe Asn Leu Lys Gly Ala Leu Ala 225 230 235 240		
Tyr Asp Pro Cys Ile Gly Gln Phe Asp Tyr Val Gln Glu Glu Ala Pro 245 250 255		
Val Val Pro Phe Val Gln Lys Asn Asn Ala Leu Phe Asn Phe Asn Ala 260 265 270		
Ser Phe Leu Ala Glu Leu Glu Ser Ile His Glu Gln Cys Gly Tyr Lys 275 280 285		
Asp Phe Ile Asp Gln Tyr Leu Val Phe Pro Ala Ser Gly Val Gln Pro 290 295 300		
Pro Lys Ala Met Asn Trp Ser Asp Pro Thr Cys Asp Val Tyr Asp Ile 305 310 315 320		
Val Asn Asn Ala Val Leu Asp Pro Asn Pro Cys Phe Asn Pro Tyr Glu 325 330 335		
Ile Asn Glu Met Cys Pro Ile Leu Trp Asp Val Leu Gly Phe Pro Thr 340 345 350		
Glu Val Asp Tyr Leu Pro Ala Gly Ala Ser Ile Tyr Phe Asp Arg Ala 355 360 365		
Asp Val Lys Arg Ala Met His Ala Pro Asn Ile Thr Trp Ser Glu Cys 370 375 380		
Ser Val Glu Ser Val Phe Val Gly Gly Asp Gly Gly Pro Glu Gln Glu 385 390 395 400		
Gly Asp Tyr Ser Ala Asn Pro Ile Glu His Val Leu Pro Gln Val Ile 405 410 415		
Glu Gly Thr Asn Arg Val Leu Ile Gly Asn Gly Asp Tyr Asp Met Val 420 425 430		

Ile Leu Thr Asn Gly Thr Leu Leu Ser Ile Gln Asn Met Thr Trp Asn  
 435 440 445

Gly Lys Leu Gly Phe Asp Thr Ala Pro Ser Thr Pro Ile Asn Ile Asp  
 450 455 460

Ile Pro Asp Leu Met Tyr Asn Glu Val Phe Ile Glu Asn Gly Tyr Asp  
 465 470 475 480

Pro Gln Gly Gly Gln Gly Val Met Gly Ile Gln His Tyr Glu Arg Gly  
 485 490 495

Leu Met Trp Ala Glu Thr Phe Gln Ser Gly His Met Gln Pro Gln Phe  
 500 505 510

Gln Pro Arg Val Ser Tyr Arg His Leu Glu Trp Leu Leu Gly Arg Arg  
 515 520 525

Asp Thr Leu  
 530

<210> 139  
 <211> 492  
 <212> PRT  
 <213> Aspergillus niger

<400> 139

Met Lys Gly Ala Ala Leu Ile Pro Leu Ala Ala Gly Ile Pro Phe Ala  
 1 5 10 15

His Gly Leu Ser Leu His Lys Arg Asp Gly Pro Ala Val Val Arg Met  
 20 25 30

Pro Ile Glu Arg Arg Ser Ala Gln Ser Leu Gln Lys Arg Asp Ser Thr  
 35 40 45

Val Gly Val Thr Leu Gln Asn Trp Asp Ala Thr Tyr Tyr Ala Val Asn  
 50 55 60

Leu Thr Leu Gly Thr Pro Ala Gln Lys Val Ser Leu Ala Leu Asp Thr  
 65 70 75 80

Gly Ser Ser Asp Leu Trp Val Asn Thr Gly Asn Ser Thr Tyr Cys Ser  
85 90 95

Ile Asp Asn Leu Cys Thr Pro Tyr Gly Leu Tyr Asn Ala Ser Glu/Ser  
100 105 110

Ser Thr Val Lys Thr Val Gly Thr His Leu Asn Asp Thr Tyr Ala Asp  
115 120 125

Gly Thr Asn Leu Tyr Gly Pro Tyr Val Thr Asp Lys Leu Thr Ile Gly  
130 135 140

Asn Thr Thr Ile Asp Asn Met Gln Phe Gly Ile Ala Glu Ser Thr Thr  
145 150 155 160

Ser Lys Arg Gly Ile Ala Gly Val Gly Tyr Lys Ile Ser Thr Tyr Gln  
165 170 175

Ala Glu His Asp Asp Lys Val Tyr Ala Asn Leu Pro Gln Ala Leu Val  
180 185 190

Asp Ser Gly Ala Ile Lys Ser Ala Ala Tyr Ser Ile Trp Leu Asp Ser  
195 200 205

Leu Glu Ala Ser Thr Gly Ser Leu Leu Phe Gly Gly Val Asn Thr Ala  
210 215 220

Lys Tyr Lys Gly Asp Leu Gln Thr Leu Pro Ile Ile Pro Val Tyr Gly  
225 230 235 240

Lys Tyr Tyr Ser Leu Ala Ile Ala Leu Thr Glu Leu Ser Val Ala Thr  
245 250 255

Asp Ser Asn Ser Ser Ser Phe Thr Asp Ser Leu Pro Leu Ser Val Ser  
260 265 270

Leu Asp Thr Gly Thr Thr Met Thr Ala Leu Pro Ser Asp Leu Val Asn  
275 280 285

Lys Val Tyr Asp Ala Leu Asn Ala Thr Tyr Asp Lys Thr Tyr Asp Met  
290 295 300

Ala Tyr Ile Asp Cys Asp Thr Arg Glu Ala Asp Tyr Asn Val Thr Tyr

305                      310                      315                      320  
 Ser Phe Ser Gly Ala Thr Ile Thr Val Ser Met Ser Glu Leu Ile Ile  
                                  325                      330                      335  
 Pro Ala Thr Glu Pro Gly Trp Pro Asp Asn Thr Cys Val Leu Gly Leu  
                                  340                      345                      350  
 Val Pro Ser Gln Pro Gly Val Asn Leu Leu Gly Asp Thr Phe Leu Arg  
                                  355                      360                      365  
 Ser Ala Tyr Val Val Tyr Asp Leu Glu Asn Asn Glu Ile Ser Leu Ala  
                                  370                      375                      380  
 Asn Thr Asn Phe Asn Pro Gly Asp Asp Asp Ile Leu Glu Ile Gly Thr  
                                  385                      390                      395                      400  
 Gly Thr Ser Ala Val Pro Gly Ala Thr Pro Val Pro Ser Ala Val Ser  
                                  405                      410                      415  
 Ser Ala Thr Gly Asn Gly Leu Ile Ser Ser Gly Thr Ala Val Pro Thr  
                                  420                      425                      430  
 Leu Ser Gly Val Thr Ile Thr Ala Thr Ala Thr Ala Thr Gly Ser Thr  
                                  435                      440                      445  
 Gly Thr Gly Ser Ser Gly Gly Ser Ser Ala Glu Ala Thr Ser Thr Ser  
                                  450                      455                      460  
 Ser Glu Gly Ala Ala Ala Gln Ala Thr Ser Asn Pro Met Asn Leu Leu  
                                  465                      470                      475                      480  
 Pro Gly Leu Ala Gly Ile Gly Leu Leu Leu Ala Leu  
                                  485                      490  
  
 <210> 140  
 <211> 611  
 <212> PRT  
 <213> *Aspergillus niger*  
  
 <400> 140  
 Met Leu Ser Ser Leu Leu Ser Gln Gly Ala Ala Val Ser Leu Ala Val  
 1                      5                      10                      15

Leu Ser Leu Leu Pro Ser Pro Val Ala Ala Glu Ile Phe Glu Lys Leu  
 20 25 30

Ser Gly Val Pro Asn Gly Trp Arg Tyr Ala Asn Asn Pro Gln Gly Asn  
 35 40 45

Glu Val Ile Arg Leu Gln Ile Ala Leu Gln Gln His Asp Val Ala Gly  
 50 55 60

Phe Glu Gln Ala Val Met Asp Met Ser Thr Pro Gly His Ala Asp Tyr  
 65 70 75 80

Gly Lys His Phe Arg Thr His Asp Glu Met Lys Arg Met Leu Leu Pro  
 85 90 95

Ser Glu Thr Ala Val Asp Ser Val Arg Asp Trp Leu Glu Ser Ala Gly  
 100 105 110

Val His Asn Ile Gln Val Asp Ala Asp Trp Val Lys Phe His Thr Thr  
 115 120 125

Val Asn Lys Ala Asn Ala Leu Leu Asp Ala Asp Phe Lys Trp Tyr Val  
 130 135 140

Ser Asp Ala Lys His Ile Arg Arg Leu Arg Thr Leu Gln Tyr Ser Ile  
 145 150 155 160

Pro Asp Ala Leu Val Ser His Ile Asn Met Ile Gln Pro Thr Thr Arg  
 165 170 175

Phe Gly Gln Ile Gln Pro Asn Arg Ala Thr Met Arg Ser Lys Pro Lys  
 180 185 190

His Ala Asp Glu Thr Phe Leu Thr Ala Ala Thr Leu Ala Gln Asn Thr  
 195 200 205

Ser His Cys Asp Ser Ile Ile Thr Pro His Cys Leu Lys Gln Leu Tyr  
 210 215 220

Asn Ile Gly Asp Tyr Gln Ala Asp Pro Lys Ser Gly Ser Lys Ile Gly  
 225 230 235 240

Phe Ala Ser Tyr Leu Glu Glu Tyr Ala Arg Tyr Ala Asp Leu Glu Arg  
 245 250 255

Phe Glu Gln His Leu Ala Pro Asn Ala Ile Gly Gln Asn Phe Ser Val  
 260 265 270

Val Gln Phe Asn Gly Gly Leu Asn Asp Gln Leu Ser Ser Ser Asp Ser  
 275 280 285

Gly Glu Ala Asn Leu Asp Leu Gln Tyr Ile Leu Gly Val Ser Ala Pro  
 290 295 300

Val Pro Ile Thr Glu Tyr Ser Thr Gly Gly Arg Gly Glu Leu Val Pro  
 305 310 315 320

Asp Leu Ser Ser Pro Asp Pro Asn Asp Asn Ser Asn Glu Pro Tyr Leu  
 325 330 335

Asp Phe Leu Gln Gly Ile Leu Lys Leu Asn Asn Ser Asp Leu Pro Gln  
 340 345 350

Val Ile Ser Thr Ser Tyr Gly Glu Asp Glu Gln Thr Ile Pro Val Pro  
 355 360 365

Tyr Ala Arg Thr Val Cys Asn Leu Tyr Ala Gln Leu Gly Ser Arg Gly  
 370 375 380

Val Ser Val Ile Phe Ser Ser Gly Asp Ser Gly Val Gly Ala Ala Cys  
 385 390 395 400

Leu Thr Asn Asp Gly Thr Asn Arg Thr His Phe Pro Pro Gln Phe Pro  
 405 410 415

Ala Ser Cys Pro Trp Val Thr Ser Val Gly Ala Thr Ser Lys Thr Ser  
 420 425 430

Pro Glu Gln Ala Val Ser Phe Ser Ser Gly Gly Phe Ser Asp Leu Trp  
 435 440 445

Pro Arg Pro Ser Tyr Gln His Ala Ala Val Gln Thr Tyr Leu Thr Lys  
 450 455 460

His Leu Gly Asn Lys Phe Ser Gly Leu Phe Asn Ala Ser Gly Arg Ala

465                      470                      475                      480  
 Phe Pro Asp Val Ser Ala Gln Gly Val Asn Tyr Ala Val Tyr Asp Lys  
                                  485                                   490                                   495  
 Gly Met Leu Gly Gln Phe Asp Gly Thr Ser Cys Ser Ala Pro Thr Phe  
                                  500                                   505                                   510  
 Ser Gly Val Ile Ala Leu Leu Asn Asp Ala Arg Leu Arg Ala Gly Leu  
                                  515                                   520                                   525  
 Pro Val Met Gly Phe Leu Asn Pro Phe Leu Tyr Gly Val Gly Ser Glu  
                                  530                                   535                                   540  
 Lys Gly Ala Leu Asn Asp Ile Val Asn Gly Gly Ser Val Gly Cys Asp  
 545                                   550                                   555                                   560  
 Gly Arg Asn Arg Phe Gly Gly Thr Pro Asn Gly Ser Pro Val Val Pro  
                                  565                                   570                                   575  
 Phe Ala Ser Trp Asn Ala Thr Thr Gly Trp Asp Pro Val Ser Gly Leu  
                                  580                                   585                                   590  
 Gly Thr Pro Asp Phe Ala Lys Leu Lys Gly Val Ala Leu Gly Glu Glu  
                                  595                                   600                                   605  
 Gly Gly Asn  
 610  
  
 <210> 141  
 <211> 478  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 141  
 Met Trp Leu Phe Leu Val Cys Ser Ile Leu Leu Pro Leu Gly Val Val  
 1                                   5                                   10                                   15  
 Asn Ala Gln Ser Gln Tyr Phe Asn Asn Lys Thr Lys Glu Phe Val Val  
                                  20                                   25                                   30  
 Asn Gly Ser Ala Ile Pro Phe Val Asp Phe Asp Ile Gly Glu Ser Tyr  
                                  35                                   40                                   45

Ala Gly Tyr Leu Pro Asn Thr Pro Ser Gly Ile Ser Ser Leu Tyr Phe  
 50 55 60

Trp Phe Phe Pro Ser Ser Asp Pro Asp Ala Ser Asp Glu Ile Thr Val  
 65 70 75 80

Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Ala Gly Ile Met Leu  
 85 90 95

Glu Asn Gly Pro Phe Leu Trp Gln Pro Gly Thr Tyr Arg Pro Val Arg  
 100 105 110

Asn Pro Tyr Ala Trp Asn Asn Leu Thr Asn Met Val Tyr Ile Asp Gln  
 115 120 125

Pro Ala Gly Thr Gly Phe Ser Leu Gly Pro Ser Thr Val Val Ser Glu  
 130 135 140

Phe Asp Val Ala Arg Gln Phe Met Asp Phe Trp Arg Arg Phe Met Lys  
 145 150 155 160

Thr Phe Asp Leu Gln Asn Arg Lys Ile Tyr Leu Thr Gly Glu Ser Tyr  
 165 170 175

Ala Gly Gln Tyr Ile Pro Tyr Ile Ala Ser Gln Met Leu Asp Gln Asp  
 180 185 190

Asp Asp Glu Tyr Phe Arg Val Ala Gly Ile Gln Ile Asn Asp Pro Tyr  
 195 200 205

Ile Asn Glu Leu Pro Val Leu Gln Asp Val Ala Thr Val Asn Gln His  
 210 215 220

Arg Ser Leu Phe Pro Phe Asn Asp Thr Phe Met Ser Gln Ile Thr Lys  
 225 230 235 240

Leu Ser Asp Asp Cys Gly Tyr Thr Ser Phe Leu Asp Asp Ala Leu Thr  
 245 250 255

Phe Pro Pro Arg Ser Gln Phe Pro Ser Val Pro Tyr Asn Ala Ser Cys  
 260 265 270



Asn Ile Trp Asp Ile Ile Asn Asn Ala Ser Leu Ala Leu Asn Pro Cys  
 275 280 285

Phe Asn Arg Tyr His Ile Pro Asp Ala Cys Pro Thr Pro Trp Asn Pro  
 290 295 300

Val Gly Gly Pro Ile Val Gly Leu Gly Pro Thr Asn Tyr Phe Asn Arg  
 305 310 315 320

Ser Asp Val Gln Lys Ala Ile Asn Ala Tyr Pro Thr Asp Tyr Phe Val  
 325 330 335

Cys Lys Asp Gly Ile Phe Pro Thr Ala Asn Gly Leu Asp Thr Ser Pro  
 340 345 350

Pro Ser Ser Leu Gly Pro Leu Pro Arg Val Ile Glu Gln Thr Asn Asn  
 355 360 365

Thr Ile Ile Ala His Gly Leu Met Asp Phe Glu Leu Leu Ala Gln Gly  
 370 375 380

Thr Leu Ile Ser Ile Gln Asn Met Thr Trp Asn Gly Lys Gln Gly Phe  
 385 390 395 400

Glu Arg Glu Pro Val Glu Pro Leu Phe Val Pro Tyr Gly Gly Ser Ser  
 405 410 415

Gly Gly Gly Val Leu Gly Thr Ala His Thr Glu Arg Gly Leu Thr Phe  
 420 425 430

Ser Thr Val Phe Ser Ser Gly His Glu Ile Pro Glu Tyr Ala Pro Gly  
 435 440 445

Ala Ala Tyr Arg Gln Leu Glu Phe Leu Leu Gly Arg Val Ala Asn Leu  
 450 455 460

Ser Thr Ile Ile Glu Gln Val Gln Ile Thr Glu Gln Asn Gly  
 465 470 475

<210> 142

<211> 210

<212> PRT

<213> Aspergillus niger

&lt;400&gt; 142

Met Ser Lys Leu Ser Ala Ala Ile Ser Lys Leu Ser Leu Ser Thr Ile  
 1 5 10 15

Ala Thr Thr Leu Leu Leu Thr Pro Pro Thr Thr Ala Tyr Phe Tyr  
 20 25 30

Lys Tyr Pro Ala Leu Phe Val Tyr Lys Asp Thr Asn Cys Thr Asp Ile  
 35 40 45

Ser Phe Ser Leu Val Tyr Pro Ser Leu Gly Asn Cys Asn Gly Gly Tyr  
 50 55 60

Tyr Asp Tyr Ala Gly Ser Phe Gln Met Phe Asn Ile Asp Ala Ala Tyr  
 65 70 75 80

Thr Cys Asn Gly Ser Asp Ser Thr Leu Met Phe Glu Met Tyr Asn Ser  
 85 90 95

Ser Gly Ser Asp Cys Gly Asp Glu Ser Asp Leu Leu Phe Arg Gln Pro  
 100 105 110

Val Thr Glu Glu Cys Thr Val Ala Asp Val Glu Ser Pro Gly Pro Leu  
 115 120 125

Glu Met Pro Val Trp Phe Glu Leu Gly Ser Leu Leu Gly Asn Cys Gly  
 130 135 140

Gly Met Ala Gly Thr Met Leu Phe Gly Val Gly Ile Leu Glu Gly Gly  
 145 150 155 160

Leu Glu Thr Lys Leu Tyr Trp Lys Cys Tyr Ser Ser Arg Leu Asn Thr  
 165 170 175

Ser Val Thr Val His Arg Leu Ser Leu Ile Leu Ser Met Gly Cys Thr  
 180 185 190

Ser Val Ser Asp Ser Tyr Asn Glu Leu Ala Ala Ala His Tyr Tyr Glu  
 195 200 205

Asp Leu  
 210

<210> 143  
 <211> 608  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 143

Met Arg His Leu Leu Ser Leu Leu Val Leu Leu Ile Ala Ser Ala Ala  
 1 5 10 15

Leu Val Ser Ala Val Pro Ala Gly Ser Ile Ile Thr Pro Gln Pro Pro  
 20 25 30

Val Glu Pro Val His Leu Leu Ser Ser Gln Pro Ser Asp Pro Arg Arg  
 35 40 45

Pro Trp Ile Arg Leu Arg Asp Trp Ile Ile Glu Ser Ile Trp Gly Ile  
 50 55 60

Glu Lys Pro Ala Ser Arg Arg Phe Pro Leu Asn Asp Ser Pro Arg Asn  
 65 70 75 80

Arg Ser Pro Pro Ser Arg Ile Leu Ala Arg Tyr Gly Ser Asp Val Val  
 85 90 95

Leu Arg Phe Ser Leu Arg Asn His Asp Glu Ala Glu Ala Leu Ala Gln  
 100 105 110

Ala Ala Asp Ile Leu Phe Leu Asp Val Trp Ala Ser Thr Pro Ala Phe  
 115 120 125

Val Asp Ile Arg Leu Ala Glu Glu Val Thr Ala Tyr Thr Pro Leu Ile  
 130 135 140

Asp Asn Leu Ala Glu Arg Ile Tyr Thr Thr Tyr Pro Ser Lys Lys Pro  
 145 150 155 160

Ile Gly Leu Glu Gly Gln Ser Gly Phe Ala Ser Ser Ser Arg Pro Ala  
 165 170 175

Pro Lys Phe Gly Asp Leu Phe Phe His Glu Tyr Gln Pro Leu Ser Val  
 180 185 190

Ile Ile Pro Trp Met Arg Leu Leu Ala Ser Met Phe Pro Ser His Val

195	200	205
Arg Met Ile Ser Val Gly	Val Ser Tyr Glu Gly	Arg Glu Ile Pro Ala
210	215	220
Leu Arg Leu Ser Ala Gly	Ser Ser Thr Ala Ala	Ser Gly Pro Arg Lys
225	230	235
Thr Ile Ile Val Thr Gly	Gly Ser His Ala Arg	Glu Trp Ile Gly Thr
	245	250
Ser Thr Val Asn His Val	Met Tyr Thr Leu Ile	Thr Lys Tyr Gly Lys
	260	265
Ser Lys Ala Val Thr Arg	Leu Leu Gln Asp Phe	Asp Trp Ile Met Ile
	275	280
Pro Thr Ile Asn Pro Asp	Gly Tyr Val Tyr Thr	Trp Glu Thr Asp Arg
	290	295
Leu Trp Arg Lys Asn Arg	Gln Arg Thr Ser Leu	Arg Phe Cys Pro Gly
305	310	315
Ile Asp Leu Asp Arg Ala	Trp Gly Phe Glu Trp	Asp Gly Gly Arg Thr
	325	330
Arg Ala Asn Pro Cys Ser	Glu Asn Tyr Ala Gly	Asp Glu Pro Phe Glu
	340	345
Gly Met Glu Ala Gln Gln	Leu Ala Gln Trp Ala	Leu Asn Glu Thr Gln
	355	360
Asn Asn Asn Ala Asp Ile	Val Ser Phe Leu Asp	Leu His Ser Tyr Ser
	370	375
Gln Thr Ile Leu Tyr Pro	Phe Ser Tyr Ser Cys	Ser Ser Ile Pro Pro
385	390	395
Thr Leu Glu Ser Leu Glu	Glu Leu Gly Leu Gly	Leu Ala Lys Ala Ile
	405	410
Arg Tyr Ala Thr His Glu	Ile Tyr Asp Val Thr	Ser Ala Cys Glu Gly
	420	425
		430

Ile Val Thr Ala Ser Ala Ala Asp Asn Asn Pro Gly Arg Phe Phe Pro  
 435 440 445

Ile Gly Gly Asn Ser Gly Gly Ser Ala Leu Asp Trp Phe Tyr His Gln  
 450 455 460

Val His Ala Thr Tyr Ser Tyr Gln Ile Lys Leu Arg Asp Arg Gly Ser  
 465 470 475 480

Tyr Gly Phe Leu Leu Pro Ser Glu His Ile Ile Pro Thr Gly Lys Glu  
 485 490 495

Ile Tyr Asn Val Val Leu Lys Leu Gly Ser Phe Leu Ile Gly Gly Asp  
 500 505 510

Ser Phe Asp Val Asp Trp Glu Ser Glu Leu Phe Asp Leu Ser Lys Asp  
 515 520 525

Glu Ser Asp Leu Asp Ser Arg Tyr Ser Lys Ser Asn Asp Arg Ser Pro  
 530 535 540

Ala Tyr Leu His Asn Ala Asn Gly Pro Leu Pro Asn Ile Asp Glu Asp  
 545 550 555 560

Glu Asp Lys Glu Trp Val Met Val Glu Glu Glu Asp Tyr Thr Asp Asp  
 565 570 575

Asp Asp Asp Asp Asp Asp Asp Asp Glu Glu Glu Glu Glu Glu Glu  
 580 585 590

Asp Thr Tyr Trp Ala Thr Glu His Thr Tyr Glu Phe Arg Arg Arg Arg  
 595 600 605

<210> 144

<211> 416

<212> PRT

<213> Aspergillus niger

<400> 144

Met Ala Phe Leu Lys Arg Ile Leu Pro Leu Leu Ala Leu Ile Leu Pro  
 1 5 10 15

Ala Val Phe Ser Ala Thr Glu Gln Val Pro His Pro Thr Ile Gln Thr  
 20 25 30  
 Ile Pro Gly Lys Tyr Ile Val Thr Phe Lys Ser Gly Ile Asp Asn Ala  
 35 40 45  
 Lys Ile Glu Ser His Ala Ala Trp Val Thr Glu Leu His Arg Arg Ser  
 50 55 60  
 Leu Glu Gly Arg Ser Thr Thr Glu Asp Asp Leu Pro Ala Gly Ile Glu  
 65 70 75 80  
 Arg Thr Tyr Arg Ile Ala Asn Phe Ala Gly Tyr Ala Gly Ser Phe Asp  
 85 90 95  
 Glu Lys Thr Ile Glu Glu Ile Arg Lys His Asp His Val Ala Tyr Val  
 100 105 110  
 Glu Gln Asp Gln Val Trp Tyr Leu Asp Thr Leu Val Thr Glu Arg Arg  
 115 120 125  
 Ala Pro Trp Gly Leu Gly Ser Ile Ser His Arg Gly Gly Ser Ser Thr  
 130 135 140  
 Asp Tyr Ile Tyr Asp Asp Ser Ala Gly Glu Gly Thr Tyr Ala Tyr Val  
 145 150 155 160  
 Val Asp Thr Gly Ile Leu Ala Thr His Asn Glu Phe Gly Gly Arg Ala  
 165 170 175  
 Ser Leu Ala Tyr Asn Ala Ala Gly Gly Glu His Val Asp Asp Val Gly  
 180 185 190  
 His Gly Thr His Val Ala Gly Thr Ile Gly Gly Lys Thr Tyr Gly Val  
 195 200 205  
 Ser Lys Asn Ala His Leu Leu Ser Val Lys Val Phe Val Gly Glu Ser  
 210 215 220  
 Ser Ser Thr Ser Val Ile Leu Asp Gly Phe Asn Trp Ala Ala Asn Asp  
 225 230 235 240  
 Ile Val Ser Lys Asn Arg Thr Ser Lys Ala Ala Ile Asn Met Ser Leu

245                      250                      255  
 Gly Gly Gly Tyr Ser Tyr Ala Phe Asn Asn Ala Val Glu Asn Ala Phe  
                          260                      265                      270  
 Asp Glu Gly Val Leu Ser Cys Val Ala Ala Gly Asn Glu Asn Arg Asp  
                          275                      280                      285  
 Ala Ala Arg Thr Ser Pro Ala Ser Ala Pro Asp Ala Ile Thr Val Ala  
                          290                      295                      300  
 Ala Ile Asn Arg Ser Asn Ala Arg Ala Ser Phe Ser Asn Tyr Gly Ser  
 305                      310                      315                      320  
 Val Val Asp Ile Phe Ala Pro Gly Glu Gln Val Leu Ser Ala Trp Thr  
                          325                      330                      335  
 Gly Ser Asn Ser Ala Thr Asn Thr Ile Ser Gly Thr Ser Met Ala Thr  
                          340                      345                      350  
 Pro His Val Thr Gly Leu Ile Leu Tyr Leu Met Gly Leu Arg Asp Leu  
                          355                      360                      365  
 Ala Thr Pro Ala Ala Ala Thr Thr Glu Leu Lys Arg Leu Ala Thr Arg  
                          370                      375                      380  
 Asn Ala Val Thr Asn Val Ala Gly Ser Pro Asn Leu Leu Ala Tyr Asn  
 385                      390                      395                      400  
 Gly Asn Ser Gly Val Ser Lys Gly Gly Ser Asp Asp Gly Asp Glu Asp  
                          405                      410                      415

<210> 145  
 <211> 455  
 <212> PRT  
 <213> Aspergillus niger

<400> 145

Met Ile Thr Leu Leu Ser Ala Leu Phe Gly Ser Val Val Tyr Ala Ala  
 1                      5                      10                      15

Thr Gln Thr Val Leu Gly Pro Glu Gly Ala Asp Pro Phe Thr Val Phe  
                          20                      25                      30

Arg Ser Pro His Ser Pro Ala Phe Ser Ile Arg Ile Gln Glu Gln Asn  
 35 40 45  
 Asp Ser Ile Cys Asp Ala Arg Ser Pro Gln Phe Thr Gly Trp Leu Asp  
 50 55 60  
 Ile Gly Pro Lys His Leu Phe Phe Trp Tyr Phe Glu Ser Gln Asn Asp  
 65 70 75 80  
 Pro Phe His Asp Pro Leu Thr Leu Trp Met Thr Gly Gly Pro Gly Asp  
 85 90 95  
 Ser Ser Met Ile Gly Leu Phe Glu Glu Val Gly Pro Cys Arg Ile Asn  
 100 105 110  
 Glu Phe Gly Asn Gly Thr Asp His Asn Pro Trp Ala Trp Thr Lys Asn  
 115 120 125  
 Ser Ser Leu Leu Phe Val Asp Gln Pro Val Asp Val Gly Phe Ser Tyr  
 130 135 140  
 Ile Asp Glu Gly Tyr Glu Leu Pro His Asp Ser Arg Glu Ala Ala Val  
 145 150 155 160  
 Asp Met His Arg Phe Leu Arg Leu Phe Ile Ser Glu Ile Phe Pro His  
 165 170 175  
 Lys Gln Phe Leu Pro Val His Leu Ser Gly Glu Ser Tyr Ala Gly Arg  
 180 185 190  
 Tyr Ile Pro Tyr Leu Ala Thr Gln Ile Leu Glu Gln Asn Glu Leu Tyr  
 195 200 205  
 Lys Asp Ser Pro Arg Ile Pro Leu Lys Ser Cys Leu Val Gly Asn Gly  
 210 215 220  
 Phe Met Ser Pro Lys Asp Ala Thr Phe Gly Tyr Trp Glu Thr Leu Cys  
 225 230 235 240  
 Thr Thr Asn Ser Gly Val Pro Ser Pro Ile Phe Asn Glu Thr Arg Cys  
 245 250 255



Asp Ile Met Ala Ala Asn Met Pro His Cys Met Asp Leu Tyr Asp Ile  
 260 265 270

Cys Ile Gln His Ser Asp Pro Ala Ile Cys His Ala Ala Gln Ser Val  
 275 280 285

Cys Tyr Asp Ser Val Val Gly Leu Met Ala Lys Leu Leu Leu Arg Met  
 290 295 300

Thr Thr Val Thr Ala Pro Cys Glu Ile Asp Glu Met Cys Tyr Ile Glu  
 305 310 315 320

Ala Ala Leu Ile Glu Arg Tyr Leu Asn Ser Pro Ser Val Trp Glu Ala  
 325 330 335

Leu Ser Pro Pro Gln Gln Val Thr Glu Tyr Lys Phe Val Ala Thr Ser  
 340 345 350

Val Ile Asp Ala Phe Ala Gln Ser Ala Asp Gly Met Val Ser Ser Ser  
 355 360 365

Lys Gln Ile Ala Phe Leu Leu Ala Asn Asn Val Asp Phe Leu Ala Tyr  
 370 375 380

Gln Gly Asn Leu Asp Leu Ala Cys Asn Thr Ala Gly Asn Leu Arg Trp  
 385 390 395 400

Ala Asn Ser Leu Ser Trp Lys Gly Gln Thr Glu Phe Thr Ala Lys Pro  
 405 410 415

Leu Leu Pro Trp Glu Ile Gln Val Ser Val Gly Glu Gly Thr Asp Glu  
 420 425 430

Thr Ser Arg Phe Ala Phe Val Thr Val Asp Asn Ala Gly His Leu Leu  
 435 440 445

Arg Asp Ser Lys Ile Ser Asn  
 450 455

<210> 146

<211> 791

<212> PRT

<213> Aspergillus niger

&lt;400&gt; 146

Met Arg Phe Leu Thr Tyr Ser Leu Pro Phe Ile Ala Ser Ala Ile Ser  
1 5 10 15

Leu Phe Gly Val Asn Val Gln Ala Arg Ser Gln Ala Pro Ser Ala Ile  
20 25 30

Arg His Val Ser Thr Leu Asp Gln Pro Thr Ile Lys Thr Pro Ser Gln  
35 40 45

Arg Val Asp His Leu Asp His Phe Asp Ile Thr Phe Asn Ile His Asp  
50 55 60

Lys His Gln Arg Ile Lys Leu Glu Leu Glu Pro Asn His Asp Ile Leu  
65 70 75 80

Ala Glu Asp Ala Ser Val Gln Tyr Leu Asp Ala Asp Gly Asn Val Arg  
85 90 95

Arg His Glu Pro Ile Ala Pro His Glu His Lys Val Phe Lys Gly Arg  
100 105 110

Ser Leu Leu Gly Arg Gly Lys Gly Met Trp Asp Pro Val Gly Trp Ala  
115 120 125

Arg Ile Tyr Leu Lys Gln Asp Gly Ser Glu Pro Leu Phe Glu Gly Val  
130 135 140

Phe Ser Ile Asp Gly Asp Asn His His Val Gln Leu Lys Ser Ala Tyr  
145 150 155 160

Met Glu Lys Lys Arg Pro Val Asp Val Asp Leu Pro Asp Ser Ala Thr  
165 170 175

Asp Tyr Met Ile Phe Tyr Arg Asp Ser Asp Met Val Arg Leu His Thr  
180 185 190

Glu Leu Lys Arg Ser Ser Leu Gly Ser Thr Ser Cys Gln Ala Asp Gln  
195 200 205

Leu Gly Phe Asn Thr Asn Pro Asn His Pro Val Leu Gln Pro Tyr Gly  
210 215 220

Gln Ala Glu Thr Asp Thr Trp Gly Ala Ile Ser Leu Asn Ser Leu Phe  
 225 230 235 240

Gly Leu Asn Lys Arg Gln Ser Asp Ile Gly Ser Val Ser Gly Asn Ala  
 245 250 255

Gly Gly Val Asn Leu Ala Ser Thr Ile Gly Asp Thr Ser Gly Cys Pro  
 260 265 270

Ser Thr Lys Gln Val Ala Leu Ile Gly Val Ala Thr Asp Cys Ala Phe  
 275 280 285

Thr Gly Ser Phe Asn Asn Glu Thr Ala Ala Lys Glu Trp Val Ile Ser  
 290 295 300

Thr Val Asn Ser Ala Ser Asn Val Tyr Glu Lys Ser Phe Asn Ile Thr  
 305 310 315 320

Ile Gly Leu Arg Asn Leu Thr Ile Thr Asp Ser Ser Cys Pro Asp Asn  
 325 330 335

Pro Pro Ala Ala Thr Ala Trp Asn Met Pro Cys Ser Ser Gly Asn Leu  
 340 345 350

Thr Ser Arg Leu Asp Leu Phe Ser Lys Trp Arg Gly Glu Gln Ser Asp  
 355 360 365

Asp Asn Ala Tyr Trp Thr Leu Met Ser Asp Cys Ala Thr Gly Asn Glu  
 370 375 380

Val Gly Leu Ser Trp Leu Gly Gln Leu Cys Asn Ser Asp Ala Ser Ser  
 385 390 395 400

Asp Gly Ser Ser Thr Val Ser Gly Thr Asn Val Val Val Arg Ser Ser  
 405 410 415

Gly Ser Asp Trp Gln Ile Phe Ala His Glu Ser Gly His Thr Phe Gly  
 420 425 430

Ala Val His Asp Cys Asp Ser Gln Thr Cys Ala Glu Asp Leu Glu Ala  
 435 440 445

Ser Ser Gln Cys Cys Pro Leu Thr Ser Ser Thr Cys Asn Ala Asn Gly  
 450 455 460

Lys Tyr Ile Met Asn Pro Thr Thr Gly Thr Asp Ile Thr Ala Phe Ser  
 465 470 475 480

Gln Cys Thr Ile Gly Asn Ile Cys Ala Ala Leu Gly Arg Asn Ser Val  
 485 490 495

Lys Ser Ser Cys Leu Ser Ala Asn Arg Asp Val Thr Thr Tyr Thr Gly  
 500 505 510

Ser Gln Cys Gly Asn Gly Ile Val Glu Ser Gly Glu Asp Cys Asp Cys  
 515 520 525

Gly Gly Glu Asp Gly Cys Gly Asp Asn Asn Cys Cys Asp Ala Lys Thr  
 530 535 540

Cys Lys Phe Lys Ser Gly Ala Val Cys Asp Asp Ser Asn Asp Ser Cys  
 545 550 555 560

Cys Ser Ser Cys Gln Phe Ser Ser Ala Gly Thr Val Cys Arg Ala Ser  
 565 570 575

Arg Gly Asp Cys Asp Val Ala Glu Thr Cys Ser Gly Asn Ser Ser Thr  
 580 585 590

Cys Pro Thr Asp Ser Phe Lys Lys Asp Gly Thr Ser Cys Gly Ser Ser  
 595 600 605

Gly Ser Gly Leu Ala Cys Ala Ser Gly Gln Cys Thr Ser Arg Asp Tyr  
 610 615 620

Gln Cys Arg Ser Val Met Gly Ser Leu Leu His Ser Asn Asp Thr Tyr  
 625 630 635 640

Ala Cys Ser Ser Phe Ser Ser Ser Cys Glu Leu Val Cys Thr Ser Pro  
 645 650 655

Lys Ile Gly Thr Cys Tyr Ser Val Asn Gln Asn Phe Leu Asp Gly Thr  
 660 665 670

Pro Cys Gly Ser Gly Gly Tyr Cys Ser Asn Gly Asp Cys Lys Gly Gln

675                      680                      685  
 Asn Val Glu Ser Trp Ile Lys Asn His Lys Gly Ile Val Ile Gly Val  
 690                      695                      700  
 Ala Cys Ala Val Gly Ala Leu Ile Leu Leu Ala Leu Met Thr Cys Ile  
 705                      710                      715                      720  
 Val Asn Arg Cys Arg Arg Ala Arg Ala Pro Lys Pro Val Pro Arg Pro  
 725                      730                      735  
 Val Pro Tyr Gly Pro Trp Pro Gly Ala Arg Pro Pro Pro Pro Pro Pro  
 740                      745                      750  
 Met Asn Gln Trp Pro Ala Arg Gly Tyr Gln Gly Leu Gly Asn Glu Pro  
 755                      760                      765  
 Pro Pro Pro Tyr Pro Gly Val Pro Gly Gln Pro Val Pro Gln His Met  
 770                      775                      780  
 Pro Pro Gln Gly Arg Tyr Ala  
 785                      790  
 <210> 147  
 <211> 481  
 <212> PRT  
 <213> Aspergillus niger  
 <400> 147  
 Met Arg Phe Leu Ser Ser Ala Ala Leu Phe Gly Leu Ala Tyr Ala Ser  
 1                      5                      10                      15  
 Thr Gln Ala Val Leu Gln Pro Glu Glu Pro Ser Asp Phe Arg Thr Phe  
 20                      25                      30  
 His Ser Pro Tyr Ser Pro His His Ser Ile Arg Ile Arg Gln Gln Asn  
 35                      40                      45  
 Glu Ser Ile Cys Ala Ala His Ser Ala Gln Tyr Thr Gly Trp Leu Asp  
 50                      55                      60  
 Ile Gly Arg Lys His Leu Phe Phe Trp Tyr Phe Glu Ser Gln Asn Asp  
 65                      70                      75                      80

Pro Ala Asn Asp Pro Leu Thr Leu Trp Met Thr Gly Gly Pro Gly Gly  
 85 90 95

Ser Ser Met Ile Gly Leu Phe Glu Glu Val Gly Pro Cys Leu Ile Asn  
 100 105 110

Glu Tyr Gly Asn Gly Thr Tyr Tyr Asn Pro Trp Gly Trp Ser Arg Asn  
 115 120 125

Ser Ser Leu Leu Phe Val Asp Gln Pro Val Asp Val Gly Phe Ser Tyr  
 130 135 140

Val Asp Glu Gly Glu Asp Leu Pro Gly Asp Ser His Gln Ala Ala Ile  
 145 150 155 160

Asp Met His Arg Phe Leu Gln Leu Phe Val Ser Glu Val Phe Pro Gln  
 165 170 175

Leu Gln Thr Leu Pro Val His Leu Ser Gly Glu Ser Tyr Ala Gly His  
 180 185 190

Tyr Val Pro Tyr Leu Gly Ser Gln Ile Val Gln Gln Asn Lys Leu Tyr  
 195 200 205

Pro Thr Glu Pro Gln Val Leu Leu His Ser Cys Leu Val Gly Asn Gly  
 210 215 220

Tyr Tyr Ser Pro Arg Asp Thr Thr Tyr Gly Tyr Trp Glu Thr Leu Cys  
 225 230 235 240

Thr Thr Asn Pro Gly Val Pro Glu Pro Val Phe Asn Arg Thr Arg Cys  
 245 250 255

Asp Ile Met Ala Ala Asn Met Pro Arg Cys Met Glu Val Ser Asp Val  
 260 265 270

Cys Val Arg Asn Pro Asp Pro Ala Ile Cys His Ala Ala Ser Glu Val  
 275 280 285

Cys Tyr Glu Gly Val Ile Gly Trp Tyr Asp Asp Glu Ser Gly Glu Gly  
 290 295 300

Gly Arg Asn Arg Phe Asp Ile Thr Ala Pro Cys Ala Leu Asp Gly Ile  
 305 310 315 320

Cys Tyr Ile Glu Ala Ala Arg Ile Glu Gln Tyr Leu Asn Thr Pro Ala  
 325 330 335

Val Trp Ala Ala Leu Ser Pro Pro Lys Glu Ile Lys Glu Tyr Lys Val  
 340 345 350

Thr Ser Asp Asn Val Ser Arg Ala Phe Asp Leu Thr Ser Asp Thr Met  
 355 360 365

Thr Pro Ala Ser Glu Gln Val Ala Phe Leu Leu Ala Asn Gln Val His  
 370 375 380

Phe Leu Ala Tyr Gln Gly Asn Leu Asp Leu Ala Cys Asn Thr Ala Gly  
 385 390 395 400

Asn Leu Arg Trp Ala His Ser Leu Pro Trp Arg Gly Gln Val Glu Phe  
 405 410 415

Ala Ser Lys Ala Leu Arg Pro Trp Ser Trp Val Asp Val Val Ser Gly  
 420 425 430

Lys Gly Gly Val Ala Gly Thr Thr Lys Glu Glu Ser Arg Phe Ala Leu  
 435 440 445

Val Thr Val Asp Gly Ala Gly His Phe Leu Pro Gln Asp Arg Pro Asp  
 450 455 460

Ile Ala Leu Asp Met Met Val Arg Trp Ile Ser Gly Ala Ser Phe Thr  
 465 470 475 480

Glu

<210> 148

<211> 319

<212> PRT

<213> Aspergillus niger

<400> 148

Met Thr Leu Leu Leu Asn Phe His Ala Leu Phe Thr Val Ile Leu Val  
 1 5 10 15

Ala Asn Leu Ser Thr Arg Cys Ser Ala Leu Leu Ser Gly Arg Asp Phe  
 20 25 30

Cys Ser Thr Pro Ala Pro Gly Glu Ser Leu Arg Ala Glu His Arg Arg  
 35 40 45

Leu Tyr Asp Val Gln Ala Gln Arg Asp Ser Thr Ala Glu Glu Ser Arg  
 50 55 60

Glu Val Val Pro Trp Ile Glu Ile Glu Thr Trp Phe His Ile Val Ser  
 65 70 75 80

Ser Asn Glu Ala Ala Asn Thr Val Ser Asp Asp Met Ile Thr Ser Gln  
 85 90 95

Leu Ser Tyr Leu Gln Lys Ala Tyr Glu Ser Ala Thr Ile Thr Tyr Arg  
 100 105 110

Leu Glu Gly Ile Thr Arg His Ile Asn Asp Ser Trp Ala Arg Asn Asp  
 115 120 125

Asp Glu Leu Gly Met Lys Asn Ala Leu Arg Arg Gly Asn Tyr Gly Thr  
 130 135 140

Leu Asn Val Tyr Phe Gln Thr Asp Leu Gln Ala Ser Ser Asp Glu Asn  
 145 150 155 160

Ser Arg Asp Tyr Pro Asn Asp Gly Asn Arg Arg Thr Asp Val Ser Asp  
 165 170 175

Gln Ser Ser Ser Thr Val Leu Gly Phe Cys Thr Leu Pro Asp Pro Ser  
 180 185 190

Val Asn Ser Ser Ser Pro Arg Ser Ser Tyr Ile Lys Asp Gly Cys Asn  
 195 200 205

Val Leu Ala Asp Ile Met Pro Gly Gly Ser Leu Ala Gln Tyr Asn Lys  
 210 215 220

Gly Gly Thr Ala Val His Glu Val Gly His Trp Asn Gly Leu Leu His  
 225 230 235 240



Thr Phe Glu Gly Glu Ser Cys Ser Pro Asp Asn Glu Gly Asp Tyr Ile  
245 250 255

Asp Asp Thr Pro Glu Gln Ser Glu Pro Thr Ser Gly Cys Pro Ala Glu  
260 265 270

Lys Asp Ser Cys Pro Asp Leu Pro Gly Leu Asp Ala Ile His Asn Phe  
275 280 285

Met Asp Tyr Ser Ser Asp Asp Cys Tyr Glu Ser Phe Thr Pro Asp Gln  
290 295 300

Ala Glu Arg Met Arg Ser Met Trp Ser Ala Met Arg Glu Gly Lys  
305 310 315

<210> 149  
<211> 639  
<212> PRT  
<213> Aspergillus niger

<400> 149

Met His Val Ser Leu Phe Leu Leu Ser Val Thr Ala Ala Phe Ala Ser  
1 5 10 15

Pro Thr Pro His Asn Tyr Val Val His Glu Arg Arg Asp Ala Leu Pro  
20 25 30

Ser Val Trp Val Glu Glu Ser Arg Leu Asp Lys Gly Ala Leu Leu Pro  
35 40 45

Met Arg Ile Gly Leu Thr Gln Ser Asn Leu Asp Arg Gly His Asp Leu  
50 55 60

Leu Met Glu Val Ser His Pro Gln Ser Ser Arg Tyr Gly Lys His Leu  
65 70 75 80

Ser Ser Glu Glu Val His Asp Leu Phe Ala Pro Ser Asn Glu Ala Val  
85 90 95

Glu Thr Val Arg Thr Trp Ile Glu Ser Ala Gly Ile Ala Pro Ser Arg  
100 105 110

Ile Ser Gln Ser Tyr Asn Lys Gln Trp Leu Gln Phe Asp Ala His Ala

[illegible]

Leu Asp Pro Gln Tyr Pro Asp Pro Ser Pro Gly Gly Tyr Ser Ser Pro  
 355 360 365

Lys Gln Cys Gly Val Tyr Thr Pro Thr Asn Val Ile Ser Ile Ser Tyr  
 370 375 380

Gly Ser Pro Glu Ala Asp Leu Pro Ile Ala Tyr Gln Arg Arg Gln Cys  
 385 390 395 400

His Glu Phe Met Lys Leu Gly Leu Gln Gly Ile Ser Val Val Val Ala  
 405 410 415

Ser Gly Asp Ser Gly Val Ala Ser Ser Thr Gly Thr Cys Phe Gly Asp  
 420 425 430

Ala Asp Asn Val Phe Val Pro Asp Phe Pro Ala Thr Cys Pro Tyr Leu  
 435 440 445

Thr Ala Val Gly Gly Thr Tyr Leu Pro Leu Gly Ala Asp Ala Ala Lys  
 450 455 460

Asp Gln Glu Ile Ala Val Thr Arg Phe Pro Ser Gly Gly Gly Phe Ser  
 465 470 475 480

Asn Ile Tyr Ala Arg Pro Ser Tyr Gln Asn His Ser Val Glu Thr Tyr  
 485 490 495

Phe Ser Thr Thr Ser Asp Asp Leu Thr Tyr Pro Tyr Tyr Ser Gly Val  
 500 505 510

Asn Tyr Thr Asp Phe Ser Asn Thr Asp Gly Val Tyr Asn Arg Ile Gly  
 515 520 525

Arg Gly Tyr Pro Asp Val Ser Ala Ile Ala Asp Asn Ile Ile Ile Tyr  
 530 535 540

Asn Gln Gly Glu Ala Thr Leu Val Gly Gly Thr Ser Ala Ala Ala Pro  
 545 550 555 560

Ala Phe Ala Ala Met Leu Thr Arg Ile Asn Glu Glu Arg Leu Ala Lys  
 565 570 575

Gly Lys Ser Thr Val Gly Phe Val Asn Pro Val Leu Tyr Glu His Pro  
580 585 590

Glu Ala Phe Arg Asp Val Thr Val Gly Ser Asn Pro Gly Cys Gly Thr  
595 600 605

Asp Gly Phe Pro Val Ala Gly Gly Trp Asp Pro Val Thr Gly Leu Gly  
610 615 620

Thr Pro Arg Phe Glu Asp Leu Met Asp Ile Phe Val Gly Asp Asp  
625 630 635

<210> 150

<211> 371

<212> PRT

<213> Aspergillus niger

<400> 150

Met Ala Ser Lys Thr Leu Leu Leu Ile Pro Ala Leu Ala Thr Ala Ala  
1 5 10 15

Leu Gly Ser Val Leu Asp Leu Asp Ile Lys Val Asp Leu Gly Thr Pro  
20 25 30

Gly Gly Pro Phe Asp Leu Met Tyr Asp Thr Gly Ser Ser Thr Leu Trp  
35 40 45

Val Leu Asp Ser Asn Cys Thr Asp Asp Cys Pro Asn Val Ser Gly Tyr  
50 55 60

Ser Arg His Gly Tyr Asn Leu Thr Ser Thr Gly Val Asn Leu Gly Val  
65 70 75 80

Asn Asp Ser Ile Ala Tyr Ser Gly Gly Thr Val Ser Gly Phe Thr Ala  
85 90 95

Thr Asp Ile Leu Thr Val Pro Asp Thr Asn Val Ser Tyr Arg Gln Ser  
100 105 110

Phe Ala Val Ile Thr Asp Ser Thr Trp Ala Ala Leu Ala Ala Asp Gly  
115 120 125

Phe Ile Gly Leu Ala Ser Ser Thr Ile Ala Phe Lys Asn Thr Thr Thr

130	135	140
Ala Val Glu Gln Met Met Gln Asp Gly Leu Leu Asp Glu Pro Arg Phe		
145	150	155 160
Ala Ile Tyr Ala Gly Ser Gly Glu Ser Thr Val Thr Asn Pro Asn Pro		
	165	170 175
Glu Asn Asn Gly Val Phe Thr Phe Gly Gly Ser His Glu Glu Thr Tyr		
	180	185 190
Ala Asp Gly Glu Leu Gln Trp Met Lys Met Leu Ser Pro Phe Glu Ile		
	195	200 205
Tyr Lys Thr Asn Leu Leu Gly Ile Gln Gly His Asn Asn Ser Asp Gly		
	210	215 220
Gln Ala Leu Ser Ser Asp Val Leu Asn Trp Tyr Gly Gln Thr Asn Leu		
225	230	235 240
Phe Asn Val Ala Gly Ala Ser Ser Ile Ser Ile Pro Asn Asp Gln Ile		
	245	250 255
Glu Ala Met Tyr Ala Leu Thr Pro Phe Ser Tyr Ala Asp Ile Ser Ser		
	260	265 270
Gly Tyr Arg Pro Leu Cys Ser Asp Phe Asn Asp Thr Trp Ser Ile Ser		
	275	280 285
Phe Thr Met Gly Phe Tyr Gly Glu Gly Val Thr Phe Asn Leu Thr Gly		
	290	295 300
Asp Gln Leu Ala Val Pro Gly Tyr Gln Asp Asp Asp His Cys Phe Pro		
305	310	315 320
Pro Phe Asn Pro Trp Asp Ser Tyr Asn Thr Ile Ile Gly Gln His Trp		
	325	330 335
Leu Ser Asn Phe Tyr Ala Val Phe Asp Phe Gly Ser Phe Asp Pro Glu		
	340	345 350
Thr Tyr Asp Ile Arg Val Gly Leu Ala Pro Leu Lys Lys Glu Tyr Leu		
	355	360 365

Pro Ser Ala  
370

<210> 151  
<211> 414  
<212> PRT  
<213> *Aspergillus niger*

<400> 151

Met Phe Pro Cys Ser Arg Ile Trp Ser Leu Leu Val Ala Ala Ala Thr  
1 5 10 15

Ala Ser Ala Val Pro Thr Ser Leu Ala Thr Thr His Leu Gln Ser Val  
20 25 30

Asp Leu Leu Leu Thr Arg Ser Ser Tyr Gly Phe Leu Thr Asp Ile Ala  
35 40 45

Leu Gly Thr Pro Gly Gln Ser Leu Pro Tyr Leu Val Asp Trp Thr Trp  
50 55 60

Thr Gly His Tyr Val Val Thr Thr Leu Cys Tyr Asn Asp Pro Thr Ala  
65 70 75 80

Thr Tyr Asp Cys Leu Asn Val Asp Gln Lys Ile Phe Asn Gln Thr Leu  
85 90 95

Ser Ser Thr Phe Ile Asn Gln Thr Asp Gln Tyr Gly Tyr Leu Tyr Trp  
100 105 110

Asp Pro Asn His Phe Tyr Phe Thr Glu Pro Ala Ala Ala Asp Val Ala  
115 120 125

Thr Asp Met Leu Arg Ile Gly Pro Thr Ala Val Asn Thr Thr Ile Gln  
130 135 140

Ala Ala Asn Phe Val Phe Asn Glu Thr Ile Ser Ala Phe Pro Phe Ser  
145 150 155 160

Gly Val Tyr Gly Leu Ser Pro Val Phe Gln Gly Asp Asn Arg Ser Val  
165 170 175

Gln Ala Ser Phe Tyr Gln Gly Trp Arg Ser Gly Ala Trp His Ser Pro  
 180 185 190

Ile Val Ser Phe Ile Tyr Cys His Asp Asn Ala Thr Lys Ala Val Cys  
 195 200 205

Ser Gly Tyr Asp Gly Leu Gln Thr Leu Gly Gly Tyr Asn Thr Ser His  
 210 215 220

Val Gln Gly Asp Ile Thr Trp Tyr Asp Ile Ile Val Thr Glu Ala Ile  
 225 230 235 240

Asn Thr Leu Asp Phe Val Tyr Ala Pro Ala Val Ile Asn Tyr Trp Ala  
 245 250 255

Leu Asn Leu Thr Arg Phe Ser Ile Gly Asp Glu Glu Gln Glu Leu Asn  
 260 265 270

Lys Thr Thr Thr Leu Asp Gly Lys Gln Ala Ala Val Ala Ala Phe Asp  
 275 280 285

His Ala Ser Tyr Gly Arg Gly Ala Pro Val Ser Val Tyr Gly Tyr Gln  
 290 295 300

Arg Leu Val Glu Leu Val Gly Ala Lys Ala Val Thr Leu Ser Asp Pro  
 305 310 315 320

Pro Asn Asn Gly Glu Gln Gly Phe Tyr Gln Phe Asp Cys Arg Asn Ser  
 325 330 335

Ser Leu Leu Pro Pro Leu Arg Tyr Glu Phe Ala Gly Ser Glu Arg Ala  
 340 345 350

Trp Glu Ile Val Pro Glu Asn Tyr Val Glu Val Leu Ala Asn Gly Thr  
 355 360 365

Asn Lys Cys Thr Phe Asn Val Arg Thr Leu Gly Asp Gly Ala Met Val  
 370 375 380

Met Gly Asn Phe Gly Glu Thr Phe Ala Ile Asp Lys Tyr Val Met Phe  
 385 390 395 400

Asp Phe Glu Lys Leu Gln Val Gly Ile Ala Asp Phe Ala Trp

405

410

<210> 152  
 <211> 480  
 <212> PRT  
 <213> Aspergillus niger

<400> 152

Met His Leu Pro Gln Arg Leu Val Thr Ala Ala Cys Leu Cys Ala Ser  
 1 5 10 15

Ala Thr Ala Phe Ile Pro Tyr Thr Ile Lys Leu Asp Thr Ser Asp Asp  
 20 25 30

Ile Ser Ala Arg Asp Ser Leu Ala Arg Arg Phe Leu Pro Val Pro Lys  
 35 40 45

Pro Ser Asp Ala Leu Ala Asp Asp Ser Thr Ser Ser Ala Ser Asp Glu  
 50 55 60

Ser Leu Ser Leu Asn Ile Lys Arg Ile Pro Val Arg Arg Asp Asn Asp  
 65 70 75 80

Phe Lys Ile Val Val Ala Glu Thr Pro Ser Trp Ser Asn Thr Ala Ala  
 85 90 95

Leu Asp Gln Asp Gly Ser Asp Ile Ser Tyr Ile Ser Val Val Asn Ile  
 100 105 110

Gly Ser Asp Glu Lys Ser Met Tyr Met Leu Leu Asp Thr Gly Gly Ser  
 115 120 125

Asp Thr Trp Val Phe Gly Ser Asn Cys Thr Ser Thr Pro Cys Thr Met  
 130 135 140

His Asn Thr Phe Gly Ser Asp Asp Ser Ser Thr Leu Glu Met Thr Ser  
 145 150 155 160

Glu Glu Trp Ser Val Gly Tyr Gly Thr Gly Ser Val Ser Gly Leu Leu  
 165 170 175

Gly Lys Asp Lys Leu Thr Ile Ala Asn Val Thr Val Arg Met Thr Phe  
 180 185 190



Gly Leu Ala Ser Asn Ala Ser Asp Asn Phe Glu Ser Tyr Pro Met Asp  
 195 200 205

Gly Ile Leu Gly Leu Gly Arg Thr Asn Asp Ser Ser Tyr Asp Asn Pro  
 210 215 220

Thr Phe Met Asp Ala Val Ala Glu Ser Asn Val Phe Lys Ser Asn Ile  
 225 230 235 240

Val Gly Phe Ala Leu Ser Arg Ser Pro Ala Lys Asp Gly Thr Val Ser  
 245 250 255

Phe Gly Thr Thr Asp Lys Asp Lys Tyr Thr Gly Asp Ile Thr Tyr Thr  
 260 265 270

Asp Thr Val Gly Ser Asp Ser Tyr Trp Arg Ile Pro Val Asp Asp Val  
 275 280 285

Tyr Val Gly Gly Thr Ser Cys Asp Phe Ser Asn Lys Ser Ala Ile Ile  
 290 295 300

Asp Thr Gly Thr Ser Tyr Ala Met Leu Pro Ser Ser Asp Ser Lys Thr  
 305 310 315 320

Leu His Ser Leu Ile Pro Gly Ala Lys Ser Ser Gly Ser Tyr His Ile  
 325 330 335

Ile Pro Cys Asn Thr Thr Thr Lys Leu Gln Val Ala Phe Ser Gly Val  
 340 345 350

Asn Tyr Thr Ile Ser Pro Lys Asp Tyr Val Gly Ala Thr Ser Gly Ser  
 355 360 365

Gly Cys Val Ser Asn Ile Ile Ser Tyr Asp Leu Phe Gly Asp Asp Ile  
 370 375 380

Trp Leu Leu Gly Asp Thr Phe Leu Lys Asn Val Tyr Ala Val Phe Asp  
 385 390 395 400

Tyr Asp Glu Leu Arg Val Gly Phe Ala Glu Arg Ser Ser Asn Thr Thr  
 405 410 415

Ser Ala Ser Asn Ser Thr Ser Ser Gly Thr Ser Ser Thr Ser Gly Ser  
 420 425 430

Thr Thr Thr Gly Ser Ser Thr Thr Thr Thr Ser Ser Ala Ser Ser Ser  
 435 440 445

Ser Ser Ser Asp Ala Glu Ser Gly Ser Ser Met Thr Ile Pro Ala Pro  
 450 455 460

Gln Tyr Phe Phe Ser Ala Leu Ala Ile Ala Ser Phe Met Leu Trp Leu  
 465 470 475 480

<210> 153  
 <211> 466  
 <212> PRT  
 <213> Aspergillus niger

<400> 153

Met Thr Ser Ser Thr Leu Arg Leu Ala Val Ala Leu Ala Leu Ser Thr  
 1 5 10 15

Cys Ser Ser Ala Leu Ser Ser Gln Arg Asp Asp Ser Leu Val Val Pro  
 20 25 30

Phe Pro Phe Gly Asn Leu Glu Asp Val His Ile Ala Lys Arg Asp Ser  
 35 40 45

Ser Lys Thr Val Glu Ala Pro Leu Val Ile Tyr Gly Asp Ser Tyr Trp  
 50 55 60

Met Asn Ala Ser Ile Gly Thr Pro Ala Gln Ser Leu Ser Phe Leu Leu  
 65 70 75 80

Asp Leu Thr Arg Ser Arg Val Glu Pro Ala Tyr Thr Leu Asp Glu Asn  
 85 90 95

Tyr Glu Cys Ser Asp Asp Glu Leu Cys Ser Glu Phe Gly Phe Tyr Lys  
 100 105 110

Pro Thr Asp Ser Ser Thr Tyr Gln His Leu Thr Tyr Thr Gln Arg His  
 115 120 125

Asp Ala Gly Val Asp Tyr Ser Tyr Leu Asp Thr Ile Thr Leu Gly Asp  
 130 135 140

His Ala Thr Asp Asn Val Pro Leu Asp Met Tyr Leu Leu Ser Tyr Ile  
145 150 155 160

Ser Tyr Ser Ser Leu Gly Leu Ser Ser Val Asn Thr Ser Phe Pro Tyr  
165 170 175

Ile Leu Val Asp Arg Gly Leu Thr Thr Ser Pro Ser Phe Ser Leu Ile  
180 185 190

Gly Asp Asn Gly Asn Thr Thr Thr Pro Ser Ile Ile Phe Gly Gly Ile  
195 200 205

Asn Thr Ser Lys Phe Asn Gly Pro Leu Gln Ala Phe Ser Phe Ala Asp  
210 215 220

His Ser Ile Thr Asn Asn Pro Phe Val Thr Val Glu Ala Asp Ser Leu  
225 230 235 240

Gln Leu Thr Thr Asn Thr Asn Asp Asn Ser Thr Tyr Pro Ile Pro Ser  
245 250 255

Ser Thr Pro Met Met Leu Arg Thr Glu Glu Leu Ile Thr Tyr Leu Pro  
260 265 270

Asn Ser Thr Val Gln Ser Leu Tyr Thr Asp Leu Asn Ile Thr Met Asp  
275 280 285

Gly Val Ile Ser Thr Ser Arg Phe Tyr Gly Val Leu Pro Cys Ala Arg  
290 295 300

Gln Glu Thr Glu Ser His Thr Ile Ser Leu Ala Ile Gly Asn Met Thr  
305 310 315 320

Phe Ser Val Ser Trp Asp Glu Leu Phe Val Pro Trp Thr Arg Asp Gly  
325 330 335

Leu Cys Lys Phe Gly Ile Gln Ala Gln Asp Ser Asp Tyr Lys Thr Arg  
340 345 350

Ala Glu Leu Gly Val Pro Phe Leu Arg Arg Met Tyr Val Ala Val Asp  
355 360 365

Tyr Asn Asn Gln Phe Val Gly Val Ala Thr Leu Lys Asp Asp Asp Asp  
 370 375 380

Gln Asn Gly Gly Glu Asp Glu Ile Val Glu Ile Gly Thr Gly Thr Ala  
 385 390 395 400

Leu Pro Ser Ala Val Gly Asp Trp Pro Ala Ser Val Thr Ala Tyr Thr  
 405 410 415

Pro Ala Ala Ser Thr Gly Thr Ala Ala Ala Thr Leu Thr Phe Thr Thr  
 420 425 430

Ala Thr Ser Ser Gly Gly Gly Val Val Pro Thr Gly Leu Ser Glu Leu  
 435 440 445

Gly Arg Ala Phe Leu Val Pro Gly Val Leu Gly Met Ala Val Leu Gln  
 450 455 460

Ala Val  
 465

<210> 154  
 <211> 543  
 <212> PRT  
 <213> Aspergillus niger

<400> 154

Met Met Arg Pro Ile Leu Leu Pro Leu Leu Gly Val Phe Leu Gln Thr  
 1 5 10 15

Ser Ser Ala Ser Asn Pro Tyr Val Met Ser Trp Ser Ser Gln Ala Tyr  
 20 25 30

Gly Pro Asp Gly Pro Trp Gln Ala Val Ser Ile Asp Val Gly Ser Asn  
 35 40 45

Gln Gln Thr Val Asp Leu Tyr Pro Gly Ala Asn Tyr Ala Ser Thr Ile  
 50 55 60

Leu Met Ser Thr Leu Cys Thr Asn Lys Thr Leu Ser Ser Thr Cys Tyr  
 65 70 75 80

Ala Ala Glu Ala Gly Thr Phe Asn Gln Asn Thr Ser Thr Thr Ala Tyr

85	90	95
Thr Thr Ala Ser Ser Trp Glu Thr Thr Tyr Trp Ala Val Glu Gly Gly		
100	105	110
Ser Gln Glu Ala Val Leu Gly Asp Glu Val Thr Leu Gly Ser Phe Val		
115	120	125
Val Pro Asn Val Ser Phe Glu Ala Ile Tyr Gln Thr Tyr Gln Thr Tyr		
130	135	140
Pro Asn Gly Ile Ala Tyr Pro Val Ser Val Gly Ser Leu Ala Leu Gly		
145	150	155
Gly Pro Tyr Leu Ser Asp Thr Val Ser Asn Ser Thr Val Leu Asn Met		
165	170	175
Ile Ala Gly Trp Leu Tyr Ser Ser Asn Asp Ile Pro Ser Tyr Ser Tyr		
180	185	190
Gly Met His Ile Gly Ser Val Asp Pro Lys Ile Pro Gly Ser Leu Ile		
195	200	205
Leu Gly Gly Tyr Asp Lys Ser Arg Val Ile Gly Asp Val Ser Ala Gln		
210	215	220
Gly Val Val Ser Ser Ser Gly Leu Leu Glu Leu Glu Leu Lys Asp Ile		
225	230	235
Gly Leu Gly Val Ala Ala Gly Ser Ser Pro Phe Ser Phe Asn Asn Glu		
245	250	255
Ser Gly Leu Phe Leu Gln Ser Ser Gly Ser Val Gln Ala Lys Thr Val		
260	265	270
Gln Ile Asp Pro Thr Lys Pro Tyr Met Tyr Leu Pro Gln Ala Thr Cys		
275	280	285
Asp Ala Ile Thr Ser Thr Met Pro Ile Ser Phe Asn Ser Ser Leu Gly		
290	295	300
Leu Tyr Phe Trp Asp Thr Thr Ser Asp Asp Tyr Leu Asn Ile Thr Ser		
305	310	315
		320

Ser Ala Ala Tyr Leu Ser Phe Val Phe Asn Met Asn Gly Val Asn Asn  
 325 330 335

Lys Asn Ile Thr Ile Lys Ile Pro Phe Ser Gln Leu Asn Leu Thr Leu  
 340 345 350

Gln Glu Pro Leu Val Asp Gln Asn Val Thr Tyr Phe Pro Cys Phe Leu  
 355 360 365

Thr Thr Ser Thr Pro Val Leu Gly Arg Ala Phe Leu Gln Ser Ala Phe  
 370 375 380

Val Gly Val Asn Trp Phe Asn Gly Asn Asn Ser Gly Thr Trp Phe Leu  
 385 390 395 400

Ala Gln Ala Pro Gly Pro Gly Tyr Ala Ser Glu Asp Ile Thr Arg Ile  
 405 410 415

Ala Val Ser Asp Thr Ser Leu Ser Ala Ser Asn Gly Thr Trp Glu Glu  
 420 425 430

Thr Trp Ala Thr Tyr Trp Gly Ile Lys Thr Ser Asp Asn Ser Ser Ser  
 435 440 445

Ser Lys Ser Gly Leu Ser Ser Gly Ala Lys Ile Gly Ile Gly Val Gly  
 450 455 460

Val Gly Val Gly Gly Ala Val Leu Ile Ala Ala Gly Ile Ala Ile Ala  
 465 470 475 480

Phe Cys Leu Arg Arg Arg Arg Gly Ala Ser Gln Glu Ala Ala Gly Glu  
 485 490 495

Gln Arg Arg Ser Met Phe Arg Gly Phe Ala Glu Leu Pro Gly Gly Ala  
 500 505 510

His Ser Glu Pro Ala Lys Glu Leu Asp Thr Lys Met His Lys Pro Pro  
 515 520 525

Gln Glu Met Met Ala Ser Gln Glu Val Glu Arg Tyr Glu Leu Gly  
 530 535 540

<210> 155  
 <211> 844  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 155

Met Arg Leu Thr Gly Gly Val Ala Ala Ala Leu Gly Leu Cys Ala Ala  
 1 5 10 15

Ala Ser Ala Ser Leu His Pro His Arg Ser Tyr Glu Thr His Asp Tyr  
 20 25 30

Phe Ala Leu His Leu Asp Glu Ser Thr Ser Pro Ala Asp Val Ala Gln  
 35 40 45

Arg Leu Gly Ala Arg His Glu Gly Pro Val Gly Glu Leu Pro Ser His  
 50 55 60

His Thr Phe Ser Ile Pro Arg Glu Asn Ser Asp Asp Val His Ala Leu  
 65 70 75 80

Leu Asp Gln Leu Arg Asp Arg Arg Arg Leu Arg Arg Arg Ser Gly Asp  
 85 90 95

Asp Ala Ala Val Leu Pro Ser Leu Val Gly Arg Asp Glu Gly Leu Gly  
 100 105 110

Gly Ile Leu Trp Ser Glu Lys Leu Ala Pro Gln Arg Lys Leu His Lys  
 115 120 125

Arg Val Pro Pro Thr Gly Tyr Ala Ala Arg Ser Pro Val Asn Thr Gln  
 130 135 140

Asn Asp Pro Gln Ala Leu Ala Ala Gln Lys Arg Ile Ala Ser Glu Leu  
 145 150 155 160

Gly Ile Ala Asp Pro Ile Phe Gly Glu Gln Trp His Leu Tyr Asn Thr  
 165 170 175

Val Gln Leu Gly His Asp Leu Asn Val Thr Gly Ile Trp Leu Glu Gly  
 180 185 190

Val Thr Gly Gln Gly Val Thr Thr Ala Ile Val Asp Asp Gly Leu Asp

195	200	205
Met Tyr Ser Asn Asp Leu Arg Pro Asn Tyr Phe Ala Ala Gly Ser Tyr		
210	215	220
Asp Tyr Asn Asp Lys Val Pro Glu Pro Arg Pro Arg Leu Ser Asp Asp		
225	230	235 240
Arg His Gly Thr Arg Cys Ala Gly Glu Ile Gly Ala Ala Lys Asn Asp		
	245	250 255
Val Cys Gly Val Gly Val Ala Tyr Asp Ser Arg Ile Ala Gly Ile Arg		
	260	265 270
Ile Leu Ser Ala Pro Ile Asp Asp Thr Asp Glu Ala Ala Ala Ile Asn		
	275	280 285
Tyr Ala Tyr Gln Glu Asn Asp Ile Tyr Ser Cys Ser Trp Gly Pro Tyr		
	290	295 300
Asp Asp Gly Ala Thr Met Glu Ala Pro Gly Thr Leu Ile Lys Arg Ala		
305	310	315 320
Met Val Asn Gly Ile Gln Asn Gly Arg Gly Gly Lys Gly Ser Val Phe		
	325	330 335
Val Phe Ala Ala Gly Asn Gly Ala Ile His Asp Asp Asn Cys Asn Phe		
	340	345 350
Asp Gly Tyr Thr Asn Ser Ile Tyr Ser Ile Thr Val Gly Ala Ile Asp		
	355	360 365
Arg Glu Gly Asn His Pro Pro Tyr Ser Glu Ser Cys Ser Ala Gln Leu		
	370	375 380
Val Val Ala Tyr Ser Ser Gly Ala Ser Asp Ala Ile His Thr Thr Asp		
385	390	395 400
Val Gly Thr Asp Lys Cys Ser Thr Thr His Gly Gly Thr Ser Ala Ala		
	405	410 415
Gly Pro Leu Ala Ala Gly Thr Val Ala Leu Ala Leu Ser Val Arg Pro		
	420	425 430



Glu Leu Thr Trp Arg Asp Val Gln Tyr Leu Met Ile Glu Ala Ala Val  
 435 440 445

Pro Val His Glu Asp Asp Gly Ser Trp Gln Asp Thr Lys Asn Gly Lys  
 450 455 460

Lys Phe Ser His Asp Trp Gly Tyr Gly Lys Val Asp Thr Tyr Thr Leu  
 465 470 475 480

Val Lys Arg Ala Glu Thr Trp Asp Leu Val Lys Pro Gln Ala Trp Leu  
 485 490 495

His Ser Pro Trp Gln Arg Val Glu His Glu Ile Pro Gln Gly Glu Gln  
 500 505 510

Gly Leu Ala Ser Ser Tyr Glu Val Thr Glu Asp Met Leu Lys Gly Ala  
 515 520 525

Asn Leu Glu Arg Leu Glu His Val Thr Val Thr Met Asn Val Asn His  
 530 535 540

Thr Arg Arg Gly Asp Leu Ser Val Glu Leu Arg Ser Pro Asp Gly Arg  
 545 550 555 560

Val Ser His Leu Ser Thr Pro Arg Arg Pro Asp Asn Gln Glu Val Gly  
 565 570 575

Tyr Val Asp Trp Thr Phe Met Ser Val Ala His Trp Gly Glu Ser Gly  
 580 585 590

Ile Gly Lys Trp Thr Val Ile Val Lys Asp Thr Asn Val Asn Glu His  
 595 600 605

Thr Gly Gln Phe Ile Asp Trp Arg Leu Asn Leu Trp Gly Glu Ala Ile  
 610 615 620

Asp Gly Ala Glu Gln Pro Leu His Pro Met Pro Thr Glu His Asp Asp  
 625 630 635 640

Asp His Ser Tyr Glu Glu Gly Asn Val Ala Thr Thr Ser Ile Ser Ala  
 645 650 655

Val Pro Thr Lys Thr Glu Leu Pro Asp Lys Pro Thr Gly Gly Val Asp  
660 665 670

Arg Pro Val Asn Val Lys Pro Thr Thr Ser Ala Met Pro Thr Gly Ser  
675 680 685

Leu Thr Glu Pro Ile Asp Asp Glu Glu Leu Gln Lys Thr Pro Ser Thr  
690 695 700

Glu Ala Ser Ser Thr Pro Ser Pro Ser Pro Thr Thr Ala Ser Asp Ser  
705 710 715 720

Ile Leu Pro Ser Phe Phe Pro Thr Phe Gly Ala Ser Lys Arg Thr Gln  
725 730 735

Val Trp Ile Tyr Ala Ala Ile Gly Ser Ile Ile Val Phe Cys Ile Gly  
740 745 750

Leu Gly Val Tyr Phe His Val Gln Arg Arg Lys Arg Ile Arg Asp Asp  
755 760 765

Ser Arg Asp Asp Tyr Asp Phe Glu Met Ile Glu Asp Glu Asp Glu Leu  
770 775 780

Gln Ala Met Asn Gly Arg Ser Asn Arg Ser Arg Arg Gly Gly Glu  
785 790 795 800

Leu Tyr Asn Ala Phe Ala Gly Glu Ser Asp Glu Glu Pro Leu Phe Ser  
805 810 815

Asp Glu Asp Asp Glu Pro Tyr Arg Asp Arg Gly Ile Ser Gly Glu Gln  
820 825 830

Glu Arg Glu Gly Ala Asp Gly Glu His Ser Arg Arg  
835 840

<210> 156

<211> 149

<212> PRT

<213> Aspergillus niger

<400> 156

Met Lys Thr Phe Ser Thr Val Thr Ser Leu Leu Ala Leu Phe Ser Ser

1                      5                      10                      15  
 Ala Leu Ala Ala Pro Val Asp Ser Ala Glu Ala Ala Gly Thr Thr Val  
                     20                      25                      30  
 Ser Val Ser Tyr Asp Thr Ala Tyr Asp Val Ser Gly Ala Ser Leu Thr  
                     35                      40                      45  
 Thr Val Ser Cys Ser Asp Gly Ala Asn Gly Leu Ile Asn Lys Gly Tyr  
                     50                      55                      60  
 Ser Asn Phe Gly Ser Leu Pro Gly Phe Pro Lys Ile Gly Gly Ala Pro  
                     65                      70                      75                      80  
 Thr Ile Ala Gly Trp Asn Ser Pro Asn Cys Gly Lys Cys Tyr Ala Leu  
                     85                      90                      95  
 Thr Tyr Asn Gly Gln Thr Val Asn Ile Leu Ala Ile Asp Ser Ala Pro  
                     100                      105                      110  
 Gly Gly Phe Asn Ile Ala Leu Glu Ala Met Asn Thr Leu Thr Asn Asn  
                     115                      120                      125  
 Gln Ala Gln Gln Leu Gly Arg Ile Glu Ala Thr Tyr Thr Glu Val Asp  
                     130                      135                      140  
 Val Ser Leu Cys Ala  
 145

<210> 157  
 <211> 296  
 <212> PRT  
 <213> Aspergillus niger

<400> 157

Met Ala Gln Ile Phe Trp Leu Ser Leu Phe Leu Leu Val Ser Trp Val  
 1                      5                      10                      15  
 Arg Ala Glu Ser Asn Arg Thr Glu Val Asp Leu Ile Phe Pro Arg Asn  
                     20                      25                      30  
 Asp Thr Phe Ala Pro Met Pro Leu Met Pro Val Val Phe Ala Val Gln  
                     35                      40                      45

Ala Pro Ser Val Ala His Lys Val Asn Thr Tyr Ile Glu Tyr Gly Tyr  
 50 55 60  
 Tyr Pro Val Gly Arg Pro Asn Glu Thr Val Ile Gly Gln Thr Asp His  
 65 70 75 80  
 Val Ser Asp Ser Thr Asn Glu Thr Thr Tyr Phe Ser Val Ser Gly Ile  
 85 90 95  
 Gly Arg Thr Phe Asn Thr Thr Gly Ser Trp Glu Leu Phe Trp Arg Leu  
 100 105 110  
 Arg Trp Thr Asn Cys Ser Ile Ser Glu Asp Ser Arg Tyr Tyr Asn Gln  
 115 120 125  
 Ser Tyr Pro Trp Ile Ser Ser Pro Tyr Ile Asp Gly Ser Leu Asn Ile  
 130 135 140  
 Asp Lys Val Tyr Glu Gly Phe His Tyr Thr Ala Tyr Asn Val Ile Val  
 145 150 155 160  
 Asp Arg Val Thr Phe Ser Thr Arg Glu Asp Ala Ser Gln Pro Asn Leu  
 165 170 175  
 Thr Thr Leu Thr Asn Ser Glu Asn Cys Asp Lys Val Ser Ser Leu Ala  
 180 185 190  
 Leu Leu Ser Ile Val Asp Ser Leu Arg Ile Pro Pro Gln Leu Pro Gln  
 195 200 205  
 Glu Asp Ile Asp Thr Val Ser Met Cys Pro Gln Leu Ala Asp Ala Arg  
 210 215 220  
 Leu Asn Ser Thr Ser Thr Ser Ser Pro Cys Ser Val Ser Ile Ser Pro  
 225 230 235 240  
 Glu Val Glu Ser Asn Ile Leu Ala Lys Ile Ala Asp Asn Glu Cys Asn  
 245 250 255  
 Asn Ala Leu His Pro Ala Val Ser Cys Thr Thr Glu Glu Thr Lys Glu  
 260 265 270

Gly Ser Ala Ser Ser His Asp His Gly His Ala Val Trp Leu Val Ile  
 275 280 285

Thr Leu Ala Phe Ala Phe Leu Phe  
 290 295

<210> 158  
 <211> 310  
 <212> PRT  
 <213> *Aspergillus niger*

<400> 158

Met Gly Gly Arg Asp Val Ala Ile Leu Ser Arg His Phe Ala Val Thr  
 1 5 10 15

Ser Ser Gln Ser Val Asn Gly Val Val Ser Gly Met Phe Gln His Thr  
 20 25 30

Val Thr Ser Ser Pro Ser Phe Thr Thr Asn Gln Phe Phe Lys Lys Lys  
 35 40 45

Phe Thr Ala Ala Ile Ala Thr Ala Ile Phe Ala Ser Val Ala Val Ala  
 50 55 60

Ala Pro Gln Arg Gly Leu Glu Ala Arg Leu Lys Ala Arg Gly Ser Ser  
 65 70 75 80

Lys Gly Ser Arg Pro Leu Gln Ala Val Ala Arg Pro Ala Ser Thr Lys  
 85 90 95

Asn Gln Thr Asn Val Glu Tyr Ser Ser Asn Trp Ser Gly Ala Val Leu  
 100 105 110

Val Glu Pro Pro Ser Ala Ala Ala Thr Tyr Thr Ala Val Thr Gly Thr  
 115 120 125

Phe Thr Val Pro Glu Pro Thr Gly Asn Ser Gly Gly Ser Gln Ala Ala  
 130 135 140

Ser Ala Trp Val Gly Ile Asp Gly Asp Thr Tyr Gly Asn Ala Ile Leu  
 145 150 155 160

Gln Thr Gly Val Asp Phe Thr Val Thr Asp Gly Glu Ala Ser Phe Asp  
 165 170 175

Ala Trp Tyr Glu Trp Tyr Pro Asp Tyr Ala Tyr Asp Phe Ser Gly Ile  
180 185 190

Asp Ile Ser Ala Gly Asp Glu Ile Val Ala Ile Val Glu Ser Tyr Thr  
195 200 205

Ser Thr Thr Gly Ile Ala Ile Ile Glu Asn Lys Ser Thr Gly Gln Lys  
210 215 220

Val Ser Lys Glu Leu Ser Ser Ser Ser Ser Leu Gly Gly Gln Asn Ala  
225 230 235 240

Glu Trp Ile Val Glu Asp Phe Glu Glu Asn Gly Ser Leu Val Asn Leu  
245 250 255

Val Asp Phe Gly Thr Val Thr Phe Thr Gly Ala Val Ala Lys Ala Ala  
260 265 270

Gly Gly Glu Ser Val Gly Leu Thr Asp Ala Thr Ile Ile Glu Ile Glu  
275 280 285

Glu Asn Gly Gln Val Val Thr Asp Val Thr Ile Asp Ser Asp Ser Glu  
290 295 300

Val Thr Ile Thr Tyr Glu  
305 310

<210> 159  
<211> 681  
<212> PRT  
<213> *Aspergillus niger*

<400> 159

Met Arg Cys Ser Leu Ile Ser Leu Leu Gly Leu Ala Ala Ile Pro Ala  
1 5 10 15

Leu Gly Gly Cys Pro Phe Ala His Thr Ala Asn Met Gly Ile Asp Asn  
20 25 30

Met Val Lys Ala His Ala His Met Ser Arg Pro Leu Ile Ala Ser Lys  
35 40 45

Ser Ser Pro Ser Thr Val Pro Thr Ser Ser Ser Thr Pro Ser Val Gly  
 50 55 60  
 Gln Lys Gly Val Phe Met Met Asn Arg Ile Ala Pro Gly Thr Ser Glu  
 65 70 75 80  
 Leu Tyr Ile Ala Asn Thr Asp Gly Ser Asn Glu Arg Pro Leu Leu Ser  
 85 90 95  
 Asn Pro Val Tyr Glu Tyr His Ala Ser Phe Ser Pro Asp Val Glu Trp  
 100 105 110  
 Ile Thr Phe Thr Ser Glu Arg Asn Gly Asp Gly Asn Ser Asp Ile Tyr  
 115 120 125  
 Arg Val Arg Thr Asn Gly Ser Asp Leu Gln Glu Leu Val Ala Thr Pro  
 130 135 140  
 Ala Val Glu Asp Ser Val Val Ile Ser Pro Asn Gly Arg Leu Ala Ala  
 145 150 155 160  
 Tyr Val Ser Thr Ala Asn Asn Met Lys Ala Asn Ile Trp Ile Leu Asp  
 165 170 175  
 Leu Gln Thr Gly Ala Gln Trp Asn Leu Thr Asn Thr Pro Thr Thr Ala  
 180 185 190  
 Ala Asn Ser Ser Leu Met Glu Ser Tyr Leu Arg Pro Ala Trp Ser Pro  
 195 200 205  
 Asp Gly Glu Trp Ile Ala Phe Ser Ser Asp Arg Asn Thr Gln Trp Asp  
 210 215 220  
 Gly His Gly Val Pro Thr Phe Leu Gly Arg Thr Gly Trp Glu Thr Thr  
 225 230 235 240  
 Gln Glu Leu Ser Leu Tyr Ala Ile Arg Pro Asn Gly Ser Asp Phe Arg  
 245 250 255  
 Gln Ile Ile Ser Lys Pro Tyr Tyr Ser Leu Gly Ser Pro Lys Trp Ser  
 260 265 270  
 Ala Asp Gly Lys Arg Ile Val Tyr Tyr Glu Met Thr Arg Glu Asp Thr

275                      280                      285  
 Tyr Asn Ala His Arg Pro Glu Thr Ile Thr Thr Ala Asn Ser Thr Ile  
 290                      295                      300  
 Met Ser Val Asp Phe Glu Thr Gly Thr Asp Val Arg Val Glu Val Ala  
 305                      310                      315                      320  
 Gly Ser Gly Val Lys Gln Phe Pro Gln Tyr Leu Asp Lys Asn Gly Thr  
 325                      330                      335  
 Ile Ala Tyr Thr Leu Lys Gly Gly Thr Ser Glu Gly Phe Tyr Thr Thr  
 340                      345                      350  
 Ala Gly Leu Tyr Val Asn Thr Thr Ser Ala Thr Leu Arg Ser Pro Ala  
 355                      360                      365  
 Trp Ser Pro Asp Gly Lys Gln Val Val Tyr Glu Lys Ser Thr Trp Ser  
 370                      375                      380  
 Ile Arg Ser Gly Tyr Lys Gln Leu Tyr Ser Trp Asp Ser Asp Trp Asp  
 385                      390                      395                      400  
 Tyr Arg Phe Thr Asp Val Phe Pro Gln Val Ser His Gln Glu Arg Val  
 405                      410                      415  
 Ala Ile Thr Gln Lys Gln Leu Gly Asn Ser Ser Ile Val Thr Leu Asn  
 420                      425                      430  
 Thr Thr Gly Gly Asp Leu Gln Leu Val Tyr Asp Pro Ser Thr Ala Asp  
 435                      440                      445  
 Phe Val Ser Asp Asp Glu Thr Thr Gly Leu Ser Ala Tyr Gln Pro Ser  
 450                      455                      460  
 Trp Ser Pro Cys Gly Glu Trp Leu Val Phe Gly Val Gly Phe Trp Phe  
 465                      470                      475                      480  
 Glu Thr Arg Glu Ala Ser Gly Gly Trp Ile Val Arg Ala Thr Ala Asn  
 485                      490                      495  
 Gly Ser Tyr Ser Glu Val Leu Val Asn Ser Ser Tyr Ser Ile Thr Glu  
 500                      505                      510



Asp Gly Ala Leu Asn Ser Gly Phe Pro Ser Phe Ser Pro Asp Gly Lys  
 515 520 525

Lys Val Val Tyr Arg Val Trp Gly Ala Asp Thr Ala Thr Tyr Gly Asn  
 530 535 540

Ala Ser Glu Ile Gly Leu Arg Val Leu Asp Leu Glu Thr Arg Lys Thr  
 545 550 555 560

Thr Val Leu Thr Thr Glu Trp Asp Asn Leu Pro Gln Phe Ser Pro Asp  
 565 570 575

Gly Glu Leu Ile Leu Phe Thr Arg Lys Thr Ser Thr Tyr Asn Tyr Asp  
 580 585 590

Val Cys Thr Ile Arg Pro Asp Gly Thr Asp Leu Arg Val Leu Thr Ser  
 595 600 605

Ser Gly Ala Asn Asp Ala His Ala Val Trp Ser Gln Asp Gly Arg Ile  
 610 615 620

Met Trp Ser Thr Gly Met Tyr Gly Phe Arg Phe Glu Cys Ala Leu Tyr  
 625 630 635 640

Gly Asp Thr Phe Gln Pro Tyr Gly Gln Val Met Ile Met Asp Ala Asp  
 645 650 655

Gly Gly Asn Lys Lys Leu Met Thr Asn Ser Met Trp Glu Asp Ser Met  
 660 665 670

Pro Leu Phe Leu Pro Arg Glu Val Leu  
 675 680

<210> 160

<211> 624

<212> PRT

<213> Aspergillus niger

<400> 160

Met Pro Pro Asp Ala Lys Ser Pro Gly Tyr Gln Pro Gly Met Ala Val  
 1 5 10 15

Leu Pro Ser Arg Pro His Pro Ala Lys Gly Lys Ala Ile Arg Phe Leu  
20 25 30

Leu Ser Leu Ala Leu Val Ala Phe Ala Ile Val Gln Leu Cys Gly Asn  
35 40 45

Phe His Lys Asn Arg Ser Val Glu Gln Gln Leu Gln Ser Gln Thr Leu  
50 55 60

Asp Asp Glu Ser Phe Lys Trp Glu Asp Val Thr Pro Thr Lys Gln Leu  
65 70 75 80

Val Tyr His Pro Cys Phe Gly Asp His Glu Cys Ala Arg Leu Ser Leu  
85 90 95

Pro Met Asn Trp Asn Arg Thr Asp Gly Glu Gly Ser Lys Ile Ala Leu  
100 105 110

Ala Val Ile Lys Leu Pro Ala Lys Val Pro Val Thr Asp Ala Arg Tyr  
115 120 125

Gly Gly Ala Ile Leu Leu Asn Pro Gly Gly Pro Gly Gly Ser Gly Val  
130 135 140

Ser Met Val Phe Arg Tyr Gly Lys Ala Ile Gln Thr Ile Val Asp Ser  
145 150 155 160

Pro Glu Ser Pro Ser Ala Asp Ser Ala Ser Gly Lys Tyr Phe Asp Val  
165 170 175

Val Ser Phe Asp Pro Arg Gly Val Asn Asn Thr Thr Pro Asn Phe Ser  
180 185 190

Cys Phe Pro Asp Pro Ala Thr Arg Lys Ala Trp Leu Leu Gln Ser Glu  
195 200 205

Ala Glu Gly Leu Leu Gly Ser Ser Glu Gly Val Phe Asp Thr Arg Trp  
210 215 220

Ala Arg Tyr Glu Ala Phe Glu Arg Leu Leu Ser Thr Ala Pro Asn Thr  
225 230 235 240

Phe Pro Val Gly Thr Asn Val Asp Ala Glu Arg Ile Arg Leu His Asn

	245		250		255
Arg Trp Lys Lys Gly Glu Glu Lys Leu Leu Tyr Trp Gly Phe Ser Tyr	260		265		270
Gly Thr Ile Leu Gly Ser Thr Phe Ala Ala Met Gln Pro His Arg Ile	275		280		285
Asn Arg Ala Val Ile Asp Gly Val Cys Asn Ala Asp Asp Tyr Tyr Ala	290		295		300
Gly Asn Trp Leu Thr Asn Leu Gln Asp Ser Asp Ala Ala Phe Asn Lys	305		310		315
Phe Phe Glu Tyr Cys Tyr Thr Ala Gly Pro Ser Ala Cys Pro Phe Ala	325		330		335
Leu Gly Gly Asp Pro Glu Asp Leu Lys Ser Arg Tyr Glu Gln Ile Leu	340		345		350
Thr Asn Leu Thr Ser Ser Pro Ile Ala Val Ser Pro Ser Gly Asn Arg	355		360		365
Gly Pro Glu Ile Ile Thr Tyr Ser Asp Val Lys Ser Leu Val Val Gln	370		375		380
Ala Leu Tyr Val Pro Leu Lys Leu Phe Asp Leu Val Ala Arg Leu Leu	385		390		395
Ala Glu Leu Glu Gln Gly Asn Gly Ser Ser Phe Ala Asp Leu Lys Tyr	405		410		415
Glu Ala Lys Gln Trp Pro Val Pro Pro Pro Cys Asp Ser Ser Ser Thr	420		425		430
Gln Tyr Lys Val Pro Gly Glu Ser Asp Gln Glu Ala Gly Arg Asn Ile	435		440		445
Leu Cys Thr Asp Gly Pro Gly Leu Asp Gly Thr Ala Lys Glu Asp Phe	450		455		460
Arg Ser Tyr Trp Asn Met Leu Arg Gly Gln Ser Lys Ala Val Gly Asp	465		470		475
					480

Phe Trp Ala Glu Val Arg Met Ser Cys Val Lys Leu Glu Thr Arg Pro  
 485 490 495

Glu Trp Arg Tyr Asp Gly Met Arg Ile Gln Gly Pro Phe Ala Gly Asn  
 500 505 510

Thr Ser His Pro Leu Leu Phe Ile Gly Asn Thr Tyr Asp Pro Val Thr  
 515 520 525

Pro Leu Arg Asn Ala His Thr Met Ala Arg Gly Phe Pro Glu Ser Ile  
 530 535 540

Val Leu Glu Gln Asn Ser Val Gly His Cys Thr Leu Ser Gly Pro Ser  
 545 550 555 560

Leu Cys Thr Ala Lys Ala Ile Arg Gln Tyr Phe Gln Thr Gly Glu Leu  
 565 570 575

Pro Asp Pro Gly Thr Val Cys Gln Val Glu Glu Leu Pro Phe Arg Leu  
 580 585 590

Ala Gly Tyr Glu Arg Ser Gln Val Met Ser Pro Gly Asp Thr Glu Leu  
 595 600 605

Met Ser Ala Leu His Ser Leu Ser Glu Phe Arg His Leu Leu Gly Ala  
 610 615 620

<210> 161

<211> 554

<212> PRT

<213> Aspergillus niger

<400> 161

Met Leu Ser Ser Leu Leu Leu Gly Gly Leu Leu Gly Leu Ala Thr Ala  
 1 5 10 15

Gln Phe Pro Pro Glu Pro Glu Gly Ile Thr Val Leu Lys Ser Lys Leu  
 20 25 30

His Glu Asn Val Thr Ile Ser Phe Lys Glu Pro Gly Ile Cys Glu Thr  
 35 40 45

Thr Pro Gly Val Arg Ser Tyr Ser Gly Tyr Val His Leu Pro Pro Ala  
 50 55 60

Ser Thr Ser Phe Phe Trp Phe Phe Glu Ala Arg Lys Asp Pro Ser Asn  
 65 70 75 80

Ala Pro Leu Ala Ile Trp Leu Asn Gly Gly Pro Gly Gly Ser Ser Leu  
 85 90 95

Met Gly Leu Leu Glu Glu Leu Gly Pro Cys Ser Ile Ala Ser Asp Ser  
 100 105 110

Lys Thr Thr Val Leu Asn Pro Trp Ser Trp Asn Asn Glu Val Asn Leu  
 115 120 125

Leu Phe Leu Asp Gln Pro Thr Gln Val Gly Phe Ser Tyr Asp Val Pro  
 130 135 140

Thr Asn Gly Thr Leu Thr Ala Asn Gly Thr Ala Phe Ala Ala His Ala  
 145 150 155 160

Leu Trp His Phe Ala Gln Thr Trp Phe Phe Glu Phe Pro His Tyr Lys  
 165 170 175

Pro Asn Asp Asp Arg Val Ser Leu Trp Ala Glu Ser Tyr Gly Gly His  
 180 185 190

Tyr Gly Pro Gly Ile Phe Arg Phe Phe Gln Gln Gln Asn Asp Lys Ile  
 195 200 205

Ala Glu Gly Thr Ala Glu Asp Gly Ala Gln Tyr Leu His Leu Asp Thr  
 210 215 220

Leu Gly Ile Val Asn Gly Leu Met Asp Met Val Ile Gln Glu Glu Ala  
 225 230 235 240

Tyr Ile Thr Trp Pro Tyr Asn Asn Val Arg Leu Ala Pro Ser Ser Phe  
 245 250 255

Asn Ser Arg Gly Phe Arg Asp Gln Ala Leu Ala Cys Glu Ala Ala Leu  
 260 265 270

Lys Glu Arg Asp Ser Gly Leu Pro His Ser Gly Lys Asn Ile Ser Glu

275	280	285
Ile Cys Gly Gly Leu Ala Leu Glu Trp Gly Asp Gly Pro Ile Thr Tyr 290 295 300		
Tyr His Thr Phe Asn Arg Gly Trp Tyr Asp Ile Ala His Pro Lys Asn 305 310 315 320		
Asp Pro Phe Pro Ala Lys His Met Leu Gly Tyr Leu Thr Gln Glu Ser 325 330 335		
Val Leu Ala Ala Leu Gly Val Pro Val Asn Phe Thr Ser Ser Ser Ser 340 345 350		
Ala Val Ala Thr Gln Phe Ile Lys Thr Phe Asp Ile Val His Gly Gly 355 360 365		
Phe Leu Asp Ala Ile Gly Tyr Leu Leu Asp Ser Gly Val Lys Val His 370 375 380		
Met Met Tyr Gly Asp Arg Asp Tyr Ala Cys Asn Trp Val Gly Gly Glu 385 390 395 400		
Lys Ala Ser Leu Ala Val Pro Tyr Ser Arg Ile Thr Glu Phe Ala Asp 405 410 415		
Thr Gly Tyr Ser Pro Leu Leu Thr Pro Asp Gly Ile Ser Gly Met Thr 420 425 430		
Arg Gln Leu Gly Asn Tyr Ser Phe Thr Arg Val Phe Gln Ala Gly His 435 440 445		
Glu Val Pro Ser Tyr Gln Pro Val Ala Ala Tyr Glu Ile Phe Met Arg 450 455 460		
Ala Thr Phe Asn Lys Asp Ile Pro Thr Gly Leu Leu Ala Val Asp Asp 465 470 475 480		
Glu Phe Gln Ser Val Gly Pro Lys Asp Thr Trp His Ile Lys Asn Ile 485 490 495		
Pro Pro Ile Met Pro Lys Pro Gln Cys Tyr Val Leu Ser Pro Gly Thr 500 505 510		

Cys Thr Pro Glu Val Trp Glu Thr Val Leu Asn Gly Ser Ala Thr Val  
 515 520 525

Lys Asp Trp Tyr Val Val Asp Asp Ser Ala Gly Val Glu Asp His Glu  
 530 535 540

Gly Phe Ser Ile Leu Gly Gly Asp Glu Leu  
 545 550

<210> 162  
 <211> 578  
 <212> PRT  
 <213> Aspergillus niger

<400> 162

Met Thr Arg Phe Gln Leu Leu Pro Leu Val Ala Gly Leu Leu Ala Pro  
 1 5 10 15

Ser Ile Ala Ala Leu Ser Ile Pro Ser Pro Gln Gln Ile Leu Asp Ser  
 20 25 30

Leu Thr Phe Gly Glu His Thr Asp Gly Phe Cys Pro Leu Ala Pro Lys  
 35 40 45

Val Glu Val Pro Asp Asp Gly Phe Phe Pro Ala Leu Lys Phe Val Glu  
 50 55 60

Asp Ala Ser Phe Lys Ser Arg Gln Val Asn Arg Leu Ser Arg Ala Val  
 65 70 75 80

Gln Val Pro Thr Ala Ile Asp Asp Tyr Met Lys Asp Pro Tyr Asp Glu  
 85 90 95

Lys Phe Ala Pro Phe Leu Asp Phe Gln Lys Leu Leu Gln Thr Leu Phe  
 100 105 110

Pro Leu Thr His Ser Tyr Ala Arg Val Asp His Ile Asn Arg Phe Gly  
 115 120 125

Leu Val Phe Thr Leu Asn Gly Thr Asp Asp Ser Leu Lys Pro Leu Leu  
 130 135 140

Phe Thr Ala His Gln Asp Val Val Pro Ile Asn Asp Pro Ala Asp Trp  
 145 150 155 160

Thr Tyr Pro Pro Phe Asp Gly His Tyr Asp Gly Glu Trp Leu Trp Gly  
 165 170 175

Arg Gly Ala Ser Asp Cys Lys Asn Val Leu Ile Gly Leu Met Ser Val  
 180 185 190

Val Glu Asp Leu Leu Ser Gln Lys Trp Glu Pro Thr Arg Thr Val Val  
 195 200 205

Leu Ala Phe Gly Phe Asp Glu Glu Ser His Gly Phe Leu Gly Ala Gly  
 210 215 220

Ser Ile Ala Lys Phe Leu Glu Lys Lys Tyr Gly Pro Asp Ser Phe Glu  
 225 230 235 240

Phe Ile Leu Asp Glu Gly Gly Met Gly Leu Glu Val Leu Asp Asp Asn  
 245 250 255

Asn Asn Gly Val Val Tyr Ala Leu Pro Gly Val Gly Glu Lys Gly Ser  
 260 265 270

Ile Asp Val Val Leu Thr Leu Ala Val Pro Gly Gly His Ser Ser Val  
 275 280 285

Pro Pro Pro His Thr Gly Ile Gly Ile Ile Ala Glu Ile Ile Tyr Glu  
 290 295 300

Leu Glu Arg Gln Asp Leu Phe Val Pro Val Leu Asp Thr His His Pro  
 305 310 315 320

Thr Arg Lys Met Leu Glu Cys Gln Val Arg His Ser Pro Ser Gln Val  
 325 330 335

Glu Pro Trp Leu Ala Ser Ala Leu Gln Ser Ser Asp Tyr Ile Ser Leu  
 340 345 350

Ala Glu Lys Leu Ala Ser Ser Arg Gly Asp Lys Phe Arg Phe Ile Leu  
 355 360 365

Gln Thr Ser Gln Ala Ala Asp Ile Ile Asn Gly Gly Val Lys Ser Asn



370                      375                      380  
 Ala Leu Pro Glu Lys Ile Asn Ala Leu Val Asn Tyr Arg Ile Ala Leu  
 385                      390                      395                      400  
 His Gln Thr Pro Asp Asp Ile Lys Asn Arg Ala Val Glu Ile Ile Ser  
                     405                      410                      415  
 Pro Ile Val Lys Lys Tyr Asn Leu Ser Leu Thr Ala Phe Pro Glu Ser  
                     420                      425                      430  
 Asp Thr Val Asp Pro Ser Leu Asn Asn His Leu Thr Leu Thr Thr Leu  
                     435                      440                      445  
 Ser Gly Ala Leu Ser Pro Ala Pro Val Ser Pro Thr Asp Ile Asp Thr  
                     450                      455                      460  
 Asp Ala Val Trp Ala Arg Phe Ser Gly Val Thr Arg Ser Val Phe Glu  
 465                      470                      475                      480  
 Ser Val Pro Ser Leu Glu Gly Arg Lys Val Val Val Ser Gly Asp Ile  
                     485                      490                      495  
 Met Thr Gly Asn Thr Asp Thr Arg Phe Tyr Trp Ala Leu Ser Arg Asn  
                     500                      505                      510  
 Ile Tyr Arg Trp Ser Pro Ser Arg Ala Gly Lys Ala Leu Asn Ile His  
                     515                      520                      525  
 Thr Val Asp Glu Arg Ile Asp Ile Asp Ile His Leu Glu Ala Met Met  
                     530                      535                      540  
 Leu Tyr Tyr Asp Leu Ile Arg Ser Phe Asp Gly Arg Thr Asp Ser Ser  
 545                      550                      555                      560  
 Val Ile Ser Ala Ala Ser Ala Ala Ala Asp Asp Glu Leu Ala His Asp  
                     565                      570                      575  
 Val Leu

<210> 163  
 <211> 456

&lt;212&gt; PRT

<213> *Aspergillus niger*

&lt;400&gt; 163

Met Lys Ser Thr Thr Leu Leu Ser Leu Ala Trp Ala Ala Gln Ser Ala  
 1 5 10 15

Tyr Ser Leu Ser Ile His Glu Arg Asp Glu Pro Ala Thr Leu Gln Phe  
 20 25 30

Asn Phe Glu Arg Arg Gln Ile Ala Asp Arg Ser Arg Arg Lys Arg Ser  
 35 40 45

Thr Ala Ser Ala Asp Leu Val Asn Leu Ala Thr Asn Leu Gly Tyr Thr  
 50 55 60

Met Asn Leu Thr Leu Gly Thr Pro Gly Gln Glu Val Ser Val Thr Leu  
 65 70 75 80

Asp Thr Gly Ser Ser Asp Leu Trp Val Asn Gly Ala Asn Ser Ser Val  
 85 90 95

Cys Pro Cys Thr Asp Tyr Gly Ser Tyr Asn Ser Ser Ala Ser Ser Thr  
 100 105 110

Tyr Thr Phe Val Asn Asp Glu Phe Tyr Ile Gln Tyr Val Asp Gly Ser  
 115 120 125

Glu Ala Thr Gly Asp Tyr Val Asn Asp Thr Leu Lys Phe Ser Asn Val  
 130 135 140

Thr Leu Thr Asn Phe Gln Phe Ala Val Ala Tyr Asp Gly Asp Ser Glu  
 145 150 155 160

Glu Gly Val Leu Gly Ile Gly Tyr Ala Ser Asn Glu Ala Ser Gln Ala  
 165 170 175

Thr Val Gly Gly Gly Glu Tyr Thr Asn Phe Pro Glu Ala Leu Val Asp  
 180 185 190

Gln Gly Ala Ile Asn Trp Pro Ala Tyr Ser Leu Trp Leu Asp Asp Leu  
 195 200 205

Asp Glu Gly Lys Gly Thr Ile Leu Phe Gly Gly Val Asn Thr Ala Lys  
 210 215 220

Tyr Tyr Gly Ser Leu Gln Thr Leu Pro Ile Val Ser Ile Glu Asp Met  
 225 230 235 240

Tyr Val Glu Phe Ala Val Asn Leu Thr Ala Val His Leu Glu Lys Asn  
 245 250 255

Gly Asn Ser Val Ser Val Asn Asn Ser Ala Thr Gln Phe Pro Ile Pro  
 260 265 270

Ala Val Leu Asp Ser Gly Thr Ala Leu Thr Tyr Ile Pro Thr Ser Ala  
 275 280 285

Ala Ala Ser Ile Tyr Glu Ala Val Gly Ala Gln Tyr Leu Ser Glu Tyr  
 290 295 300

Gly Tyr Gly Val Ile Glu Cys Asp Val Lys Asp Glu Asp Phe Thr Phe  
 305 310 315 320

Leu Phe Asp Phe Gly Ser Phe Asn Met Ser Val Asp Ile Ser Glu Met  
 325 330 335

Ile Leu Glu Ala Ser Ser Asp Met Thr Asp Met Asn Val Cys Thr Phe  
 340 345 350

Gly Leu Ala Val Ile Glu Asn Glu Ala Leu Leu Gly Asp Thr Phe Leu  
 355 360 365

Arg Ser Ala Tyr Val Val Tyr Asp Leu Gly Asn Asn Glu Ile Ser Leu  
 370 375 380

Ala Lys Ala Asn Phe Asn Pro Gly Glu Asp His Val Leu Glu Ile Gly  
 385 390 395 400

Thr Gly Ser Asp Ala Val Pro Lys Ala Thr Gly Ala Thr Ala Thr Gly  
 405 410 415

Ala Ala Ala Thr Ser Thr Ala Ser Ser Asp Lys Ser Asp Lys Glu Ser  
 420 425 430

Ser Ala Thr Val Pro Arg Ser Gln Ile Val Ser Leu Val Ala Gly Val

435                      440                      445  
 Leu Val Gly Val Phe Leu Val Leu  
 450                      455  
  
 <210> 164  
 <211> 664  
 <212> PRT  
 <213> *Aspergillus niger*  
  
 <400> 164  
 Met Leu Val Arg Gln Leu Ala Leu Ala Leu Ala Ile Ala Ala Leu Ser  
 1                      5                      10                      15  
  
 Asp Ala Ile Pro Thr Ser Ile Lys His Val Leu His Glu Lys Arg His  
 20                      25                      30  
  
 Lys Pro Ala Ser Asp Trp Val Lys Gly Ala Arg Val Glu Ser Asp Ala  
 35                      40                      45  
  
 Val Leu Pro Met Arg Ile Gly Leu Ala Gln Asn Asn Leu Asp Lys Gly  
 50                      55                      60  
  
 Tyr Asp Phe Leu Met Glu Val Ser Asp Pro Lys Ser Ser Lys Tyr Gly  
 65                      70                      75                      80  
  
 Gln Tyr Trp Ser Ala Asp Glu Val His Asp Ile Phe Ser Pro Ser Glu  
 85                      90                      95  
  
 Glu Ala Val Glu Ala Val Arg Glu Trp Leu Val Ala Ser Gly Ile His  
 100                      105                      110  
  
 Pro Ser Arg Val Val His Ser Asp Asn Lys Gly Trp Leu Ala Phe Asp  
 115                      120                      125  
  
 Ala Tyr Ala His Glu Ala Glu Arg Leu Phe Met Thr Glu Phe His Glu  
 130                      135                      140  
  
 His Glu Ser Asp Arg Ser Ala Lys Ile Arg Val Gly Cys Asp Gln Tyr  
 145                      150                      155                      160  
  
 His Val Pro Glu His Ile Gln Lys His Ile Asp Tyr Ile Thr Pro Gly  
 165                      170                      175

Val Lys Leu Thr Gln Val Val Lys Arg Thr Asn Lys Val Lys Arg Ala  
 180 185 190  
 Ser Gln Leu Ala His Ser Ser Lys Ala Lys Ser Ala Ala Gln Gly Pro  
 195 200 205  
 Gln Pro Leu Pro Asn Lys Ala Lys Phe Leu Pro Glu Asp Leu Arg Gly  
 210 215 220  
 Cys Gly Tyr Asn Ile Thr Pro Ser Cys Ile Lys Ala Leu Tyr Gln Ile  
 225 230 235 240  
 Pro Asp Ala Lys Thr Ala Thr Pro Asn Asn Ser Leu Gly Leu Tyr Glu  
 245 250 255  
 Gln Gly Asp Tyr Phe Ala Lys Ser Asp Leu Asp Leu Phe Tyr Lys Glu  
 260 265 270  
 Tyr Ala Pro Trp Val Pro Gln Gly Thr Tyr Pro Ile Pro Ala Leu Ile  
 275 280 285  
 Asp Gly Ala Asn Tyr Ser Val Pro Ser Tyr Ser Ser Leu Asn Thr Gly  
 290 295 300  
 Glu Ser Asp Ile Asp Ile Asp Met Ala Tyr Ser Leu Leu Tyr Pro Gln  
 305 310 315 320  
 Gln Val Thr Leu Tyr Gln Val Asp Asp Gln Leu Tyr Glu Pro Val Glu  
 325 330 335  
 Val Asp Thr Thr Asn Leu Phe Asn Thr Phe Leu Asp Ala Leu Asp Gly  
 340 345 350  
 Ser Tyr Cys Thr Tyr Ser Ala Tyr Gly Glu Thr Gly Asp Asp Pro Ser  
 355 360 365  
 Ile Asp Pro Val Tyr Pro Asp Thr Arg Pro Gly Gly Tyr Lys Gly Lys  
 370 375 380  
 Leu Gln Cys Gly Val Tyr Lys Pro Thr Asn Val Ile Ser Ala Ser Tyr  
 385 390 395 400

Gly Gln Ser Glu Ala Asp Leu Pro Val Ser Tyr Thr Lys Arg Gln Cys  
 405 410 415  
 Asn Glu Phe Met Lys Leu Gly Leu Gln Gly His Ser Ile Leu Phe Ala  
 420 425 430  
 Ser Gly Asp Tyr Gly Val Ala Ser Phe Ala Gly Asp Gly Asp Glu Asn  
 435 440 445  
 Gly Cys Leu Gly Pro Glu Gly Lys Ile Phe Asn Pro Gln Tyr Pro Ser  
 450 455 460  
 Asn Cys Pro Tyr Val Thr Ser Val Gly Gly Thr Met Leu Tyr Gly Tyr  
 465 470 475 480  
 Gln Thr Val Asn Asp Ser Glu Ser Val Met His Val Asn Leu Gly Gly  
 485 490 495  
 Thr Ala Ser Asn Phe Ser Thr Ser Gly Gly Phe Ser Asn Tyr Phe Pro  
 500 505 510  
 Gln Pro Ala Tyr Gln Phe Ala Ala Val Glu Gln Tyr Phe Gln Ser Ala  
 515 520 525  
 Asn Leu Ser Tyr Pro Tyr Tyr Ser Glu Phe Glu Val Asp Val Asn Thr  
 530 535 540  
 Thr Lys Gly Leu Tyr Asn Arg Leu Gly Arg Ala Tyr Pro Asp Val Ser  
 545 550 555 560  
 Ala Asn Gly Ala His Phe Arg Ala Tyr Met Asp Gly Tyr Asp Tyr His  
 565 570 575  
 Trp Tyr Gly Ser Ser Leu Ala Ser Pro Leu Phe Ala Ser Val Leu Thr  
 580 585 590  
 Leu Leu Asn Glu Glu Arg Phe Ala Ile Gly Lys Gly Pro Val Gly Phe  
 595 600 605  
 Val Asn Pro Val Leu Tyr Ala Tyr Pro Gln Val Leu Asn Asp Ile Thr  
 610 615 620  
 Asn Gly Thr Asn Ala Gly Cys Gly Thr Tyr Gly Phe Ser Ala Ile Glu

625                      630                      635                      640  
 Gly Trp Asp Pro Ala Ser Gly Leu Gly Thr Pro Asn Tyr Pro Leu Met  
                                 645                      650                      655  
 Lys Glu Leu Phe Leu Ser Leu Pro  
                                 660  
  
 <210> 165  
 <211> 520  
 <212> PRT  
 <213> Aspergillus niger  
  
 <400> 165  
 Met Arg Val Thr Thr Ala Ile Ala Ser Leu Leu Leu Val Gly Ser Ala  
 1                                  5                                  10                                  15  
  
 Thr Ser Leu Gln Asn Pro His Arg Arg Ala Val Pro Pro Pro Leu Ser  
                                 20                                  25                                  30  
  
 His Arg Ser Val Ala Ser Arg Ser Val Pro Val Glu Arg Arg Thr Thr  
                                 35                                  40                                  45  
  
 Asp Phe Glu Tyr Leu Thr Asn Lys Thr Ala Arg Phe Leu Val Asn Gly  
                                 50                                  55                                  60  
  
 Thr Ser Ile Pro Glu Val Asp Phe Asp Val Gly Glu Ser Tyr Ala Gly  
 65                                  70                                  75                                  80  
  
 Leu Leu Pro Asn Thr Pro Thr Gly Asn Ser Ser Leu Phe Phe Trp Phe  
                                 85                                  90                                  95  
  
 Phe Pro Ser Gln Asn Pro Glu Ala Ser Asp Glu Ile Thr Ile Trp Leu  
                                 100                                  105                                  110  
  
 Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Gln Glu Asn  
                                 115                                  120                                  125  
  
 Gly Pro Phe Leu Trp Gln Pro Gly Thr Tyr Lys Pro Val Pro Asn Pro  
                                 130                                  135                                  140  
  
 Tyr Ser Trp Thr Asn Leu Thr Asn Val Val Tyr Ile Asp Gln Pro Ala  
 145                                  150                                  155                                  160

Gly Thr Gly Phe Ser Pro Gly Pro Ser Thr Val Asn Asn Glu Glu Asp  
 165 170 175  
 Val Ala Ala Gln Phe Asn Ser Trp Phe Lys His Phe Val Asp Thr Phe  
 180 185 190  
 Asp Leu His Gly Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly  
 195 200 205  
 Met Tyr Val Pro Tyr Ile Ala Asp Ala Met Leu Asn Glu Glu Asp Thr  
 210 215 220  
 Thr Tyr Phe Asn Leu Lys Gly Ile Gln Ile Asn Asp Pro Ser Ile Asn  
 225 230 235 240  
 Ser Asp Ser Val Met Met Tyr Ser Pro Ala Val Arg His Leu Asn His  
 245 250 255  
 Tyr Asn Asn Ile Phe Gln Leu Asn Ser Thr Phe Leu Ser Tyr Ile Asn  
 260 265 270  
 Ala Lys Ala Asp Lys Cys Gly Tyr Asn Ala Phe Leu Asp Lys Ala Ile  
 275 280 285  
 Thr Tyr Pro Pro Pro Ser Pro Phe Pro Thr Ala Pro Glu Ile Thr Glu  
 290 295 300  
 Asp Cys Gln Val Trp Asp Glu Val Val Met Ala Ala Tyr Asp Ile Asn  
 305 310 315 320  
 Pro Cys Phe Asn Tyr Tyr His Leu Ile Asp Phe Cys Pro Tyr Leu Trp  
 325 330 335  
 Asp Val Leu Gly Phe Pro Ser Leu Ala Ser Gly Pro Asn Asn Tyr Phe  
 340 345 350  
 Asn Arg Ser Asp Val Gln Lys Ile Leu His Val Pro Pro Thr Asp Tyr  
 355 360 365  
 Ser Val Cys Ser Glu Thr Val Ile Phe Ala Asn Gly Asp Gly Ser Asp  
 370 375 380



Pro Ser Ser Trp Gly Pro Leu Pro Ser Val Ile Glu Arg Thr Asn Asn  
385 390 395 400

Thr Ile Ile Gly His Gly Trp Leu Asp Tyr Leu Leu Phe Leu Asn Gly  
405 410 415

Ser Leu Ala Thr Ile Gln Asn Met Thr Trp Asn Gly Lys Gln Gly Phe  
420 425 430

Gln Arg Pro Pro Val Glu Pro Leu Phe Val Pro Tyr His Tyr Gly Leu  
435 440 445

Ala Glu Leu Tyr Trp Gly Asp Glu Pro Asp Pro Tyr Asn Leu Asp Ala  
450 455 460

Gly Ala Gly Tyr Leu Gly Thr Ala His Thr Glu Arg Gly Leu Thr Phe  
465 470 475 480

Ser Ser Val Tyr Leu Ser Gly His Glu Ile Pro Gln Tyr Val Pro Gly  
485 490 495

Ala Ala Tyr Arg Gln Leu Glu Phe Leu Leu Gly Arg Ile Ser Ser Leu  
500 505 510

Ser Ala Lys Gly Asn Tyr Thr Ser  
515 520

<210> 166  
<211> 551  
<212> PRT  
<213> Aspergillus niger

<400> 166

Met Arg Gly Ser Arg Leu Val Leu Leu Leu Pro Leu Ala Ala Leu Ser  
1 5 10 15

Cys Ala Met Pro Glu Asn Glu Trp Ser Ser Thr Ile Arg Arg Gln Leu  
20 25 30

Pro Lys Ala Ser Thr Gly Val Lys Ser Ile Lys Thr Pro Asn Asn Val  
35 40 45

Thr Ile Arg Tyr Lys Glu Pro Gly Thr Glu Gly Ile Cys Glu Thr Thr  
50 55 60

Pro Gly Val Lys Ser Tyr Ser Gly Tyr Val Asp Leu Ser Pro Glu Ser  
65 70 75 80

His Thr Phe Phe Trp Phe Phe Glu Ser Arg Arg Asp Pro Glu Asn Asp  
85 90 95

Pro Val Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile  
100 105 110

Gly Leu Phe Glu Glu Leu Gly Pro Cys His Ile Thr Pro Glu Tyr Glu  
115 120 125

Ser Ile Ile Asn Gln Tyr Ser Trp Asn Glu Val Thr Asn Leu Leu Phe  
130 135 140

Leu Ser Gln Pro Leu Gly Val Gly Phe Ser Tyr Ser Glu Thr Glu Ala  
145 150 155 160

Gly Ser Leu Asn Pro Phe Thr Gly Ala Val Glu Asn Ala Ser Phe Ala  
165 170 175

Gly Val Gln Gly Arg Tyr Pro Val Ile Asp Ala Thr Ile Ile Asp Thr  
180 185 190

Thr Asp Ile Ala Ala Arg Ala Thr Trp Glu Val Leu Gln Gly Phe Leu  
195 200 205

Ser Gly Leu Ser Gln Leu Asp Ser Glu Val Lys Ser Lys Glu Phe Asn  
210 215 220

Leu Trp Thr Glu Ser Tyr Gly Gly His Tyr Gly Pro Ala Phe Phe Asn  
225 230 235 240

His Phe Tyr Glu Gln Asn Ser Lys Ile Ala Ser Gly Glu Val Asn Gly  
245 250 255

Val Gln Leu Asn Phe Asn Ser Leu Gly Ile Ile Asn Gly Ile Ile Asp  
260 265 270

Ala Ala Ile Gln Ala Asp Tyr Tyr Ala Asp Phe Ala Val Asn Asn Thr  
275 280 285

Tyr Gly Ile Lys Ala Val Asn Asp Thr Val Tyr Asn Tyr Met Lys Phe  
 290 295 300  
 Ala Asn Thr Met Pro Asn Gly Cys Gln Asp Gln Val Ala Ser Cys Lys  
 305 310 315 320  
 Leu Thr Asn Arg Thr Ser Leu Ser Asp Tyr Ala Ile Cys Thr Glu Ala  
 325 330 335  
 Ala Asn Met Cys Arg Asp Asn Val Glu Gly Pro Tyr Tyr Gln Phe Gly  
 340 345 350  
 Gly Arg Gly Val Tyr Asp Ile Arg His Pro Tyr Asn Asp Pro Thr Pro  
 355 360 365  
 Pro Ser Tyr Phe Val Asp Tyr Leu Lys Lys Asp Ser Val Met Asp Ala  
 370 375 380  
 Ile Gly Val Asp Ile Asn Tyr Thr Glu Ser Ser Gly Glu Val Tyr Tyr  
 385 390 395 400  
 Ala Phe Gln Gln Thr Gly Asp Phe Val Trp Pro Asn Phe Ile Glu Asp  
 405 410 415  
 Leu Glu Glu Ile Leu Gln Leu Pro Val Arg Val Ser Leu Ile Tyr Gly  
 420 425 430  
 Asp Ala Asp Tyr Ile Cys Asn Trp Phe Gly Gly Gln Ala Ile Ser Leu  
 435 440 445  
 Ala Val Asn Tyr Pro His Ala Ala Gln Phe Arg Ala Ala Gly Tyr Thr  
 450 455 460  
 Pro Met Thr Val Asp Gly Val Glu Tyr Gly Glu Thr Arg Glu Tyr Gly  
 465 470 475 480  
 Asn Phe Ser Phe Thr Arg Val Tyr Gln Ala Gly His Glu Val Pro Tyr  
 485 490 495  
 Tyr Gln Pro Ile Ala Ala Leu Gln Leu Phe Asn Arg Thr Leu Phe Gly  
 500 505 510

Trp Asp Ile Ala Ala Gly Thr Thr Gln Ile Trp Pro Glu Tyr Ser Thr  
515 520 525

Asn Gly Thr Ser Gln Ala Thr His Thr Glu Ser Phe Val Pro Leu Ser  
530 535 540

Thr Ala Ser Ser Thr Val Asn  
545 550

<210> 167  
<211> 623  
<212> PRT  
<213> Aspergillus niger

<400> 167

Met Pro Phe Pro Phe Ser Ser Ala Leu Leu Gly Tyr Ile Leu Thr Thr  
1 5 10 15

Ser Thr Thr Leu Thr Ser Leu Val Ala Gly Gln Tyr Tyr Pro Pro Thr  
20 25 30

Pro Glu Asp Leu Thr Val Ile His Ser Glu Ile Phe Pro Gly Ala Arg  
35 40 45

Ile Ser Tyr Lys Gln Pro Leu Gly Ile Cys Thr Thr Thr Pro Ser Thr  
50 55 60

Pro Ser Tyr Ser Gly Tyr Ile His Leu Pro Pro His Thr Leu Thr Asn  
65 70 75 80

Leu Ser Ile Pro Gly Ile Ser Ile Ser Gln Pro Tyr Pro Ile Asn Thr  
85 90 95

Phe Phe Trp Tyr Phe Pro Ser Arg His His His Asn Asn Asp Thr Ser  
100 105 110

Pro Leu Thr Ile Trp Met Asn Gly Gly Pro Gly Gly Ser Ser Met Ile  
115 120 125

Gly Leu Phe Gln Glu Asn Gly Pro Cys Thr Val Asn Thr Asp Ser Asn  
130 135 140

Ser Thr Ala Tyr Asn Pro Trp Ser Trp Asn Glu Tyr Val Asp Met Leu  
145 150 155 160

Tyr Ile Glu Gln Pro Val Gln Thr Gly Phe Ser Tyr Asp Val Leu Arg  
 165 170 175

Asn Gly Thr Leu Asp Leu Asn Glu Thr Phe Leu Val Gly Thr Leu Pro  
 180 185 190

Ser Gln Asp Val His Gly Thr Val Asn Gly Thr Val Asn Gly Gly Arg  
 195 200 205

Ala Leu Trp Val Ala Leu Gln Val Trp Leu Gly Glu Phe Ser Glu Tyr  
 210 215 220

Val Ser Ser Val Asp Gly Asn Gly Gly Gly Asp Asp Arg Val Ser Ile  
 225 230 235 240

Trp Thr Glu Ser Tyr Gly Gly Arg Tyr Gly Pro Ala Tyr Thr Ala Leu  
 245 250 255

Phe Gln Glu Met Asn Glu Arg Ile Glu Ser Gly Glu Val Ser Thr Gly  
 260 265 270

Lys Lys Ile His Leu Asp Thr Leu Gly Ile Ile Asn Gly Cys Val Asp  
 275 280 285

Leu Leu Val Gln Val Pro Ser Phe Pro Glu Gln Ala Tyr Asn Asn Thr  
 290 295 300

Tyr Gly Ile Glu Gly Ile Asn Arg Thr Leu Tyr Asp Arg Ala Met Asp  
 305 310 315 320

Ser Trp Ser Lys Pro Gly Gly Cys Arg Asp Met Ile Ile Glu Cys Arg  
 325 330 335

Asp Ala Gly Glu Leu Gly Asp Pro Leu Ile Ile Cys Glu Glu Ala Ser  
 340 345 350

Asp Tyr Cys Ser Arg Glu Ile Lys Ser Leu Tyr Thr Asn Thr Ser Gly  
 355 360 365

Arg Gly Tyr Tyr Asp Ile Ala His Phe Thr Pro Asp Ala Ala Leu Val  
 370 375 380

Pro Tyr Phe Val Gly Phe Leu Asn Arg Pro Trp Val Gln Lys Ala Leu  
385 390 395 400

Gly Val Pro Val Asn Tyr Thr Met Ser Ser Glu Ala Val Gly Asn Ser  
405 410 415

Phe Ala Ser Thr Gly Asp Tyr Pro Arg Asn Asp Pro Arg Gly Met Ile  
420 425 430

Gly Asp Ile Gly Tyr Leu Leu Asp Ser Gly Val Lys Val Ala Met Val  
435 440 445

Tyr Gly Asp Arg Asp Tyr Ala Cys Pro Trp Arg Gly Gly Glu Asp Val  
450 455 460

Ser Leu Leu Val Glu Tyr Glu Asp Ala Glu Lys Phe Arg Ala Ala Gly  
465 470 475 480

Tyr Ala Glu Val Gln Thr Lys Ser Ser Tyr Val Gly Gly Leu Val Arg  
485 490 495

Gln Tyr Gly Asn Phe Ser Phe Thr Arg Val Phe Gln Ala Gly His Glu  
500 505 510

Val Pro Phe Tyr Gln Pro Glu Thr Ala Tyr Glu Ile Phe Asn Arg Ala  
515 520 525

Gln Phe Asn Trp Asp Ile Ala Thr Gly Gly Ile Ser Leu Glu Gln Asn  
530 535 540

Gln Ser Tyr Gly Thr Glu Gly Pro Ser Ser Thr Trp His Ile Lys Asn  
545 550 555 560

Glu Val Pro Glu Ser Pro Glu Pro Thr Cys Tyr Leu Leu Ala Met Asp  
565 570 575

Ser Thr Cys Thr Asp Glu Gln Arg Glu Arg Val Leu Ser Gly Asp Ala  
580 585 590

Val Val Arg Asp Trp Val Val Val Asp Asp Ile Glu Ala Glu Ser Ser  
595 600 605

Phe Ser Gly Val Gly Asp Gln Leu Ala Gln Val Pro Leu Gly His  
 610 615 620

<210> 168  
 <211> 439  
 <212> PRT  
 <213> Aspergillus niger

<400> 168

Met Arg Thr Ser Thr Leu Leu Leu Leu Trp Ser Thr Ala Gly Ala Ala  
 1 5 10 15

Leu Ala Ser Pro Tyr Pro Leu Pro Asp Ser Gln Val Val Phe Ala Ala  
 20 25 30

Asp His Glu Val Pro Asn Thr Gln Gly Lys His Val Val Asp Glu Ala  
 35 40 45

Ile Leu Ser Ala Leu Asn Ala His Ser Asp Pro Val Ala Ala Met Val  
 50 55 60

Ser Leu Arg Pro Glu Thr Ala Ala Phe Leu Ala Glu Pro Arg Leu Leu  
 65 70 75 80

His Ile Arg Gly Glu Glu Lys Ala Glu Trp Met Thr Glu Gly Asp Lys  
 85 90 95

Leu Arg Leu Arg Gln Arg Gly Lys Lys Phe Met Asp Ile Thr Glu His  
 100 105 110

Gln Asp Phe Tyr Ala Glu Gln Ala Met Ala Ser Phe Ala Gly Asp Pro  
 115 120 125

Asn Leu Pro Lys Leu Ser His Lys Gly Leu Val Lys Pro Leu Phe Ser  
 130 135 140

Gln Ile Glu Thr Glu Arg Met His Asp Ile Leu Gln His Met Thr Ser  
 145 150 155 160

Tyr Tyr Asn Arg Tyr Tyr Gly Asp Tyr His Gly Glu Met Ser Ser Glu  
 165 170 175

Trp Leu His Asp Tyr Ile Ala Ala Ile Ile Ser Lys Ser Pro Phe Arg  
 180 185 190

Thr His Ile Ser Leu Glu Tyr Phe Thr His Pro Phe Arg Gln Ser Ser  
195 200 205

Ile Ile Ala Arg Phe Glu Pro Lys Val Arg Ser Phe Ser Gln Pro Leu  
210 215 220

Thr Ile Ile Gly Ala His Gln Asp Ser Ala Asn Tyr Leu Phe Pro Leu  
225 230 235 240

Leu Pro Ala Pro Gly Ala Asp Asp Asp Cys Ser Gly Thr Val Ser Ile  
245 250 255

Leu Glu Ala Phe Arg Val Leu Ala Glu Asn Gly Tyr Thr Pro Lys Asp  
260 265 270

Gly Pro Val Glu Phe His Trp Tyr Ala Ala Glu Glu Ala Gly Leu Leu  
275 280 285

Gly Ser Gln Ala Ile Ala Arg Tyr Lys Lys Glu Gln Gly Ala Lys Ile  
290 295 300

Asp Ala Met Met Glu Phe Asp Met Thr Ala Phe Ile Ala Arg Asn Ala  
305 310 315 320

Thr Glu Thr Ile Gly Phe Val Ala Thr Gln Ala Asp Ala Ala Leu Thr  
325 330 335

Asn Trp Ala Leu Asn Leu Ser Arg Glu Tyr Ile Ser Ile Pro Ala Glu  
340 345 350

Val Tyr Glu Leu Gly Pro Asn Ala Gly Ser Asp Tyr Met Ser Tyr Thr  
355 360 365

Lys Leu Asn Tyr Pro Ala Ala Phe Ala Ser Glu Gly Asn Pro Leu Ala  
370 375 380

Gly Gly Ser Phe Pro Gly Glu Met Asp Pro Tyr Val His Gly Ile Lys  
385 390 395 400

Asp Arg Met Asp Val Asp Asp Glu Thr Gly Val Phe Ser Ile Glu His  
405 410 415



Met Ala Arg Phe Ser Glu Leu Ala Ile Ala Phe Val Val Glu Gln Ala  
 420 425 430

Gly Trp Asp Asn Thr Trp Arg  
 435

<210> 169  
 <211> 526  
 <212> PRT  
 <213> Aspergillus niger

<400> 169

Met Arg Ser Phe Ser Val Val Ala Ala Ala Ser Leu Ala Leu Ser Trp  
 1 5 10 15

Ala Ser Leu Ala Gln Ala Ala Arg Pro Arg Leu Val Pro Lys Pro Ile  
 20 25 30

Ser Arg Pro Ala Ser Ser Lys Ser Ala Ala Thr Thr Gly Glu Ala Tyr  
 35 40 45

Phe Glu Gln Leu Leu Asp His His Asn Pro Glu Lys Gly Thr Phe Ser  
 50 55 60

Gln Arg Tyr Trp Trp Ser Thr Glu Tyr Trp Gly Gly Pro Gly Ser Pro  
 65 70 75 80

Val Val Leu Phe Asn Pro Gly Glu Val Ser Ala Asp Gly Tyr Glu Gly  
 85 90 95

Tyr Leu Thr Asn Asp Thr Leu Thr Gly Val Tyr Ala Gln Glu Ile Gln  
 100 105 110

Gly Ala Val Ile Leu Ile Glu His Arg Tyr Trp Gly Asp Ser Ser Pro  
 115 120 125

Tyr Glu Val Leu Asn Ala Glu Thr Leu Gln Tyr Leu Thr Leu Asp Gln  
 130 135 140

Ser Ile Leu Asp Met Thr Tyr Phe Ala Glu Thr Val Lys Leu Gln Phe  
 145 150 155 160

Asp Asn Ser Ser Arg Ser Asn Ala Gln Asn Ala Pro Trp Val Met Val

	165		170		175
Gly Gly Ser Tyr Ser Gly Ala Leu Thr Ala Trp Thr Glu Ser Ile Ala	180		185		190
Pro Gly Thr Phe Trp Ala Tyr His Ala Thr Ser Ala Pro Val Glu Ala	195		200		205
Ile Tyr Asp Phe Trp Gln Tyr Phe Tyr Pro Ile Gln Gln Gly Met Ala	210		215		220
Gln Asn Cys Ser Lys Asp Val Ser Leu Val Ala Glu Tyr Val Asp Lys	225		230		240
Ile Gly Lys Asn Gly Thr Ala Lys Glu Gln Gln Glu Leu Lys Glu Leu		245		250	255
Phe Gly Leu Gly Ala Val Glu His Tyr Asp Asp Phe Ala Ala Val Leu		260		265	270
Pro Asn Gly Pro Tyr Leu Trp Gln Asp Asn Asp Phe Val Thr Gly Tyr		275		280	285
Ser Ser Phe Phe Gln Phe Cys Asp Ala Val Glu Gly Val Glu Ala Gly		290		295	300
Ala Ala Val Thr Pro Gly Pro Glu Gly Val Gly Leu Glu Lys Ala Leu	305		310		315
Ala Asn Tyr Ala Asn Trp Phe Asn Ser Thr Ile Leu Pro Asn Tyr Cys		325		330	335
Ala Ser Tyr Gly Tyr Trp Thr Asp Glu Trp Ser Val Ala Cys Phe Asp		340		345	350
Ser Tyr Asn Ala Ser Ser Pro Ile Phe Thr Asp Thr Ser Val Gly Asn		355		360	365
Pro Val Asp Arg Gln Trp Glu Trp Phe Leu Cys Asn Glu Pro Phe Phe		370		375	380
Trp Trp Gln Asp Gly Ala Pro Glu Gly Thr Ser Thr Ile Val Pro Arg	385		390		395
					400

Leu Val Ser Ala Ser Tyr Trp Gln Arg Gln Cys Pro Leu Tyr Phe Pro  
 405 410 415

Glu Val Asn Gly Tyr Thr Tyr Gly Ser Ala Lys Gly Lys Asn Ser Ala  
 420 425 430

Thr Val Asn Ser Trp Thr Gly Gly Trp Asp Met Thr Arg Asn Thr Thr  
 435 440 445

Arg Leu Ile Trp Thr Asn Gly Gln Tyr Asp Pro Trp Arg Asp Ser Gly  
 450 455 460

Val Ser Ser Thr Phe Arg Pro Gly Gly Pro Leu Val Ser Thr Ala Asn  
 465 470 475 480

Glu Pro Val Gln Ile Ile Pro Gly Gly Phe His Cys Ser Asp Leu Tyr  
 485 490 495

Met Glu Asp Tyr Tyr Ala Asn Glu Gly Val Arg Lys Val Val Asp Asn  
 500 505 510

Glu Val Lys Gln Ile Lys Glu Trp Val Glu Glu Tyr Tyr Ala  
 515 520 525

<210> 170

<211> 424

<212> PRT

<213> Aspergillus niger

<400> 170

Met Gln Leu Leu Gln Ser Leu Ile Val Ala Val Cys Phe Ser Tyr Gly  
 1 5 10 15

Val Leu Ser Leu Pro His Gly Pro Ser Asn Gln His Lys Ala Arg Ser  
 20 25 30

Phe Lys Val Glu Arg Val Arg Arg Gly Thr Gly Ala Leu His Gly Pro  
 35 40 45

Ala Ala Leu Arg Lys Ala Tyr Arg Lys Tyr Gly Ile Ala Pro Ser Ser  
 50 55 60

Phe Asn Ile Asp Leu Ala Asp Phe Lys Pro Ile Thr Thr Thr His Ala  
 65 70 75 80

Ala Ala Gly Ser Glu Ile Ala Glu Pro Asp Gln Thr Gly Ala Val Ser  
 85 90 95

Ala Thr Ser Val Glu Asn Asp Ala Glu Phe Val Ser Pro Val Leu Ile  
 100 105 110

Gly Gly Gln Lys Ile Val Met Thr Phe Asp Thr Gly Ser Ser Asp Phe  
 115 120 125

Trp Val Phe Asp Thr Asn Leu Asn Glu Thr Leu Thr Gly His Thr Glu  
 130 135 140

Tyr Asn Pro Ser Asn Ser Ser Thr Phe Lys Lys Met Asp Gly Tyr Thr  
 145 150 155 160

Phe Asp Val Ser Tyr Gly Asp Asp Ser Tyr Ala Ser Gly Pro Val Gly  
 165 170 175

Thr Asp Thr Val Asn Ile Gly Gly Ala Ile Val Lys Glu Gln Ala Phe  
 180 185 190

Gly Val Pro Asp Gln Val Ser Gln Ser Phe Ile Glu Asp Thr Asn Ser  
 195 200 205

Asn Gly Leu Val Gly Leu Gly Phe Ser Ser Ile Asn Thr Ile Lys Pro  
 210 215 220

Glu Ala Gln Asp Thr Phe Phe Ala Asn Val Ala Pro Ser Leu Asp Glu  
 225 230 235 240

Pro Val Met Thr Ala Ser Leu Lys Ala Asp Gly Val Gly Glu Tyr Glu  
 245 250 255

Phe Gly Thr Ile Asp Lys Asp Lys Tyr Gln Gly Asn Ile Ala Asn Ile  
 260 265 270

Ser Val Asp Ser Ser Asn Gly Tyr Trp Gln Phe Ser Thr Pro Lys Tyr  
 275 280 285

Ser Val Ala Asp Gly Glu Leu Lys Asp Ile Gly Ser Leu Asn Thr Ser

290                                      295                                      300  
 Ile Ala Asp Thr Gly Thr Ser Leu Met Leu Leu Asp Glu Asp Val Val  
 305                                      310                                      315                                      320  
 Thr Ala Tyr Tyr Ala Gln Val Pro Asn Ser Val Tyr Val Ser Ser Ala  
                                      325                                      330                                      335  
 Gly Gly Tyr Ile Tyr Pro Cys Asn Thr Thr Leu Pro Ser Phe Ser Leu  
                                      340                                      345                                      350  
 Val Leu Gly Glu Ser Ser Leu Ala Thr Ile Pro Gly Asn Leu Ile Asn  
                                      355                                      360                                      365  
 Phe Ser Lys Val Gly Thr Asn Thr Thr Thr Gly Gln Ala Leu Cys Phe  
                                      370                                      375                                      380  
 Gly Gly Ile Gln Ser Asn Gly Asn Thr Ser Leu Gln Ile Leu Gly Asp  
 385                                      390                                      395                                      400  
 Ile Phe Leu Lys Ala Phe Phe Val Val Phe Asp Met Arg Gly Pro Ser  
                                      405                                      410                                      415  
 Leu Gly Val Ala Ser Pro Lys Asn  
                                      420  
 <210> 171  
 <211> 548  
 <212> PRT  
 <213> Aspergillus niger  
 <400> 171  
 Met Arg Ile Asp Ser Ala Ala Leu His Leu Val Pro Val Leu Leu Gly  
 1                                      5                                      10                                      15  
 Gln Val Gly Ala Leu Gln Leu Pro Leu Val Gln Asp Ser Asn Ser Gln  
                                      20                                      25                                      30  
 Trp Gln Lys Pro Asn Ala Gly Asp Lys Pro Leu Ile Ser Ser Pro Leu  
                                      35                                      40                                      45  
 Leu Gln Glu Gln Val Lys Ala Glu Asn Leu Leu Asp Arg Ala Arg Gln  
 50                                      55                                      60

Leu Tyr Lys Ile Ala Glu Leu Gly Glu Asp Glu Tyr Asn His Pro Thr  
 65 70 75 80

Arg Val Ile Gly Ser Lys Gly His Leu Gly Thr Leu Asp Tyr Ile Tyr  
 85 90 95

Ser Thr Leu Thr Asp Leu Gly Asp Tyr Tyr Thr Val Val Asn Gln Ser  
 100 105 110

Phe Pro Ala Val Ser Gly Asn Val Phe Glu Ser Arg Leu Val Leu Gly  
 115 120 125

His Asp Val Pro Lys Ser Ala Thr Pro Met Gly Leu Thr Pro Pro Thr  
 130 135 140

Arg Asn Lys Glu Pro Val Tyr Gly Ser Leu Val Ala Val Ser Asn Leu  
 145 150 155 160

Gly Cys Glu Ala Ser Asp Tyr Ser Ser Asn Leu Lys Gly Ala Val Ala  
 165 170 175

Phe Ile Ser Arg Gly Ser Cys Pro Phe Gly Thr Lys Ser Gln Leu Ala  
 180 185 190

Gly Lys Ala Gly Ala Val Ala Ala Val Ile Tyr Asn Asn Glu Arg Gly  
 195 200 205

Asp Leu Ser Gly Thr Leu Gly Asn Pro Thr Pro Asp His Val Ala Thr  
 210 215 220

Phe Gly Ile Ser Asp Glu Asp Ala Ala Pro Val Leu Glu Lys Leu Asn  
 225 230 235 240

Lys Gly Glu Lys Val Asp Ala Ile Ala Tyr Val Asp Ala Ile Val Glu  
 245 250 255

Thr Ile His Thr Thr Asn Ile Ile Ala Gln Thr Thr Asp Gly Asp Pro  
 260 265 270

Asn Asn Cys Val Met Leu Gly Gly His Ser Asp Ser Val Ala Glu Gly  
 275 280 285

Pro Gly Ile Asn Asp Asp Gly Ser Gly Thr Leu Thr Leu Leu Glu Leu  
 290 295 300

Ala Thr Leu Leu Thr Gln Phe Arg Val Asn Asn Cys Val Arg Phe Ala  
 305 310 315 320

Trp Trp Ala Ala Glu Glu Gly Leu Leu Gly Ser Asp Tyr Tyr Val  
 325 330 335

Ser Val Leu Thr Pro Glu Glu Asn Arg Lys Ile Arg Leu Phe Met Asp  
 340 345 350

Tyr Asp Met Leu Gly Ser Pro Asn Phe Ala Tyr Gln Val Tyr Asn Ala  
 355 360 365

Thr Asn Ala Val Asn Pro Glu Gly Ser Glu Glu Leu Arg Asp Leu Tyr  
 370 375 380

Thr Asp Phe Tyr Glu Asp His Gly Phe Asn Tyr Thr Tyr Ile Pro Phe  
 385 390 395 400

Asp Gly Arg Ser Asp Tyr Asp Ala Phe Ile Arg His Gly Ile Pro Gly  
 405 410 415

Gly Gly Ile Ala Thr Gly Ala Glu Gly Ile Lys Thr Val Glu Glu Ala  
 420 425 430

Asp Met Phe Gly Gly Val Ala Gly Gln Trp Tyr Asp Pro Cys Tyr His  
 435 440 445

Gln Ile Cys Asp Thr Val Ala Asn Val Asn Leu Thr Ala Trp Glu Trp  
 450 455 460

Asn Thr Lys Leu Val Ala His Ser Ile Ala Thr Tyr Ala Lys Ser Phe  
 465 470 475 480

Asp Gly Phe Pro Glu Arg Ser Asp Glu Pro Ile Ser Pro Ala Ala Phe  
 485 490 495

Glu Glu Pro Lys Tyr His Gly His Ala Leu Gln Leu Leu Arg Gly Asn  
 500 505 510

Thr Thr Gly Thr Gln Ser Val Leu Trp Gly Ala Gln Ile Gln Asn Gly

515

520

525

Thr Ala Ala Ser Val Leu Asn Leu Leu Ser Ile Arg Arg Arg Gly Thr  
530 535 540

Phe Ser Leu Ser  
545